HIV2/SIV POL

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                                                   -> Pol reading frame (-1 from Gag) P15
CONSENSUS-A   VLELWKGGTLGETVPSTQKTgLLEmWQ?RThHGKlPrkTG?FFRdgp?GKeapQlPrgPssaGAdTNSTp     67
ROD                                                --R---T--L----------------------     32
NIHZ                                               --W----W-L---G--------P---N-----     32
ISY                                                --W---AWTM-----------KF---N-----     32
ST                              --R------G------M-----G---V--M------F-C--NP---------     52
BEN                             ------V--A--------G---R---V--T----S----D--PS-------S     52
CAM2                                               --G----W-L------F------T--N-----     32
D194          ------------------------V--V--------G---R------T--A----------S--------     70
GH1                             ---------D--R---M-----R-----SM-------------S--------     52
UC2                             ---------A--------GQ--G-----LT-------------S--------     52
MDS                             ---------D--Y---V--Q--G----W-L-----------G----N-----     52
KR                              ---------I--C---------W----W-M----S----D--P---------     52
CONSENSUS-B                     KtGMLEMWk?RTHHVKMPRKTGgFFRVRtLGKEASQlPhdPsasGsdtICtP     51
D205                            ---------N----------------------------------------     52
UC1                             ---------T------------W-----------------------------     52
EHOACG                          -A------TA------------------P-------F-R.-GTP-DSA--A-     51
CONSENSUS-SD  VLELWE?gTLCKAMQsPKKTGmLEMWkNGPCYGQMPr?TggFFRaWpmGKEAPQFPHGpdASGAD?NCSp     67
MM251         ------G------------------------------Q------P-S-----------SS-----A----     70
MM32H         ------RR-----------------------------Q------P-S-----------SS-----A----     70
MM239         ------R------------------------------Q------P-S-----------SS-----A----     70
MM142         ------GR-----------------------------KQ------P--L----------SS-----A----     70
MNE           ------R--------N-----L----T----------Q--R---L-------------N-----A----     70
SMMH4                                               K---------------------------T----     33
SMMH9                                          ---K---------------------------T---x     36
SMMPBJ                                         ---K-S-------------------------T----     36
6P6                                            ---K-S-------------------------T----     36
CONSENSUS-STM                 RPEKTRLLEMWTTGPSDGQMPRKTGGFFRLWPMGKEAPQLPHGPNTSGADANCPS     55
STM                           -------------------------------------------------------     55

                                                   P15 peptide \/ Protease
CONSENSUS-A   ?rsssgptgeiyAArekaegAE.?etiQrgDrgLtApRagrdt?Qr??dRGlAaPQFSLWkRPVVTAyiE    131
ROD           SG----S----------T-R--.R----GS----------G--I-GATN---------------------    101
NIHZ          IG-------------K--K---.R--V-GS------F------M-G.D--------------------H--    100
ISY           NG--------VH-----T-R--.TK----S----A-S--R---T--.D---------------------    100
ST            D-P-R---R-VH-------R--.R-A---S----P-A-ET---M--.D--------------------HV-    120
BEN           G-----TV---------------.G-------G--A----E---S--.G----------------------    120
CAM2          IG----S----------------.T--------------TR-GPM-G.DN------------------H--    100
D194          N------V-----------R--.G----G--G----------AP--.G-----T-------------F--    138
GH1           S-----SI-K----G-R-----.G-------GR-------KS-S--.G----------------------    120
UC2           S--G---VR--F--G-------.G----G--GR----------S--.G----------------------    120
MDS           S---------------------.R----------A-----K--M-G.DN--F--------N------H--    120
KR            S-P--R-AR-VL----E--R--.N----G---------TR---T--.G---F----------------V-    120
CONSENSUS-B   DePSrgHDTSGgDtICaPCRSSsGDAekLHadgEtaErEpRETLQG.GDRGFAAPQFSLWRRPVVkAcIE    120
D205          ------------------------------------T----------.-----------------------    121
UC1           -G----------------------------E---------------.------------------R----    121
EHOACG        ----IR-----C-S--T-----R---KE---TR-E--G-Q------.--------------------T--    120
CONSENSUS-SD  RgsSCGS??eLH??GQk????.............AE??QrE?LQG.GdrGFAAPQFSLWRRPvVTA?IE    110
MM251         --P----AK---AV--A..................--RK---A---.--------------------H--    121
MM32H         --P----AK---AA--AAERK..............--RK---A---.--------------------H--    125
MM239         --P----AK---AV--AAERK..............--RK---A---.--------------------H--    125
MM142         -RT----AK---AL--A..................--RK---A---.--------------------H--    121
MNE           --P----AKK--AV--T..................--RK-K-A---.--------------------H--    121
SMMH4         -------TE---ED---...................--GE---T---.--------------------Y--     84
