Sequences in the *Vif* Alignment

COMMON NAME	LOCUS	ACC #	FIRST AUTHOR	REFERENCE
SUBTYPE A:				
U455	HIVU455	M62320	Oram,J.D.	ARHR 6, 1073 (1990)
IBNG	HIVIBNG	L39106	Howard,R.M.	ARHR 10: 1755 (1994)
IFA86	HIVIFA86	Z30637	Wieland,U.	Virol. 203, 43 (1994)
SUBTYPE B:				
SF2	HIVSF2	K02007	Sanchez-Pescador,R.	Science 227, 484 (1985)
LAI	HIVLAI	K02013	Wain-Hobson,S.	Cell 40, 9 (1985)
HXB2R	HIVHXB2R	K03455	Starcich,B.	Science 227, 538 (1985)
LW123	HIVLW123	U12055	Reitz,M.	ARHR 10, 1143 (1994)
NL43	HIVNL43	M19921	Buckler,C.E.	JVI 59: 284 (1986)
NY5CG	HIVNY5CG	M38431	Theodore,T.	PNAS 83: 5038 (1986)
MN	HIVMN	M17449	Gurgo,C.	Virol. 164, 531 (1988)
JRCSF	HIVJRCSF	M38429	Koyanagi,S.	Science 236: 819 (1987)
JRFL	HIVJRFL	M74978	O'Brien,W.A.	Nature 348, 69 (1990)
NH52	HIVNH52	L07424	Weidt,G.	Unpublished (1992)
OYI	HIVOYI	M26727	Wain-Hobson,S.	AIDS 3: 707 (1989)
CAM1	HIVCAM1	D10112	McIntosh,A.	Unpublished (1991)
HAN	HIVHAN	U43141	Sauermann,U.	ARHR 6, 813 (1990)
D31	HIVD31	U43096	Dietrich,U.	Unpublished (1992)
RF	HIVRF	M17451	Starcich,B.R.	Cell 45, 637 (1986)
YU2	HIVYU2	M93258	Li,Y.	JVI 65, 3973 (1991)
BCSG3C	HIVBCSG3C	L02317	Ghosh,S.K.	Virol. 194, 858 (1993)
IFA70	HIVIFA70	Z30632	Wieland,U.	Virol. 203, 43 (1994)
IFA19	HIVIFA19	Z30686	Wieland,U.	Virol. 203, 43 (1994)
IFA65	HIVIFA65	Z30630	Wieland,U.	Virol. 203, 43 (1994)
P896	HIVP896	M96155	Collman,R.	JVI 66, 7517 (1992)
YU10	HIVYU10	M93259	Li,Y.	JVI 65, 3973 (1991)
IFA10	HIVIFA10	Z30679	Wieland,U.	Virol. 203, 43 (1994)
3202A12	HIV3202A12	U34603	Guillon,C.	ARHR 11, 1537 (1995)
3202A21	HIV3202A21	U34604	Guillon,C.	ARHR 11, 1537 (1995)
MANC	HIVMANC	U23487	Zhu,T.	Nature 3745, 503 (1995)
WEAU160	HIVWEAU160	U21135	Ghosh,S.	Unpublished (1995)
SUBTYPE D:				
ELI	HIVELI	K03454	Alizon,M.	Cell 46, 63 (1986)
Z2Z6	HIVZ2Z6	M22639	Theodore,T.	Unpublished (1988)
Z6	HIVZ6	K03458	Srinivasan,A.	Gene 52, 71 (1987)
NDK	HIVNDK	M27323	Spire,B.	Gene 81, 275 (1989)
SUBTYPE O:				
MVP5180	HIVMVP5180	L20571	Gurtler,L.G.	JVI 68, 1581 (1994)
ANT70C	HIVANT70C	L20587	Vanden Haesevelde,M.	JVI 68, 1586 (1994)
HYBRIDS:				
AD_MAL	HIVMAL	K03456	Alizon,M.	Cell 46, 63 (1986)
CPZ:				
CPZGAB	SIVCPZGAB	X52154	Huet,T.	Nature 345, 356 (1990)
CPZANT	SIVCPZANT	U42720	Vanden Haesevelde,M.	Virol. In Press (1996)

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Subtypes C, and E-H are not currently represented in VIF. The sequence MAL has been identified as a likely hybrid in this region. It is presented with respect to a duplicate of the subtype A consensus.

