Figure 1A. WT–Vif Consensus sequence

```
Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1               5                  10                  15

Arg Ile Arg Thr Trp Lys Ser Leu Val Lys His His Met Tyr Val Ser
            20                  25                  30

Gly Lys Ala Arg Gly Trp Phe Tyr Arg His His Tyr Glu Ser Pro His
        35                  40                  45

Pro Arg Ile Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
    50                  55                  60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
65                  70                  75                  80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Lys Arg Tyr Ser Thr
                85                  90                  95

Gln Val Asp Pro Glu Leu Ala Asp Gln Leu Ile His Leu His Tyr Phe
            100                 105                 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Lys Ala Leu Leu Gly His Ile
        115                 120                 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
    130                 135                 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
145                 150                 155                 160

Pro Pro Leu Pro Ser Val Thr Lys Leu Thr Glu Asp Arg Trp Asn Lys
                165                 170                 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
            180                 185                 190
```

Figure 1B. Consensus sequence alignments

```
                ....|....|  ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
                     5          15         25         35         45         55
HXB2            MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG
BRU             MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG
SF2             MENRWQVMIV WQVDRMRIRT WKSLVKHHMY ISKKAKGWFY RHHYESTHPR VSSEVHIPLG
PV22            MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG
MN              MENRRQVMIV WQADRMRIRT WKSLVKHHMY ISKKAKGRFY RHHYESTHPR ISSEVHIPLG
F12Vif          MENRWQVMIV WQVDRMRIRT WISLVKHHIY ISKKAKGWFY KHHYESTNPR ISSEVHIPLG
Consensus       MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG

                ....|....|  ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
                     65         75         85         95        105        115
HXB2            DARLVITTYW GLHTGERDWH LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI
BRU             DARLVITTYW GLHTGERDWH LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI
SF2             DAKLVITTYW GLHTGEREWH LGQGVAIEWR KKKYSTQVDP GLADQLIHLH YFDCFSESAI
PV22            DARLVITTYW GLHTGERDWH LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI
MN              DARLVITTYW GLHTGERDWH LGQGVSIEWR KKRYSTQVDP DLADHLIHLH YFDCFSDSAI
F12Vif          DARLVVTTYW GLHTGERDWN LGQGVSIEWR KKRYSTQVDP GLADQLIHRY YFDCFSESAI
Consensus       DARLVITTYW GLHTGERDWH LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI

                ....|....|  ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
                    125        135        145        155        165        175
HXB2            RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK PPLPSVTKLT EDRWNKPQKT
BRU             RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK PPLPSVTKLT EDRWNKPQKT
SF2             KNAILGYRVS PRCEYQAGHN KVGSLQYLAL AALITPKKTK PPLPSVKKLT EDRWNKPQKT
PV22            RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK PPLPSVTKLT EDRWNKPQKT
MN              RKAILGHRVS PICEFQAGHN KVGPLQYLAL TALITPKKIK PPLPSVKKLT EDRWNKPQKT
F12Vif          RNAILGNVVR LSCEYQAGHN KIGSLQYLAL AALITPKKIK PPLPSVTKLT EDRWNKPQKT
Consensus       RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK PPLPSVTKLT EDRWNKPQKT

                ....|....|  ..
                    185
HXB2            KGHRGSHTMN GH
BRU             KGHRGSHTMN GH
SF2             KGHRGSHTMN GH
PV22            KGHRGSHTMN GH
MN              KGHRGSHTIN GH
F12Vif          KGHRRNHTMN GH
Consensus       KGHRGSHTMN GH
```

Figure 1C. NL4-3 Vif sequence

```
MENRWQVMIVWQVDRMRINTWKRLVKHHMYISRKAKDWFYRHHYESTNPKISSEVHIPLGDAKLVITTYWGLHTGERDWH
LGQGVSIEWRKKRYSTQVDPDLADQLIHLHYFDCFSESAIRNTILGRIVSPRCEYQAGHNKVGSLQYLALAALIKPKQIK
PPLPSVRKLTEDRWNKPQKTKGHRGSHTMNGH
```

Figure 2. F12-Vif

Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1 5 10 15

Arg Ile Arg Thr Trp **Ile** Ser Leu Val Lys His His **Ile** Tyr Ile Ser
20 25 30

Lys Lys Ala Lys Gly Trp Phe Tyr **Lys** His His Tyr Glu Ser Thr **Asn**
35 40 45

Pro Arg Ile Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
50 55 60

Val **Val** Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp **Asn**
65 70 75 80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Lys Arg Tyr Ser Thr
85 90 95

Gln Val Asp Pro Gly Leu Ala Asp Gln Leu Ile His **Arg** Tyr Tyr Phe
100 105 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Asn Ala Ile Leu Gly **Asn** **Val**
115 120 125

Val **Arg** **Leu** **Ser** Cys Glu Tyr Gln Ala Gly His Asn Lys **Ile** Gly Ser
130 135 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
145 150 155 160

Pro Pro Leu Pro Ser Val Thr Lys Leu Thr Glu Asp Arg Trp Asn Lys
165 170 175

Pro Gln Lys Thr Lys Gly His Arg **Arg** **Asn** His Thr Met Asn Gly His
180 185 190