SMMH9         -------TE---EG---...................--GE---T---.-NG-----------------Y--     87
SMMPBJ        -------TE---ED---...................--GE---T---.-NG-------------I---Y--     87
6P6           -------TE---ED---...................--GE---T---.-NG-------------I---Y--     87
CONSENSUS-STM RRPSCGSAEKLHAAGQE.................AEREQEDTLQG.GDRGFAAPQFSLWRRPVVTAHIE    106
STM           -----------------.................-----------.-----------------------    106
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CONSENSUS-A   gQPVEVLLDTgAdDSIVAGieLGsNYsPKiVGGIGGFINTKEyKnvEI?VLnKrVrATIMTGDTPINIFG   200
ROD           -----------------------N-----------------------E----K----------------   171
NIHZ          ----------R-N---------------------------------E--G---K--------------   170
ISY           D-----------------------------------------D---R----K----------------   170
ST            -------------------V----------------------------R--------------------   190
BEN           D----------------------D--T---------------------K--------------------   190
CAM2          -----------------------------------------------E--G------------------   170
D194          D----------------------D--T---------------------K--------------------   208
GH1           V-------------------Q--D--V---------------I--I--K---------------------   190
UC2           D----------------------D--T--V------------------K---------------------   190
MDS           -----------------------------------------------E--G------------------   190
KR            ------------------------------------------------K----K-K--------------   190
CONSENSUS-B   GQsVEVLLDTGaDDSIVAGIELGSNYTPKIVGGIGGFINTkEYKdVEIEVVGKRVRATiMTGDTPINIFG   190
D205          -----------V------------------------------------------------------------   191
UC1           --P---------------------------------------------------------------------   191
EHOACG        ----------------------------------------N---N-------------V-----------   190
CONSENSUS-D                                                                         x     1
FORTC2                                                                              -     1
CONSENSUS-SD  ?QPvEVLLDTGADDSIVaGIELGP?YTPKIVGGIGGFINTKEYK?VkI?VLGK?IKGTIMTGDTPINIFG   175
MM251         G----------------T------H-------------------N---E----R----------------   191
MM32H         G----------------T-----LH-------------------N-E-E----R----------------   195
MM239         G----------------T------H-------------------N-E-E----R----------------   195
MM142         G----------------T------H-------------------N-E-E----R----------------   191
MNE           G--A--------------------H-------------------N---E----R----------------   191
SMMH4         E-----------------------N-------------------D---K----V----------------   154
SMMH9         E--I--------------------N-------------------D---K----V----------------   157
SMMPBJ        E-----------------------N-------------------D---K----V----------------   157
6P6           E-----------------------N-------------------D---K----V----------------   157
CONSENSUS-STM GQPVEVLLDTGADDSIVAGIELGLQYTPKVVGGIGGFINTKEFKNVNIEVLGKKIKGTIMTGDTPINIFG   176
STM           ---------------------------------------------------------------------   176

                 Protease \/ Reverse Transcriptase
CONSENSUS-A   RNiLtaLGMSLNlpvAkiePiKimLKPGKDGP?lrQWPLTkEKiEALkEICEKMEkEGQLEEAPPTNPYN   269
ROD           -----------------V--------------K-------------------------------------   241
NIHZ          --V-----------------------------R-K-----------------------------------   240
ISY           --------------------V-VT--------KQ------R------R-------R--------------   240
ST            -------------------------------K----------------------R--------------   260
BEN           ----------------------VT--------R-K-----------------------------------   260
CAM2          --------------------------------R-------------------------------------   240
D194          ----AT-----------LD---VT--------R-K--------------------R--------------   278
GH1           --------------I-------VT--------R--------------R----------------------   260
UC2           ----------------R------T--------R-K--------V--------------------------   260
MDS           --------------------------------K----------------------R--------------   260
KR            -----------------VD---VI--------KV----------------------R--------------   260
S52907                    MA---V--------------K-------------------------------------    58
CONSENSUS-B   RNILNtLGMTLNFPVAkiEPVKV?LKPgKDGPKIRQWPLSkEKILALKEICEKMeKEGQLEEApPTNPYN   259
D205          -----------------V-----E----------------R-----------------------------   261
UC1           -----------------------K-------------------------------------------   261
EHOACG        -----S----------R------Q---E-----------------------------------------   260
CONSENSUS-D   RNLLTELGMSLNFPVAKIEPVKVRLKPGMDGPKLRQWPLSKEKIEALKEICEKMEREGQLEEAPPTNPYN    71
FORTC2        ---------------------------------------------------------------------    71