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                                                                <- pol cds
CONSENSUS-A   ATGGAAAACAGATGGCAGGTGATGATTGTgTGGCAGGTAGACAGGATGAgGATTAGAACATGGAAcAGTT     70
U455          ----------------------------A-------------------A--------------------     70
IBNG          ------------------------------------------------------------------T----     70
IFA86         ----------------------------------------------------------------------     70

CONSENSUS-B   ATGGAAAaCAGAtGGcagGTGATGaTTGTGTGGCAaGtAGACAGGATGAGGATTAgaaCATGGAaaAGtt     70
SF2           ----------------------------------------------------------------------     70
LAI           ----------------------------------------------------------------------     70
HXB2R         ----------------------------------------------------------------------     70
LW123         ----------------------------------------------------------------------     70
NL43          -------------------------------------------------------AC-----------A-     70
NY5CG         -------------------------------------------------------AC-----------A-     70
MN            ------------C------------------------C--------------------------------     70
JRCSF         ----------------------------------------------------------------------C----     70
JRFL          ----------------------------------------------------------------------     70
NH52          ------------------------G--------------------------------G------------     70
OYI           ----------------------------------------------------------------------     70
CAM1          ----------------------------------------------------------------------C     70
HAN           ---------------GCA-----------------------------------------------------C----     70
D31           -----------------------------------G-----------------------------G--C-     70
RF            ----------------------------------------------------------------------     70
YU2           -----------------------------------G---------------------G------------     70
BCSG3C        ----------------------------------------------------------------------T-----     70
IFA70         ----------------------------------------------------------------------     70
IFA19         ----------------------------------------------------------------------     70
IFA65         ----------------------------------------------------------------------C----     70
P896          ----------------------------------------------------------------------     70
YU10          -----------------------------------G---------------------G------------     70
IFA10         ---------------------------------------------------------G------------     70
3202A12       ---------------------------------------------------------G------------     70
3202A21       ---------------------------------------------------------G------------     70
MANC          -------G---------------------------G--------------------------------C-     70
WEAU160       ----------------------------------------------------------------------     70

CONSENSUS-D   ATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTA?aACATGGAAAAGTT     69
ELI           -------------------------------------------------------A--------------     70
Z2Z6          -------------------------------------------------------G--------------     70
Z6            -------------------------------------------------------G--------------     70
NDK           -------------------------------------------------------AC-------------     70

CONSENSUS-O   ATGGAAAACAGATGGCAGGTACTGATAGTATGGCAA?T?GACAGACAGAAAGTGAAAGC?TGGAACAGCC     67
MVP5180       -------------------------------------A-A--------------------A----------     70
ANT70         -------------------------------------G-G--------------------G----------     70

CONSENSUS-A   ATGGAAAACAGATGGCAGGTGATGATTGTgTGGCAGGTAGACAGGATGAgGATTAGAACATGGAAcAGTT     70
AD_MAL        ----------------------------------------G------------------------C------     70

CONSENSUS-CPZ ATG?????????????????GT?AT???TGTGTGGCAAGTAGACAG?ATGAGGATTAA?A??TGGAA????T     43
CPZGAB        ---GAAAACAGATGGCAG--G--GAT------------------A-----------G-CT-----TAGT-     70
CPZANT        ---ACTGCATCGGTCGGC--C--CGC------------------G-----------T-TC-----ATCC-     70
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CONSENSUS-A   TAGTAAAACATCAtATGTATGTCTC?AAGAAAGCTaAgGGTTGGTTTTATAGACATCACTtTGAAaGTAG    139
U455          -------------C-----------C---------C-A----------------------A---------    140
IBNG          -------------------------A-----------------------------------------    140
IFA86         -------------------------T--------------------------------------T----    140

CONSENSUS-B   TAGTaAAACACCATATgTATattTCAggGAAAGCtaagggatGGtttATAgACAtCACTAtGAAAGcac    140
SF2           --------------------------AA---------A-----------------------------T--    140
LAI           --------------------G---------------G-------------------------------C-    140
HXB2R         --------------------G---------------G-------------------------------C-    140
LW123         --------------------G---------------G-------------------------------C-    140
NL43          --------------------------A------------AC--------------------------T--    140
NY5CG         --------------------------A------------AC--------------------------T--    140
MN            --------------------------AA---------A---C----------------------------    140
JRCSF         ------------------------------------------A------A------------------    140
JRFL          ---------------------C----------------------A------------------------    140
NH52          --------------------------C------------------------------------------    140
OYI           --------------------G-----AA------------------------------------------    140
CAM1          ----G-----------------------------------AA-----C---------C--------------    140
HAN           ----------------A---TG----C-----------AAC---G------------------------    140
D31           --------------------G--------------G--AA-----------A------------------    140
RF            --------------------------A-------------------------------------------    140
YU2           -----------------------------------G-----------------------------TC-    140
BCSG3C        --------------------------A-------A-----------------------------------    140
IFA70         --------------------G---------------G-------------------------------C-    140
IFA19         ----T--------------------------------A--------------------------------    140
IFA65         --------------------------AA------C---A-----G-C---------------------T    140
P896          ---------------------------------------------C------------------------    140
YU10          -----------------------------------G-----------------------------TC-    140
IFA10         ---------------------------------------A--G------C---------------------A    140
3202A12       ---------------------AG---AA-------G--A----------------------------T--    140
3202A21       ---------------------AG---AA-------G--A----------------------------T--    140
MANC          ---------------------------------------A------C-----A------------------    140
WEAU160       --------------------------AA-----------------C---------------C--------    140

CONSENSUS-D   TAGTAAAAcACCATATGTATGTTTCAAAGAAAGCTA?CAGATGGTTTTATAGACATCACTATGAcAGCCc    138
ELI           -----------------------------------A----------------------------A-----    140
Z2Z6          -----------------------------------G---------------------------------    140
Z6            -----------------------------------G---------------------------------    140
NDK           --------T---------------------------A--------------------------------A    140