Figure 3A. Chim1

```
Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1               5                  10                  15

Arg Ile Arg Thr Trp Ile Ser Leu Val Lys His His Ile Tyr Ile Ser
            20                  25                  30

Lys Lys Ala Lys Gly Trp Phe Tyr Lys His His Tyr Glu Ser Thr Asn
        35                  40                  45

Pro Arg Ile Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Arg Leu
    50                  55                  60

Val Val Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp Asn
65                  70                  75                  80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Lys Arg Tyr Ser Thr
                85                  90                  95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu His Tyr Phe
            100                 105                 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Asn Thr Ile Leu Gly Arg Ile
        115                 120                 125

Val Ser Pro Arg Cys Glu Tyr Gln Ala Gly His Asn Lys Val Gly Ser
    130                 135                 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Lys Pro Lys Gln Ile Lys
145                 150                 155                 160

Pro Pro Leu Pro Ser Val Arg Lys Leu Thr Glu Asp Arg Trp Asn Lys
                165                 170                 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
            180                 185                 190
```

Figure 3B. Chim1

MENRWQVMIVWQVDRMRIRTWISLVKHHIYISKKAKGWFYKHHYESTNPRISSEVHIPLGDAR
*LVVTTYWGLHTGERDWNLGQGVSI*EWRKKRYSTQVDPDLADQLIHLHYFDCFSESAIRNTI
LGRIVSPRCEYQAGHNKVGSLQYLALAALIKPKQIKPPLPSVRKLTEDRWNKPQKTKGHR
GSHTMNGH

Figure 4A. Chim2

```
Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1               5                  10                  15

Arg Ile Asn Thr Trp Lys Arg Leu Val Lys His His Met Tyr Ile Ser
            20                  25                  30

Arg Lys Ala Lys Asp Trp Phe Tyr Arg His His Tyr Glu Ser Thr Asn
        35                  40                  45

Pro Lys Ile Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Lys Leu
    50                  55                  60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
65                  70                  75                  80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Lys Arg Tyr Ser Thr
                85                  90                  95

Gln Val Asp Pro Gly Leu Ala Asp Gln Leu Ile His Arg Tyr Tyr Phe
            100                 105                 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Asn Ala Ile Leu Gly Asn Val
        115                 120                 125

Val Arg Leu Ser Cys Glu Tyr Gln Ala Gly His Asn Lys Ile Gly Ser
    130                 135                 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
145                 150                 155                 160

Pro Pro Leu Pro Ser Val Thr Lys Leu Thr Glu Asp Arg Trp Asn Lys
                165                 170                 175

Pro Gln Lys Thr Lys Gly His Arg Arg Asn His Thr Met Asn Gly His
            180                 185                 190
```

Figure 4B. Chim2

MENRWQVMIVWQVDRMRINTWKRLVKHHMYISRKAKDWFYRHHYESTNPKISSEVHIP
LGDAKLVITTYWGLHTGERDWHLGQGVSIE*WRKKRYSTQVDPGLADQLIHRYYFDCFSESAI*
RNAILGNVVRLSCEYQAGHNKIGSLQYLALAALITPKKIKPPLPSVTKLTEDRWNKPQKTKGHRR
NHTMNGH

Figure 5A. Chim3

```
Met Glu Asn Arg Trp Gln Val Met Ile Val Trp Gln Val Asp Arg Met
1               5                  10                  15

Arg Ile Asn Thr Trp Lys Arg Leu Val Lys His His Met Tyr Ile Ser
            20                  25                  30

Arg Lys Ala Lys Asp Trp Phe Tyr Arg His His Tyr Glu Ser Thr Asn
        35                  40                  45

Pro Lys Ile Ser Ser Glu Val His Ile Pro Leu Gly Asp Ala Lys Leu
    50                  55                  60

Val Ile Thr Thr Tyr Trp Gly Leu His Thr Gly Glu Arg Asp Trp His
65                  70                  75                  80

Leu Gly Gln Gly Val Ser Ile Glu Trp Arg Lys Lys Arg Tyr Ser Thr
                85                  90                  95

Gln Val Asp Pro Asp Leu Ala Asp Gln Leu Ile His Leu His Tyr Phe
            100                 105                 110

Asp Cys Phe Ser Glu Ser Ala Ile Arg Asn Thr Ile Leu Gly Asn Val
        115                 120                 125

Val Arg Leu Ser Cys Glu Tyr Gln Ala Gly His Asn Lys Ile Gly Ser
    130                 135                 140

Leu Gln Tyr Leu Ala Leu Ala Ala Leu Ile Thr Pro Lys Lys Ile Lys
145                 150                 155                 160

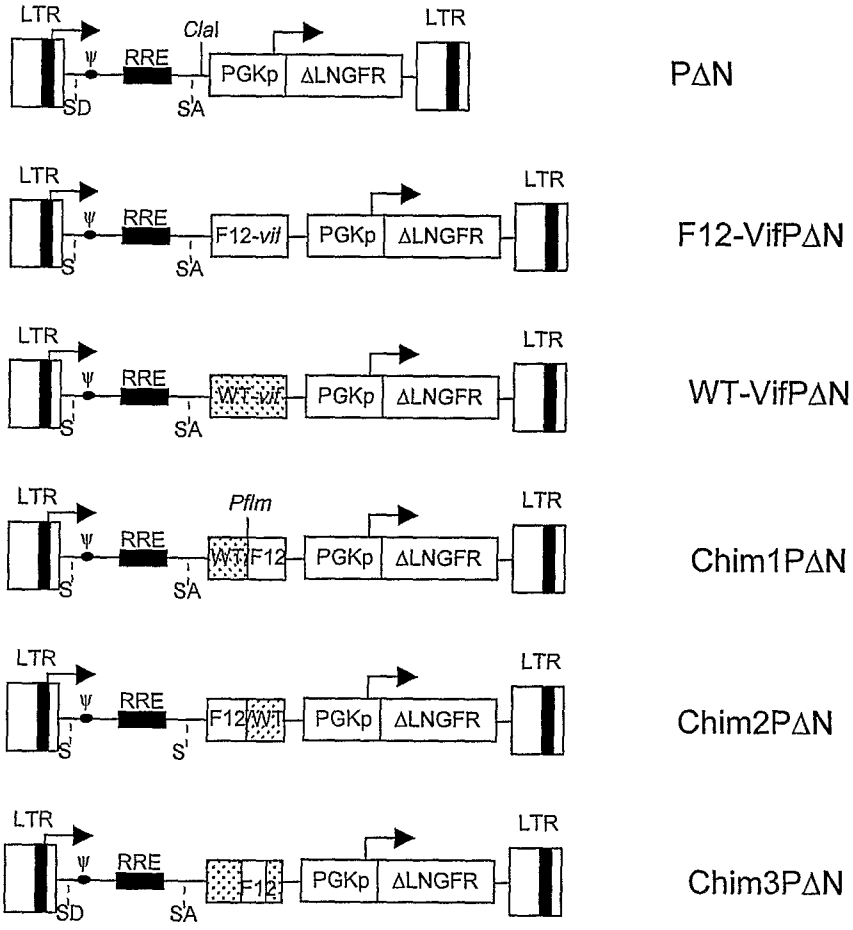
Pro Pro Leu Pro Ser Val Thr Lys Leu Thr Glu Asp Arg Trp Asn Lys
                165                 170                 175

Pro Gln Lys Thr Lys Gly His Arg Gly Ser His Thr Met Asn Gly His
            180                 185                 190
```