CONSENSUS-SD  RNLLTA?gMSLNlPIAKVeP?KvtLKPGKdGPKLrQWPLSKEKI?ALREICEKMEKDGQLEeAPPTNPYN   242
MM251         ------L-------------V--------V----K---------V-------------------------   261
MM32H         ------L-------------V--A----------K---------V-------------------------   265
MM239         ------L-----F-------V--A----------K---------V-------------------------   265
MM142         ------L-------------V-SP----------K---------V-------------------------   261
MNE           ------LE----F-------V----------------------V-------------------------   261
SMMH4         ------M-------------I--------E--------------I-------------------------   224
SMMH9         ------M-----------x-I-----------------------I----------------x--------   227
SMMPBJ        ------M-------------I-----------------------I-------------------------   227
6P6           ------M-------------I-----------------------I-------------------------   227
CONSENSUS-STM RNLLTALGMSLNFPVAKVEPVKVTLKPGKDGPKIKQWPLSKEKIEALKEICEKMEKDGQLEEAPPTNPYN   246
STM           ---------------------------------------------------------------------   246
CONSENSUS-E                                                           xKEGQLERAPPTNPYN    16
PAR                                                                   ----------------    16
CONSENSUS-B   RNILNtLGMTLNFPVAkiEPVKV?LKPgKDGPKIRQWPLSkEKILALKEICEKMeKEGQLEEApPTNPYN   259
BA_7312AR                                                             x--------S------    16
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CONSENSUS-A   TPTFAIkKKDKNKWRMLIDFRELNkVTQdFTEiQLGIPHPAGLAKKrRItvLDvGDAYFSIPLhEDFRqY    339
ROD           ----------------------------------------------------------------------P-    311
NIHZ          ----------------------------------------------------------------------    310
ISY           -------------------------------V-----------------------------Y------    310
ST            ----------------------------------------------K-----------------------    330
BEN           ----------------------------------------------K--SI-------------------    330
CAM2          ------R---------------------------------------------------------------    310
D194          ------------------------R---------------------K-----------------------    348
GH1           ------------------------R---------------------K-----------------------    330
UC2           ------------------------R---------------------K----------------Y----P-    330
MDS           ------R---------------------------------------------------------------    330
KR            ----------------------------E-----------------------I-----------------    330
S52907        ----------------------------------------------------------------------P-    128
CONSENSUS-B   tPTFAIKKkDKNKWRMLIDFRELNKVTQ?FTEvQLGIPHPAGlaeKrRITV?DVGDAYFS?PLDP?FRQY    325
D205          ----------------------------D---#---------GRK-#----I--------I----N----    329
UC1           --------R-------------------D----------------------L--------I----N----    331
EHOACG        S---------------------------E---------------S-K----L--------V----D----    330
CONSENSUS-D   TPTFAIKKKDKSKWRMLIDFRELNKVTQDFTEVQLGVPHPAGLAKRRRITVLDVGDAYFSIPLDKEFRQY    141
FORTC2        ----------------------------------------------------------------------    141
CONSENSUS-SD  TPTFAIKkkDkNKWRmLIDFRELNkVTQDFTEVQLGIPHPaGLAKR?RITVLDvGDAYFSIPLDEEFRQY    311
MM251         ------------------------R---------------------K------I----------------    331
MM32H         ------------------------R---------------------K------I----------------    335
MM239         ------------------------R---------------------K------I----------------    335
MM142         ------------------------R---------------------K------I----------------    331
MNE           ---------------I------------------------------K-----------------------    331
SMMH4         ----------------------------------------------R-----------------------    294
SMMH9         -------xx-G-----------------------------x-----R-----------------------    297
SMMPBJ        ----------------------------------------------R-----------------------    297
6P6           ----------------------------------------------R-----------------------    297
CONSENSUS-STM TPTFAIKKKDKNKWRMLIDFRELNKVTQDFTEIQLGIPHPAGLAKRRRITVLDVGDAYFSIPLDEGFRQY    316
STM           ----------------------------------------------------------------------    316
CONSENSUS-E   TPTFAIRKKDKSKWRMLIDFRELNKATQDFTEVQLGIPHPAGLKEMEQITVLDIGDAYFSVPLDPEFRQY     86
PAR           ----------------------------------------------------------------------     86
CONSENSUS-B   tPTFAIKKkDKNKWRMLIDFRELNKVTQ?FTEvQLGIPHPAGlaeKrRITV?DVGDAYFS?PLDP?FRQY    325
BA_7312AR     ----------------------------E-------------WP-------I--------V----D----     86

CONSENSUS-A   TAFTLPsvNNaEPgKRYiYKVlPQGWKGSPAIFQytMRQvLEPFRKANpDvI?iQYMDDILIASDRTdLE    408
ROD           -----------------------------------H-------------K---I-----------------    381