CONSENSUS-O   T?GTGAAATACCATAA?TACA?GTCTA??AAG?CCG?GAACTGG?G?TA?AG?CATCATTATGAATCCAG    126
MVP5180       -G--------------A----T-----AG---G---C-------C-T--T--G-----------------    140
ANT70         -A--------------G----G-----GA---A---A-------T-G--C--A-----------------    140

CONSENSUS-A   TAGTAAAACATCAtATGTATGTCTC?AAGAAAGCTaAgGGTTGGTTTTATAGACATCACTtTGAAaGTAG    139
AD_MAL        -------------------------A-----------AAA--------------------A------C--    140

CONSENSUS-CPZ TAGT?AAA?A?CA?AT?T????G?C?AAA??????A?A???TGG???TA?AGACATCATTATGA??A???     83
CPZGAB        ----T---T-T--T--T-ATAG-T-A---AAGGCA-G-GGT---TTT--C--------------TC-CCC    140
CPZANT        ----G---C-C--C--A-GGGA-A-T---GTACTT-A-CCA---AAG--T--------------AA-TGA    140
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CONSENSUS-A   gCATcCAAaAGtAaGTTCAGAAGTACACATCCCACTAGGGGAt......GCTAGaTTAGTAGTAAGAACA    203
U455          A---T---G--------------------------------A......----------------------    204
IBNG          -------------T------------------------------.......-----G---------------    204
IFA86         -----------C------------------------------......----------------------    204

CONSENSUS-B   TcAtCCaAgaatAAGTTCAGAaGTACAcATCCCactAGGGGAt......GctAgatTgGTAaTAAcAACA    204
SF2           ----------G----------------------C---------......----A----------------    204
LAI           ------------------------------------------......----------------------    204
HXB2R         ------------------------------------------......----------------------    204
LW123         ------------------------------------------......----------------------    204
NL43          -A------A----------------------------------......----A---A------------    204
NY5CG         -A------A----------------------------------......----A---A------------    204
MN            ------------------------------------------......----------------------    204
JRCSF         -A--------G----------------A---------------......----------------------    204
JRFL          ------------------------------------------......----------------------    204
NH52          ------G-------------------------------------.......--G-A----------------    204
OYI           ------------------------------------------.......----CC------G--------    204
CAM1          ----------------------------------------G.....--------A---G--------    204
HAN           -A--------G------------------------------A.....----A----------------    204
D31           -A----------------------------------------......----------------------    204
RF            ---------------------G-------------C-------.......-AA--G---------------    204
YU2           ------------------------------------------.....----A----------------    204
BCSG3C        ---C----A----------------------------------.....----------------------    204
IFA70         ------------------------------------------.....----------------------    204
IFA19         -A---------C-----------------------------A.....----A----------------    204
IFA65         ---------G-A-----------------------------.....----A----------------    204
P896          -A----------------------------------------.....----A-------G--------    204
YU10          ------------------------------------------.....----A----------------    204
IFA10         ------------------------------------------.....------------G--------    204
3202A12       ----------------------------------G-------G.....------C--------------    204
3202A21       ----------------------------------G-------G.....------C--------------    204
MANC          -A--------G-----------------------T--------.....----A-----------A----    204
WEAU160       ---------------------------T--------------A......-G--A---A------------    204

CONSENSUS-D   CCACCCAAAAATAAGTTCAGAAGTACACAT?CCACTAGGAGAA......GCTAgaCTGGTAgTAAaAACA    201
ELI           ------------------------------C------------......------------A--------    204
Z2Z6          ------------------------------T------------......----TG---------------    204
Z6            ------------------------------T------------......----------------------    204
NDK           ------------------------------C------------......----------------C----    204

CONSENSUS-O   ?AATCCAA?AGT?AGTTC????GT?TATATTCCAGTAG??G??......GC??AT?TAGT?GT?ACCACA    173
MVP5180       G-------A---C-----GGCG--G-------------CA-AA.......--TG--A----G--C------    204
ANT70         A-------G---T-----AAGT--A-------------GG-TG.......--CC--G----A--A------    204

CONSENSUS-A   gCATcCAAaAGtAaGTTCAGAAGTACACATCCCACTAGGGGAt......GCTAGaTTAGTAGTAAGAACA    203
AD_MAL        ------------------------------------------......----------------------    204

CONSENSUS-CPZ T?A?CCAAA????G?????GAA?TACA?ATACC??T???A???T????????AAATT??TAGTGACA???    119
CPZGAB        -A-T-----AGTT-CTTCT---A----C-----TT-CAG-GAT-AT...TCT-----AA--------ACC    207
CPZANT        -C-C-----GAAA-GAGAA---G----T-----AC-ACC-ACA-TGGATAAA-----GG--------GTG    210
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CONSENSUS-A   TATTGGGGTCTGCATACAGGAGAAagAGACTGGCACTTGGGTCAtGGGGTCTCCATAGAATGGAgGCaGA   273
U455          -------------------------A-------------------------------------------T--   274
IBNG          ------------------------C--------------------------------------A-----   274
IFA86         ---------------------------------------------G-------------------------   274