Figure 5B. Chim3

MENRWQVMIVWQVDRMRINTWKRLVKHHMYISRKAKDWFYRHHYESTNPKISSEVHI
PLGDAKLVITTYWGLHTGERDWHLGQGVSIEWRKKRYSTQVDPDLADQLIHLHYFDCF
SESAIRNTIL*GNVV**RLS**CEYQAGHNKIGSLQYLALAALITPKKIKPPLPSVTKLT*EDRWNKPQK
TKGHRGSHTMNGH

Figure 6. Schematic representation of the PΔN, WT-VifPΔN, F12-VifPΔN, Chim1PΔN, Chim2PΔN, and Chim3PΔN lentiviral vectors in their proviral forms.



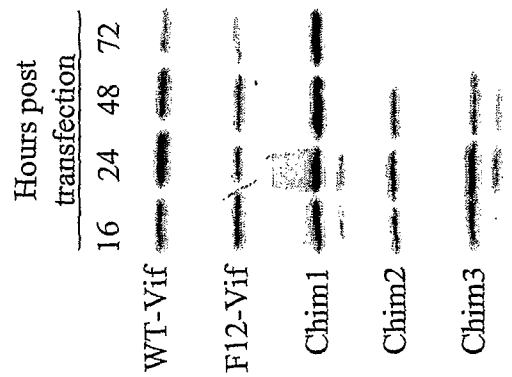

Hours post transfection
16 24 48 72
WT-Vif
F12-Vif
Chim1
Chim2
Chim3

Figure 7

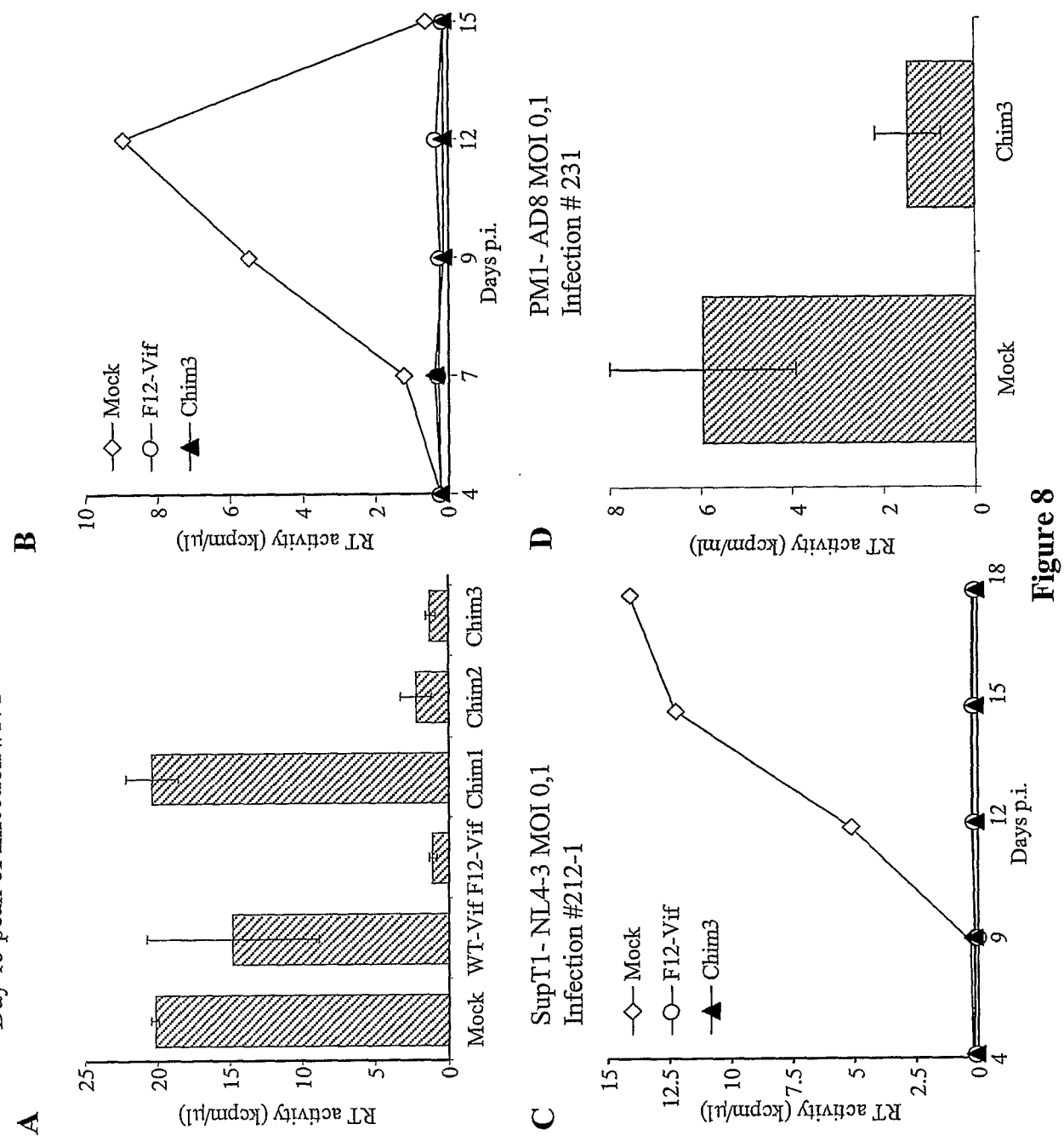

A
CEM A3.01- NL4-3 MOI 0,1
Day 15 peak of Infection #171
RT activity (kcpm/µl)
Mock
WT-Vif
F12-Vif
Chim1
Chim2
Chim3
B
CEMss- NL4-3 MOI 0,1
Infection #213-3
RT activity (kcpm/µl)
Mock
F12-Vif
Chim3
Days p.i.
C
SupT1- NL4-3 MOI 0,1
Infection #212-1
RT activity (kcpm/µl)
Mock
F12-Vif
Chim3
Days p.i.
D
PM1- AD8 MOI 0,1
Infection # 231
RT activity (kcpm/ml)
Mock
Chim3

Figure 8

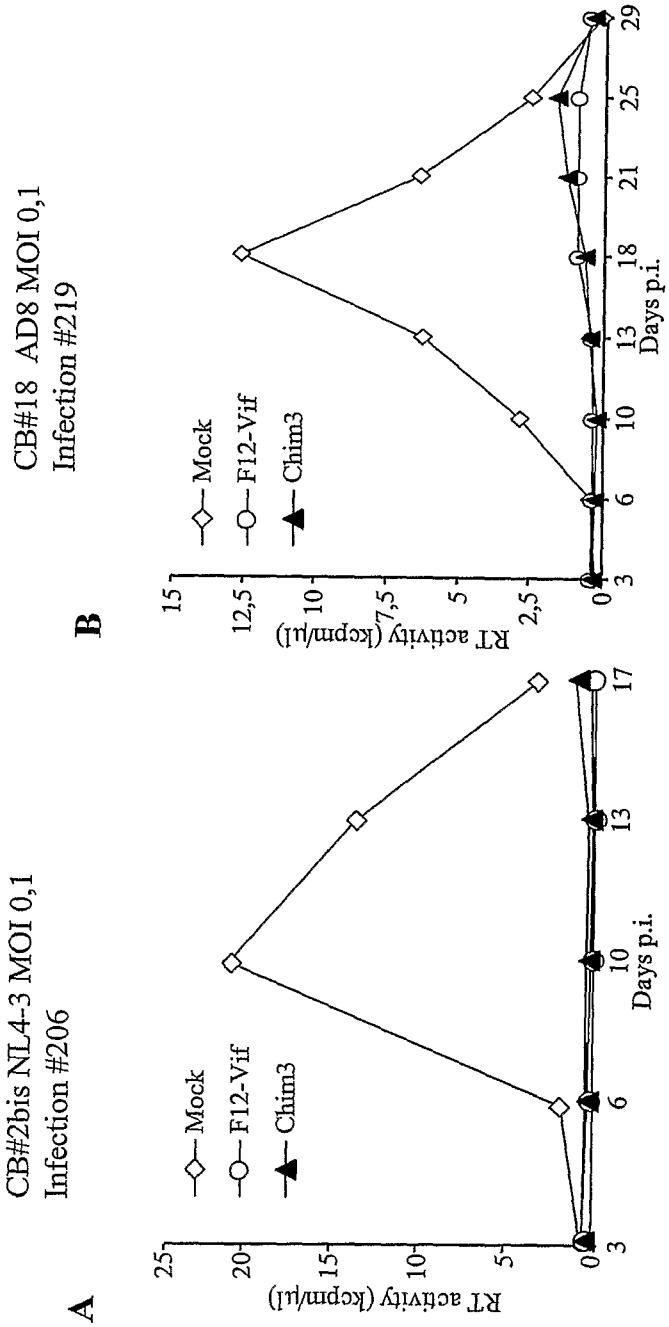

A
CB#2bis NL4-3 MOI 0,1
Infection #206
RT activity (kcpm/µl)
Days p.i.
Mock
F12-Vif
Chim3
B
CB#18 AD8 MOI 0,1
Infection #219
RT activity (kcpm/µl)
Days p.i.
Mock
F12-Vif
Chim3