CONSENSUS-B   TaTTGGGGTCTgCAtACAggAgAAAGAGAcTGGCAttTgGGtCAgGGAGtCtCcaTaGAATGGAGGAaaa   274
SF2           ----------------------------A-----------C---------G------------------   274
LAI           -----------------------------------C--------------------------------   274
HXB2R         ----------------------------------------------------------------------   274
LW123         ----------------------------------------------------------------------   274
NL43          ----------------------------------------------------------------------   274
NY5CG         ----------------------------------------------------------------------   274
MN            --------------------------------------A-------------------------------   274
JRCSF         ------------------------------------------------------------G----------C--   274
JRFL          ------------------------------------------------------G---------------   274
NH52          -----------A------TA-1                                                   225
OYI           ----------------------------A-----------C-------C---T----------------   274
CAM1          ------------------------------------------------------------------C--   274
HAN           ----------------------------------------C-------C--------------------   274
D31           -----------------------------------A-----C--T------------------------   274
RF            ----------------------------------------------------------------------   274
YU2           --------------C-------------------------------------------------------   274
BCSG3C        ----------------------------T--------------T---------G---------------   274
IFA70         ----------------------------------------------------------------------   274
IFA19         ----------------------------T-------------------------------------G-   274
IFA65         --------------A-------------------------------------------------------   274
P896          ----------------------------------------------------------------------   274
YU10          --------------C-------------------------------------------------------   274
IFA10         -T--------------------------------------------------------------------   274
3202A12       ----------------------------------------C----------------------------   274
3202A21       ----------------------------------------C----------------------------   274
MANC          ------------------------------------------------C--------------------   274
WEAU160       ---------------------------------------------A------------------------C   274

CONSENSUS-D   TATTGGGGTCTGCATACAGGAGAAAgAGA?TGGCATCTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAA   270
ELI           ----------------------------A-----------------------------------------   274
Z2Z6          ----------------------------C-----------------------------------------   274
Z6            ----------------------------C-----------------------------------------   274
NDK           -------------------------A---A-----------------------------------------   274

CONSENSUS-O   TATTGGGGATT?ATGCCAGGGGAAAGAGA?GAACA?TTGGGACATGGGGTTAGTATAGAATGGC??TA?A   237
MVP5180       -----------A-----------------G-----C----------------------------AA--C-   274
ANT70         -----------G-----------------T-----T----------------------------GT--T-   274

CONSENSUS-A   TATTGGGGTCTGCATACAGGAGAAagAGACTGGCACTTGGGTCAtGGGGTCTCCATAGAATGGAgGCaGA   273
AD_MAL        --------------A----------A--------------------------------------------   274

CONSENSUS-CPZ T??TGGG??TTA??????GGAGAA?G??C?TGGCA?TTAGG?CATGG?GT???CAT??AATGGAG????G   163
CPZGAB        -AT----CC---AGCCCA------A-GG-C-----T-----C-----A--CTC---TC-------GCTA-   277
CPZANT        -TC----GA---CAATGT------C-CC-A-----C-----A-----T--GAG---AG-------ATGT-   280
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CONSENSUS-A   AAAGATATAGCACACAAgTAGAtCCTGACcTAGCAGACCAaCTgATTCACCTGcATTATTTTgAcTGTTT    343
U455          ----------------------------------------T--A--------------------------    344
IBNG          -----------------A----C------T-----------------------T--------A-T-----    344
IFA86         ----------------------------------------------------------------------    344

CONSENSUS-B   aGagATAtAgCAcACAAGTAgacCCTgaccTAGCAGACCaaCTAATTCAtctgtAttAcTTTGAtTGTTT    344
SF2           ---A-----------------------G-------------------------C----T-----------    344
LAI           ----------------------------A-----------------------------------C-----    344
HXB2R         ----------------------------A-----------------------------------C-----    344
LW123         ----------------------------A-----------------------------------C-----    344
NL43          -------------------------------------------------------C-C--T-----------    344
NY5CG         -------------------------------------------------------C-C--T-----------    344
MN            ----------------------------------------C------------C----------------    344
JRCSF         G---------------------------------------------------------------------    344
JRFL          ---------A-------------------------------------------------------------    344
OYI           ---------------------------G----------------------ACA-----T-----------    344
CAM1          --G------A----------------------------------------------C--T-----------    344
HAN           G-------------------------A----------------------C--------T-----------    344
D31           ---------------------------G--------------------------C--T-----------    344
RF            G----------------------------------------------C-----C--T-----------    344
YU2           ----------------------------------------------------------------------    344
BCSG3C        ----------------------------------------------------------------------    344
IFA70         ----------------------------A-----------------------------------C-----    344
IFA19         -------------------------------------------------------C----------------    344
IFA65         --------------------AC-------A---------------------------------------    344
P896          ---------------------------G-----------G--------------------------------    344
YU10          ----------------------------------------------------------------------    344
IFA10         G--------------------G------------------------------C----------------    344
3202A12       ----------------------T----G------------------------------T-----------    344
3202A21       ----------------------T----G------------------------------T-----------    344
MANC          --G----C----T--------------G------------------------------T-----------    344
WEAU160       ---------------------------------------------------------C-T-----------    344