Figure 9

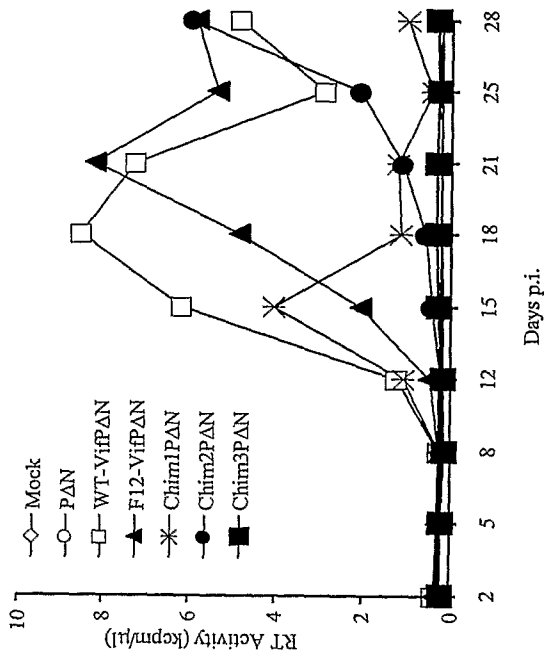

CEM A3.01 NL4-3Δ-vifX4 MOI 0,1
Infection #179
Mock
PΔN
WT-VifPΔN
F12-VifPΔN
Chim1PΔN
Chim2PΔN
Chim3PΔN
RT Activity (kcpm/µl)
Days p.i.
0
2
4
6
8
10
2
5
8
12
15
18
21
25
28

Figure 10

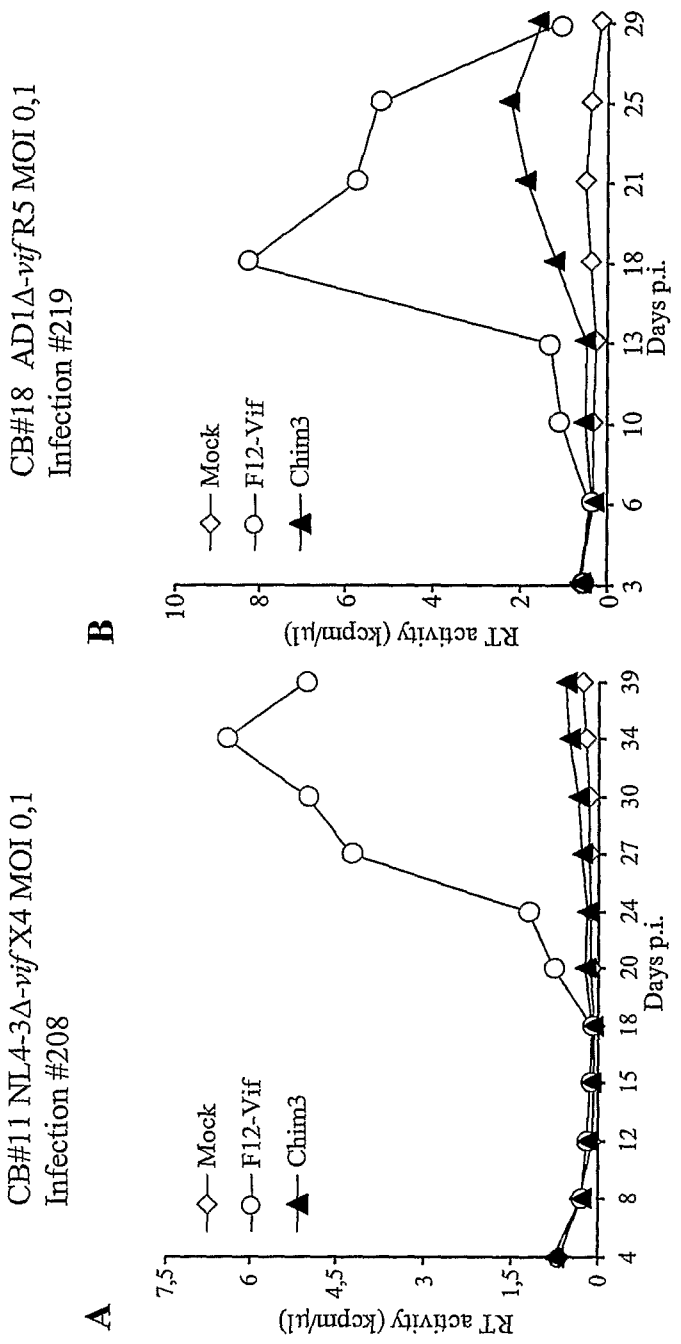

A
CB#11 NL4-3Δ-vif X4 MOI 0,1
Infection #208
RT activity (kcpm/µl)
Days p.i.
Mock
F12-Vif
Chim3
B
CB#18 AD1Δ-vif R5 MOI 0,1
Infection #219
RT activity (kcpm/µl)
Days p.i.
Mock
F12-Vif
Chim3

Figure 11

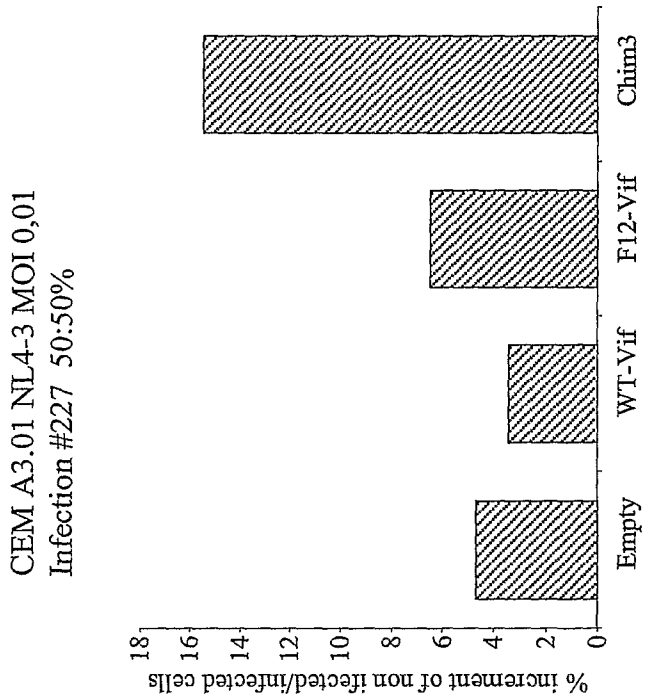

CEM A3.01 NL4-3 MOI 0,01
Infection #227 50:50%
% increment of non ifected/infected cells
0
2
4
6
8
10
12
14
16
18
Empty
WT-Vif
F12-Vif
Chim3