CONSENSUS-D   GGAGATATAGCACACAAGTAGACCCTGGCCTGGCAGACCAACTAATTCATATGTATTATTTTGATTGTTT    340
ELI           ----------------------------------------------------------------------    344
Z2Z6          ----------------------------------------------------------------------    344
Z6            ----------------------------------------------------------------------    344
NDK           ----------------------------------------------------------------------    344

CONSENSUS-O   AG?AGTATAAAACACAGATTGA?CCTGAAACAGCAGACAGGATGATACATCTGCATTATTT?AC?TGTTT    303
MVP5180       --G--------------------T-------------------------------------C--A-----    344
ANT70         --A--------------------C-------------------------------------T--C-----    344

CONSENSUS-A   AAAGATATAGCACACAAgTAGAtCCTGACcTAGCAGACCAaCTgATTCACCTGcATTATTTTgAcTGTTT    343
AD_MAL        -----------------C------------------------------T---T-C--------T-----    344

CONSENSUS-CPZ GA???TAT?TCACACA?GT?GA?CC????ACAGC?GAT??A?TGAT?CAC????A?TATTT????TG?TT    207
CPZGAB        --TCT---G-------G--G--T--CTTC-----A---AG-T----C---TCTC-A-----TGAT--C--    347
CPZANT        --AAG---A-------A--A--C--AGAA-----T---CA-A----A---CAAT-T-----CCCC--T--    350
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CONSENSUS-A   TTCAGAcTCTGCCATAAGgAaAGCCATATTAGGAgAAaTAGTTAGACCTAGGTGTGAATATCAAGCAGGA    413
U455          ------A-------------G-------------C------------------------------------    414
IBNG          ------------------A-----------------------------------------------------    414
IFA86         -------------------------------------G--------------------------------    414

CONSENSUS-B   TTCAGAaTCtGCtATAAgaaatgCcatAtTAGGAcatatAGtTAgtcCTAggTGTGAATaTCaAGCAGGa    414
SF2           -----------------A----------------T---G------------------------------    414
LAI           ------C--------------G---T-------------------C------------------------    414
HXB2R         ------C--------------G---T----------C--------C------------------------    414
LW123         ------C--------------G---T----------C--------C------                     396
NL43          ----------------------A------------G----------------------------------    414
NY5CG         ----------------------A------------G----------------------------------    414
MN            ------C-----C--------G----------------G-----------TT-------T----------    414
JRCSF         ------------------G------------------------------A------------------    414
JRFL          ---------------------------------------------------A------------------    414
OYI           ----------------------------C-----A---------------------------C-------    414
CAM1          ---------------------G------G------GAT-------C------------------------    414
HAN           -----------------------------------G----------------------------------    414
D31           -----------------------------------G-----G---C-----T----------G-------    414
RF            ---------------------GC-ATC-------------------------------------------    414
YU2           ---------------------G------------T---G------------------------------    414
BCSG3C        ------------C--------------------------------------------------------    414
IFA70         ------C--------------G---T----------C--------C------------------------    414
IFA19         --------------------G-----------------------------------------G-------    414
IFA65         ------------C------C-A--------------C-------T-T----T------------------    414
P896          ------C--------------GT----------------------C-----T------------------    414
YU10          ----------------------------------T---G------------------------------    414
IFA10         --------------------G-----------------G------A------------------------    414
3202A12       -------------------------------------G--------------------------------    414
3202A21       -------------------------------------G--------------------------------    414
MANC          ---------------------------------------------C------------------------    414
WEAU160       ------G--C---------------------------T------T------------------------G    414

CONSENSUS-D   TtCAGAA?CTGC?ATAAGAAAAGCCATATTAGGAcATATAGT?AGTC?TAGgTGTGAGTATCAAGCAGGA    406
ELI           -------T----T---------------------G-------T----C----------------------    414
Z2Z6          -------G----C------------------------------C----A----------------------    414
Z6            -------G----C------------------------------C----A----------------------    414
NDK           -G-----T----T------------------------------T----C---T------------------    414

CONSENSUS-O   TACAG?ATCAGCA?TCAGGAA?GCCAT?CTAGG?CAGAGAGT?CTGACCAAGTGTGAATACC???CAGGA    364
MVP5180       -----A-------A-------G-----T-----G--------G-------------------TGG-----    414
ANT70         -----C-------G-------A-----C-----A--------A-------------------CTA-----    414

CONSENSUS-A   TTCAGAcTCTGCCATAAGgAaAGCCATATTAGGAgAAaTAGTTAGACCTAGGTGTGAATATCAAGCAGGA    413
AD_MAL        ------A-----------AC--------------C-T--------T-----------T------------    414