Figure 12

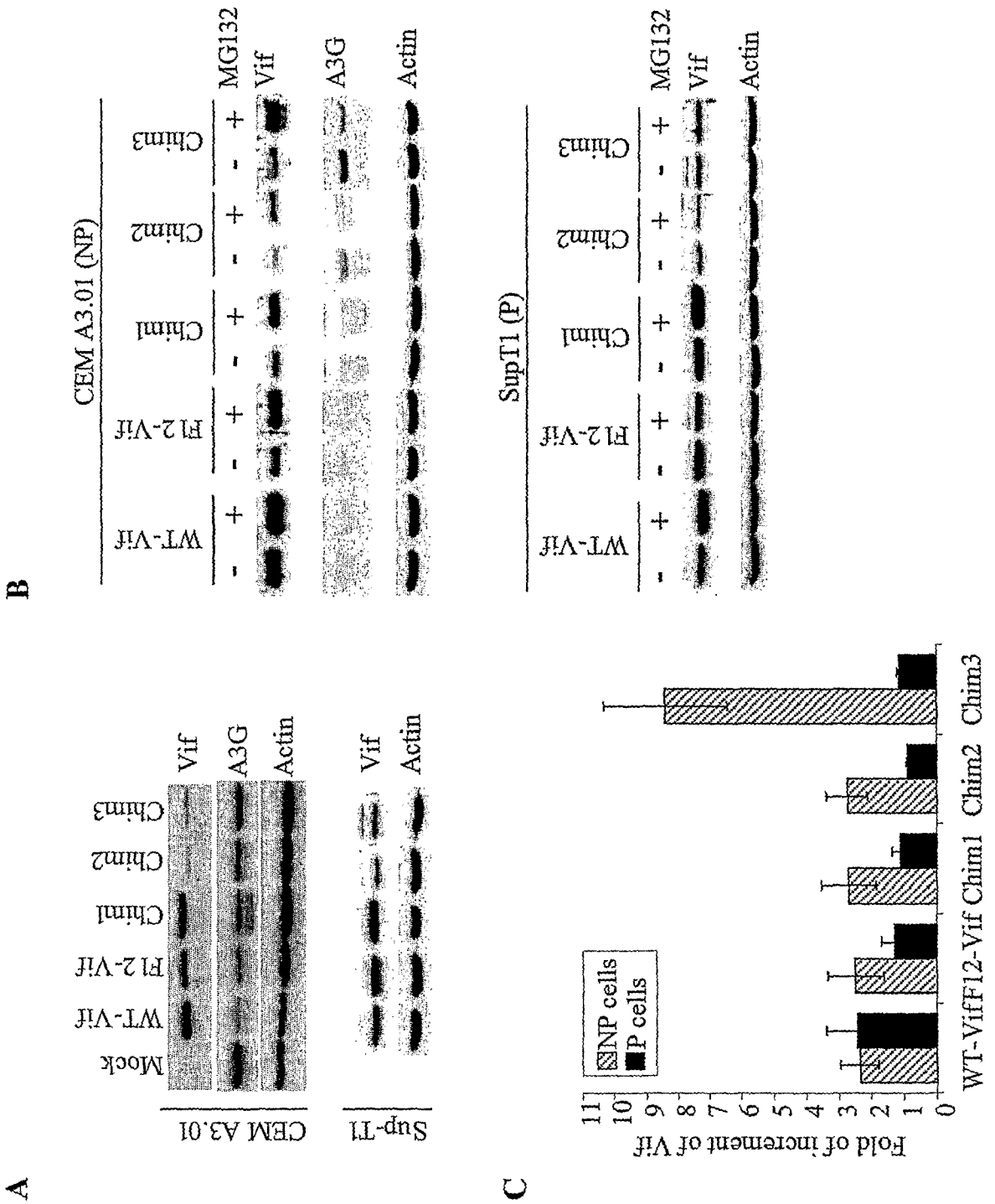

A
Mock
WT-Vif
F1 2-Vif
Chim1
Chim2
Chim3
Vif
A3G
Actin
CEM A3.01
Sup-T1
Vif
Actin
B
CEM A3.01 (NP)
WT-Vif
F1 2-Vif
Chim1
Chim2
Chim3
MG132
Vif
A3G
Actin
SupT1 (P)
WT-Vif
F1 2-Vif
Chim1
Chim2
Chim3
MG132
Vif
Actin
C
Fold of increment of Vif
NP cells
P cells
WT-Vif
F12-Vif
Chim1
Chim2
Chim3

Figure 13

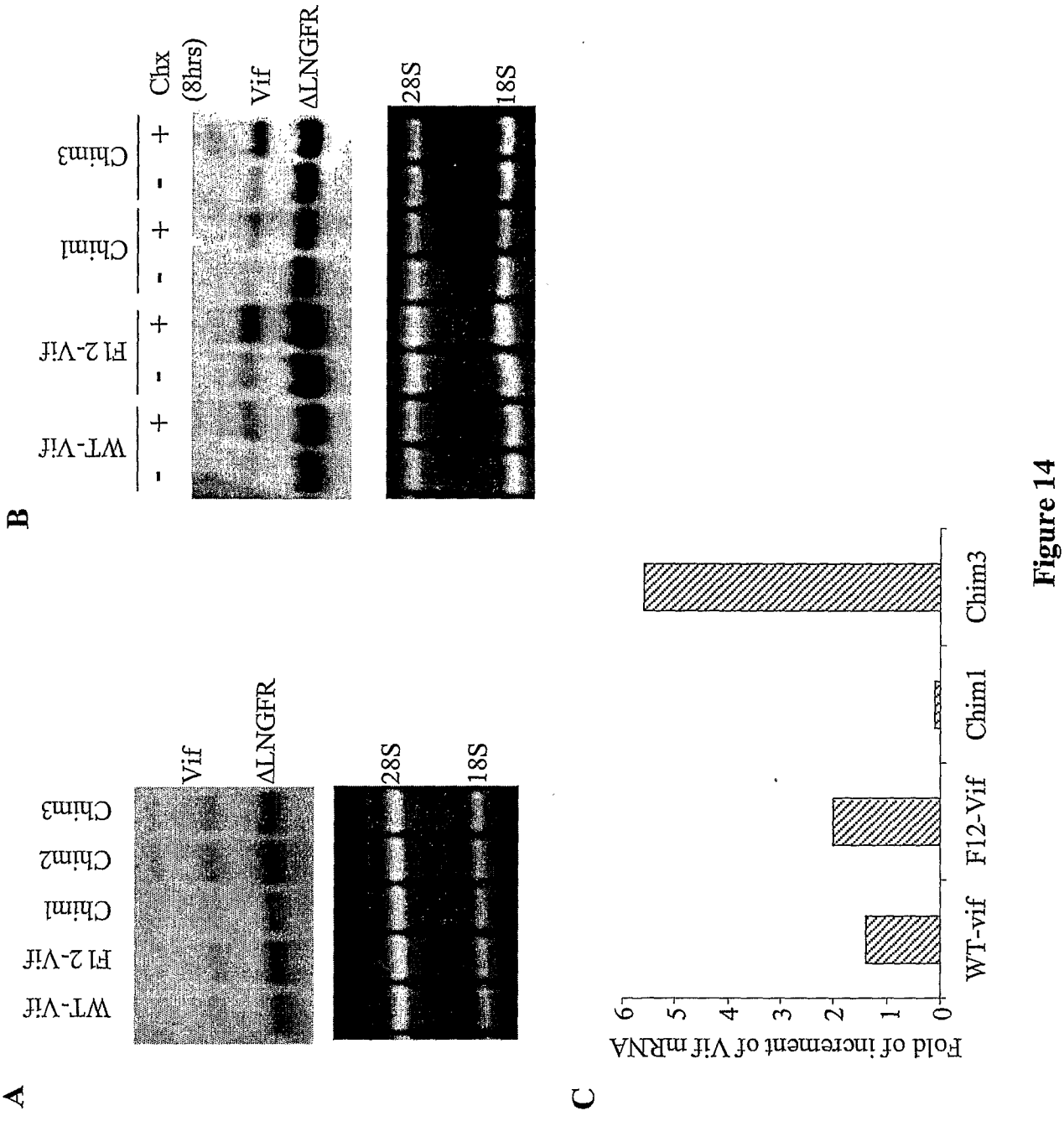

A
WT-Vif
F12-Vif
Chim1
Chim2
Chim3
Vif
ΔLNGFR
28S
18S
B
WT-Vif
F12-Vif
Chim1
Chim3
Chx (8hrs)
Vif
ΔLNGFR
28S
18S
C
Fold of increment of Vif mRNA
0
1
2
3
4
5
6
WT-vif
F12-Vif
Chim1
Chim3

Figure 14

CHIM3

ATCGATGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGA
TGAGGATTAACACATGGAAAAGATTAGTAAAACACCATATGTATATTTCAAGGAAAGC
TAAGGACTGGTTTTATAGACATCACTATGAAAGTACTAATCCAAAAATAAGTTCAGAA
GTACACATCCCACTAGGGGATGCTAAATTAGTAATAACAACATATTGGGGTCTGCATA
CAGGAGAAAGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAAGA
GATATAGCACACAAGTAGACCCTGACCTAGCAGACCAACTAATTCATCTGCACTATTTT
GATTGTTTTTCAGAATCTGCTATAAGAAATACCATATTAGGAAATGTAGTTAGACTTAG
TTGTGAATATCAAGCAGGACATAACAAGATAGGATCTCTACAATACTTGGCACTAGCA
GCATTAATAACACCAAAAAAGATAAAGCCACCTTTGCCTAGTGTTACGAAACTGACAG
AGGACAGATGGAACAAGCCCCAGAAGACCAAGGGCCACAGAGGGAGCCATACAATGA
ATGGACACTAGCATCGAT

FIGURE 15

Chim2

TATCGATGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAACACATGGAAAA
GATTAGTAAAACACCATATGTATATTTCAAGGAAAGCTAAGGACTGGTTTTATAGACATCACTATGAAAGTACTAATCCA
AAAATAAGTTCAGAAGTACACATCCCACTAGGGGATGCTAAATTAGTAATAACAACATATTGGGGTCTGCATACAGGAGA
AAGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAatggaggaaaaagagatatagcacacaagtagaccctggcctag
cagaccaactaattcatcggtattattttgattgtttttcagaatctgctataagaaatgccatactaggaaatgtagtt
agacttagttgtgaatatcaagcaggacataacaagataggatctctacaatacttggcactagcagcattaataacacc
aaaaaagataaagccacctttgcctagtgttacgaaactgacagaggatagatggaacaagccccagaagaccaagggcc
acagaaggaaccatacaatgaatggacactagatcgatA

ATCGATGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAACACATGGAAAAG
ATTAGTAAAACACCATATGTATATTTCAAGGAAAGCTAAGGACTGGTTTTATAGACATCACTATGAAAGTACTAATCCAA
AAATAAGTTCAGAAGTACACATCCCACTAGGGGATGCTAAATTAGTAATAACAACATATTGGGGTCTGCATACAGGAGAA
AGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAAGAGATATAGCACACAAGTAGACCCTGGCCTAGC
AGACCAACTAATTCATCGGTATTATTTTGATTGTTTTTCAGAATCTGCTATAAGAAATGCCATACTAGGAAATGTAGTTA
GACTTAGTTGTGAATATCAAGCAGGACATAACAAGATAGGATCTCTACAATACTTGGCACTAGCAGCATTAATAACACCA
AAAAAGATAAAGCCACCTTTGCCTAGTGTTACGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCA
CAGAAGGAACCATACAATGAATGGACACTAGATCGATA

Figure 16

ATCGATGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGG
ATGAGGATTAACACATGGAAAAGATTAGTAAAACACCATATGTATATTTCAAGGAAAG
CTAAGGACTGGTTTTATAGACATCACTATGAAAGTACTAATCCAAAAATAAGTTCAGAA
GTACACATCCCACTAGGGGATGCTAAATTAGTAATAACAACATATTGGGGTCTGCATA
CAGGAGAAAGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAAGA
GATATAGCACACAAGTAGACCCTGACCTAGCAGACCAACTAATTCATCTGCACTATTT
TGATTGTTTTTCAGAATCTGCTATAAGAAATACCATATTAGGACGTATAGTTAGTCCTA
GGTGTGAATATCAAGCAGGACATAACAAGGTAGGATCTCTACAGTACTTGGCACTAG
CAGCATTAATAAAACCAAAACAGATAAAGCCACCTTTGCCTAGTGTTAGGAAACTGAC
AGAGGACAGATGGAACAAGCCCCAGAAGACCAAGGGCCACAGAGGGAGCCATACAA
TGAATGGACACTAGCATCGAT

Figure 17 – NL4-3

ATCGATGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGAT
GAGGATTAGAACATGGATAAGTTTAGTAAAACACCATATATATATTTCAAAGAAAGCTAAG
GGATGGTTTTATAAACATCACTATGAAAGCACTAATCCAAGAATAAGTTCAGAAGTACACA
TCCCACTAGGGGATGCTAGATTGGTAGTAACAACATATTGGGGTCTGCATACAGGAGAA
AGAGACTGGAATTTAGGCCAGGGAGTCTCCATAGAATGGAGGAAAAAGAGATATAGCAC
ACAAGTAGACCCTGGCCTAGCAGACCAACTAATTCATCGGTATTATTTTGATTGTTTTTCA
GAATCTGCTATAAGAAATGCCATACTAGGAAATGTAGTTAGACTTAGTTGTGAATATCAAG
CAGGACATAACAAGATAGGATCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAA
AAAAGATAAAGCCACCTTTGCCTAGTGTTACGAAACTGACAGAGGATAGATGGAACAAG
CCCCAGAAGACCAAGGGCCACAGAAGGAACCATACAATGAATGGACACTAG

Figure 18 F12-Vif