CONSENSUS-CPZ T?CAGA????GC??TCAGA??AGC?AT??TAGG??A?????TA??G?C????TG??A?TACAA??A?GGA    245
CPZGAB        -G----AACT--CA-----AG---T--AT----GC-GCTTG--GC-C-TCGT--TG-A-----AG-A---    417
CPZANT        -T----TCAA--AG-----CA---A--CC----AG-AAGAA--TT-A-ATAC--CC-C-----GA-G---    420
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                 5'sj \/
CONSENSUS-A   CATAAcAAGGTAGGATC?CTaCAATATTTGGCaCTG...AAaGCaTTA.........GTAgCaCCAAcAA    470
U455          -----------------T--------------T---...---------.........---A-C-------    472
IBNG          -----T-----------G------------------...--T--T---.........-------------    472
IFA86         -----------------A--G---------------...---------.........----------A--    472

CONSENSUS-B   CATAacAAGGTAGGatCtCTACAgTACtTgGCACTA...gCAGCaTTa.........atAacAcCAAaaa    472
SF2           -----------------------A------------...---------.........-------------    472
LAI           -----------------------A------------...---------.........-------------    472
HXB2R         -----------------------A------------...---------.........-------------    472
NL43          -----------------------------------...---------.........----A-------C    472
NY5CG         -----------------------------------...---------.........----A-------C    472
MN            ---------------C--------------------...A--------.........-------------    472
JRCSF         ----G------------------------------...A--------.........----A--------    472
JRFL          --------------G----------------------...A--------.........----A-T------    472
OYI           -----------------------A------------...--------G.........----A--------    472
CAM1          -----------------------------------...A--------...........---G---------    472
HAN           ----G------------------A------------...---------.........-C-----------    472
D31           -----------------------------------...------G---.........-------------    472
RF            --------------------------C--------...---------.........-C-----------    472
YU2           -----------------------------------...A--------.........-------------    472
BCSG3C        --------------------------C-A------...---------.........-------------    472
IFA70         -----------------------A------------...---------.........-------------    472
IFA19         -----T------------------------------...A--------.........G----------G-    472
IFA65         -----A-----------G------------------...---------.........----A--------    472
P896          -----------------------------------...---------.........-C--------G--    472
YU10          -----------------------------------...A--------.........-------------    472
IFA10         -----------------------------------...A--------.........-------------    472
3202A12       -----------------------A------------...---------.........----A--------    472
3202A21       -----------------------A------------...---------.........----A--------    472
MANC          -----------------------------------...--------G.........-------------    472
WEAU160       -----------------------A------------...A--------.........-------------    472

CONSENSUS-D   CATA?CAAGGTAGGATCCtTACAGTATTTGGCACTA...aCAGCATTA.........aTAGCACCAAAAa    463
ELI           ----A-------------C-----------------...---------.........------------C    472
Z2Z6          ----G------------------------------...---------.........G------------    472
Z6            ----G------------------------------...---------.........-------------    472
NDK           ----A------------------------------...G--------.........-------------    472

CONSENSUS-O   CATAGTCAGGTAGGGACACTACAA?T??TAGC??T?...A?AGCAGTA.........GT?AAAG?AA?AA    412
MVP5180       ------------------------T-CT----CT-G...-A-------..........--G----T--A--    472
ANT70         ------------------------C-GC----TC-A...-G-------..........--A----C--G--    472

CONSENSUS-A   CATAAcAAGGTAGGATC?CTaCAATATTTGGCaCTG...AAaGCaTTA.........GTAgCaCCAAcAA    470
AD_MAL        -----------------TT----G-----------A...-C-------.........A---------A--    472

CONSENSUS-CPZ CA?AG?CAGGTAGG??C??T?CAGT??TT?GC??T????AA?????TA??????????AT?????A???    275
CPZGAB        --C--G--------AT-CT-A----TC--G--CC-A...--AGCTT--.........AT--CAGAG-GAA    475
CPZANT        --T--T--------GA-AC-G----AT--A--TT-TTGT--GATCC--GAATTCAGAGG--ACCCC-AGG    490
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                                                vpR cds ->
CONSENSUS-A   aGgCAAAGCCACCTTTGCCTAGTgTTAaGAAgTTAaCAGAaGAtAGATGGAAcgAGCCCCAGAAGACCAG    540
U455          G-----------------------------A--------G------------A----------------    542
IBNG          --A------------------------G-------G-------C--------A-----------------    542
IFA86         -----------------------C--------------------------------------------    542

CONSENSUS-B   aGAtAAaGCCACCtTTgCCTAgTGTTa?gAAACTgACAGAgGAtAGATGGAACAAgCCCCaGAAgACCAA    541
SF2           ---C-----------------------A-----------------------------------------    542
LAI           --------------------------C-----------------------------------------    542
HXB2R         --------------------------C-----------------------------------------    542
LW123                                                                   T---------    406
NL43          --------------------------G---------------C--------------------------    542
NY5CG         --------------------------G---------------C--------------------------    542
MN            --------------------------A-----------------------------------------    542
JRCSF         --------------------------A------A----------------------------------    542
JRFL          --------------------------A------A----------------------------------    542
OYI           --------------------------C------A----------------------------------    542
CAM1          --------------------------G---------------------------A--------------    542
HAN           ---------------------T-----CA-----------A----------------------------    542
D31           --------------------------GCA---------------C----------------G---------    542
RF            --------------------------A-----------------------------------------    542
YU2           ---C-----------------------AA----------------------------------------    542
BCSG3C        G-------------------------CA-----A----------------------------------    542
IFA70         --------------------------C-----------------------------------------    542
IFA19         --------------------------A-----------------------------------------    542
IFA65         ---A--G--------------------A-----------------------------------------    542
P896          G------------C--T----------C-----------------------------------------    542
YU10          ---C-----------------------A-----------------------------------------    542
IFA10         ---C-----------------------G-----------------------------------------    542
3202A12       ---C-----------------------C-----------------------------------------    542
3202A21       --------------------------C-----------------------------------A-----    542
MANC          ---C-----------------------C-----------------------------------------    542
WEAU160       --------------------------A-----------------------------------------    542

CONSENSUS-D   AGATAAAGCC?CCTTTGCCTAGTGTTAGGAAG?TAACAGAAGATAGATGGAACAAGCCCCAGaAGACCAa    531
ELI           ----------A---------------------C-----------------------------C------G    542
Z2Z6          ----------G---------------------T-----------------------------------    542
Z6            ----------G---------------------T-----------------------------------    542
NDK           ----------A---------------------C-----------------------------------    542

CONSENSUS-O   G?A??AAGCCTCCCCTACCCAGTGTCCAGA?ATTAACAGAAGATAGATGGAACAAGC?C??GA?AATCAG    474
MVP5180       -A-AT-------------------------G--------------------------C-TG--A------    542
ANT70         -C-GG-------------------------A--------------------------A-CT--G------    542

CONSENSUS-A   aGgCAAAGCCACCTTTGCCTAGTgTTAaGAAgTTAaCAGAaGAtAGATGGAACgAGCCCCAGAAGACCAG    540
AD_MAL        --A---G--------------------G----C--------------------A--------C------A    542

CONSENSUS-CPZ G?C??AGA??AC??TT?CCTAGT?T??C?A??TTAACAGA?GATAGATGGAACAAGC?CC??AGGA??A?    324
CPZGAB        -G-AT---CC--CT--A------G-CG-C-AA--------G----------------A--AG----CC-A    545
CPZANT        -T-CA---AG--AG--C------C-GT-T-TC--------A----------------C--GC----TG-G    560
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HIV1 VIF

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CONSENSUS-A   GGGCCACAGAGGGAgCCGT?CaaTGAATgGaCActAG   576
U455          -------------------A-GC-----A-G--T      576
IBNG          -------------------C-----------------   579
IFA86         --------------A----T-----------------   579

CONSENSUS-B   GGGCCACAGAGggAGCCataCAATgaaTGGaCAC?AG   577
SF2           ----------------------------------     576
LAI           ------------------C---------------     576
HXB2R         ------------------C---------------     576
LW123         ------------------C---------------T--  443
NL43          ----------------------------------     576
NY5CG         ----------------------------------     576
MN            ------------------------C-----G---     576
JRCSF         ----------------------------------     576
JRFL          ----------------------------------     576
OYI           ----------------------------------     576
CAM1          ------------C---------------------     576
HAN           -------------------------C--------     576
D31           ----------------------------------     576
RF            ----------------------------------     576
YU2           -----------------GC---------------     576
BCSG3C        ------------------------------------T--  579
IFA70         ------------------C---------------T--  579
IFA19         ------------------------------------T--  579
IFA65         -------------------T--------------T--  579
P896          --------------------------C-------T--  579
YU10          -----------------GC---------------T--  579
IFA10         -------------------T--------------T--  579
3202A12       -----------------------------------T--  579
3202A21       -----------------------------------T--  579
MANC          -----------A----------------------T--  579
WEAU160       -----------------------------------T--  579

CONSENSUS-D   GGGCCaCA?AGGgAGCCATACAATGAATGGaCAT      564
ELI           --------G---------------------G---     576
Z2Z6          --------A-------------------------     576
Z6            --------A---.--------------            567
NDK           -----G--G-------------------------     576

CONSENSUS-O   GGACCAGCTA??GAGCC?TTCAATGAATGG?CAC?AG   506
MVP5180       ----------GG-----A------------A---T--  579
ANT70         ----------AA-----C------------G---     576

CONSENSUS-A   GGGCCACAGAGGGAgCCGT?CaaTGAATgGaCActAG   576
AD_MAL        -----------------ACA-------------T      576

CONSENSUS-CPZ GG?CCAC??AGAGAACC???CCAGGAATGGGCAT      352
CPZGAB        --T----CA--------TTA--------------      579
CPZANT        --G----AG--------AA1                    579
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                                                                <- pol cds
CONSENSUS-A   ATGGAAAACAGATGGCAGGTGATGATTGTgTGGCAGGTAGACAGGATGAgGATTAGAACATGGAAcAGTT     70
CONSENSUS-B   ------------------------------------a-----------------------------a----     70
CONSENSUS-D   ------------------------------------A-------------------?---------A----     69
CONSENSUS-O   --------------------AC----A--A-----A?-?-----ACA--AAG-G-A-G-?--------CC     67
CONSENSUS-CPZ ---?????????????????--?--???---------A--------?----------A?-??-----????-     43

CONSENSUS-A   TAGTAAAACATCAtATGTATGTCTC?AAGAAAGCTaAgGGTTGGTTTTATAGACATCACTtTGAAaGTAG    139
CONSENSUS-B   ----------C---------a-t--Agg------------a-------------------A------c-c    140
CONSENSUS-D   ----------C-----------T--A----------?CA-A-------------------A---c--CCc    138
CONSENSUS-O   -?--G---T-C----A?--CA?G--T-??--G?-CG?-AAC---?G?--?--?-----T-A----TCC--    126
CONSENSUS-CPZ ----?---?-?--?--?-????G?----A??????-?A???---???--?--------T-A---??A???     83

CONSENSUS-A   gCATcCAAaAGtAaGTTCAGAAGTACACATCCCACTAGGGGAt......GCTAGaTTAGTAGTAAGAACA    203
CONSENSUS-B   T-------g-a--------------------------------.....--------g---a---c----    204
CONSENSUS-D   C--C------A-------------------?--------A--A.....------C-G-------a----    201
CONSENSUS-O   ?A------?---?-----????--?T-T--T---G---??-??......--??AT?----?--?-CC---    173
CONSENSUS-CPZ T?-?-----????G?????---?----?--A--??-???A???T????????-A---??----G-C-???    119

CONSENSUS-A   TATTGGGGTCTGCATACAGGAGAAagAGACTGGCACTTGGGTCAtGGGGTCTCCATAGAATGGAgGCaGA    273
CONSENSUS-B   ------------------------------------t--------g--A------------------A-a-    274
CONSENSUS-D   ------------------------------?-----TC-------G--A------------------A-A-    270
CONSENSUS-O   --------AT-?ATGC----G--------?GAA--?-----A--------TAGT---------C??T-?-    237
CONSENSUS-CPZ -??----??T-A??????------?-??C?-----?--A--?-----?--???---??-------????G    163

CONSENSUS-A   AAAGATATAGCACACAAgTAGAtCCTGACcTAGCAGACCAaCTgATTCACCTGcATTATTTTgAcTGTTT    343
CONSENSUS-B   -G--------------------c--------------------A-----t---t----c-----t-----    344
CONSENSUS-D   GG--------------------C----G---G-----------A-----TA--T----------T-----    340
CONSENSUS-O   -G?AG----AA-----GA-T--?-----AAC-------AGGA----A--T-----------?AC?-----    303
CONSENSUS-CPZ G-???---?T------?--?--?--????AC---?--T??-?----?---????-?-----????--?--    207

                  \/ 3'sj
CONSENSUS-A   TTCAGAcTCTGCCATAAGgAaAGCCATATTAGGAgAAaTAGTTAGACCTAGGTGTGAATATCAAGCAGGA    413
CONSENSUS-B   ------a-----t-----a--t------------c-t--------t------------------------    414
CONSENSUS-D   ------A?----?-----A---------------c-T-----?--T-?---------G------------    406
CONSENSUS-O   -A---?A--A--A?-C-----?-----?C----?C-G-G---?CTGA-C-A---------C-???-----    364
CONSENSUS-CPZ -?----????--??-C--A??---?--??----??-?????-A??G?-????--??-?--CA-??A?---    245

                 5'sj \/
CONSENSUS-A   CATAAcAAGGTAGGATC?CTaCAATATTTGGCaCTG...AAaGCaTTA.........GTAgCaCCAAcAA    470
CONSENSUS-B   -----------------t-----g--C--------A...gC-------.........a--a------a--    472
CONSENSUS-D   ----?------------Ct----G-----------A...-C-------.........a---------A--    463
CONSENSUS-O   ----GTC-------GA-A------?T??-A--??-?...-?----G--..........--?AA-G?--?--    412
CONSENSUS-CPZ --?-G?C-------??--?-?--G-??--?--??-????--?????--??????????-T?????-???    275

                                                   vpR cds ->
CONSENSUS-A   aGgCAAAGCCACCTTTGCCTAGTgTTAaGAAgTTAaCAGAaGAtAGATGGAAcgAGCCCCAGAAGACCAG    540
CONSENSUS-B   --At-----------------------?---AC-g-----g------------A---------------A    541
CONSENSUS-D   --AT------?----------------G----?--------------------A---------------a    531
CONSENSUS-O   G?A??-----T--CC-A--C-----CC---?A---------------------A---?-??--?A-T---    474
CONSENSUS-CPZ G?C??-GA??--??--?------?-??C?-??--------?------------A---?--??-G--??-?    324

CONSENSUS-A   GGGCCACAGAGGGAgCCGT?CaaTGAATgGaCActAG                                    576
CONSENSUS-B   -----------------a-a--------------?--                                    577
CONSENSUS-D   --------?--------A-A-------------T                                       564
CONSENSUS-O   --A---GCT-??-----?-T----------?---?--                                    506
CONSENSUS-CPZ --?----??--A--A--??--C-G------G--T                                       352
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