NIHZ          ---------------------------------------I--------E---I-----------------    380
ISY           ------------------------------------------------IV-----------------    380
ST            -------I-------------S----------------------------I-L-----------------    400
BEN           ------A---M-----------------------------------------L--------------G--    400
CAM2          ----------------------------------------------S---I-----------------    380
D194          -------------E---V----------------FM---I------------L--------------G--    418
GH1           ----------------------------------H-----------------L--------------G--    400
UC2           ----------V---------------------------I------------L--------------G--    400
MDS           ----------------------------------------------Q---I-----------------    400
KR            ------T----------------------------H-----------------LV----------------    400
S52907        -----------------------------------H-------------K---I-----------------    198
CONSENSUS-B   TAFTLPs?NNAEPGKRYiYKVLPQGWKGSpaIfQYsMrKVLDPFRkAN?DV?IIQYMDDIL?ASDRSDLE    391
D205          -------V---------------------QS-C---------------S--I---------I--------    399
UC1           -------I-----------------------------------------S--I---------I--------    401
EHOACG        ------AV---------L-----------------T-A----------N--T---------V--------    400
CONSENSUS-D   TTFTLPSVNNREPGKRYIYKVLPQGWKGSPAIFQYTMRNILEPFRKANSDVTLIQYMDDILIASDRTDLE    211
FORTC2        ----------------------------------------------------------------------    211
CONSENSUS-SD  TAFTLPSVNNAEPGKRYIYKVLPQGWKGSPAIFq?TmRnVLEPFRKANPDVTL?QYMDDILiASDRTDLE    379
MM251         -----------------------------------Y---H--------------V----------------    401
MM32H         -----------------------------------Y---H--------------V----------------    405
MM239         -----------------------------------Y---H--------------V----------------    405
MM142         -----------------------------------Y---H--------------V----------------    401
MNE           -----------------------------------H------------------V-------V--------    401
SMMH4         -----------------------------------Y------------------I----------------    364
SMMH9         ----------------------------------xH-x----------------I----------------    367
SMMPBJ        -----------------------------------H------------------I----------------    367
6P6           -----------------------------------H------------------I----------------    367
CONSENSUS-STM TAFTLPSVNNAEPGKRYIYKVLPQGWKGSPAIFQYTMRNILEPFRRANPDVTLIQYMDDILIASDRTDLE    386
STM           ----------------------------------------------------------------------    386
CONSENSUS-E   TAFTIPSVNNQEPGKRYIYKVLPQGWKGSPAVFQETMRQVLEPFRKANSDVLLIQYMDDLLIGSNRSMTE    156
PAR           ----------------------------------------------------------------------    156
CONSENSUS-B   TAFTLPs?NNAEPGKRYiYKVLPQGWKGSpaIfQYsMrKVLDPFRkAN?DV?IIQYMDDIL?ASDRSDLE    391
BA_7312AR     -------I-------------------------------------R--N--T---------V--------    156
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CONSENSUS-A   HDkvvLQLKELLNgLGFSTPdEKFQKDPPyqWMGyELWPTKWKLQkiQLPQKevWTVNDIQKLVGvLNWA   478
ROD           --R----------------------------H----------------------I-----------------   451
NIHZ          ------------------------------R--------------------------------------   450
ISY           ----------------------------------------------------------------------   450
ST            --R-------------------------------------------R------------------------   470
BEN           ------------------------------F----C-----------L-----DI----------------   470
CAM2          -------------N----------------R--------------------------------------   450
D194          ------------------------------F-----------------------I----------------   488
GH1           ------------------------------L----------------L------I----------------   470
UC2           --------------------E--------F-----------------------T-----------I----   470
MDS           --R----------S----------------R--------------------------------------   470
KR            --RT--------------------------K--------------------------------------   470
S52907        --R-I-------------------------H----------------------I----------------   268
CONSENSUS-B   HDrVVSQLKELLNdMGFSTPEEKFQKDPPFkWMGYELWPKkWKLQKIQlPEkEVWTVNdIQKLVGVLNWA   461
D205          ------------------------------------------------------------A-----------   469
UC1           ----------------------------------------R-----------------------------   471
EHOACG        -------------N----------------------------------------------------------   470
CONSENSUS-D   HDKVVLQLKELLNDLGFLTPEEKFQKDPPYHWMGYELWPTKWKLQKIELPQREDWTVNDIQKLVGVLNWA   281
FORTC2        ----------------------------------------------------------------------   281
CONSENSUS-SD  HDRVVLQlKELLNsIGFStPEEKFQKDPPFQWMGYELWPTKWKLQKIELPQrETWTVNdIQKLVGVLNWA   449
MM251         ----------------------------------------------------------------------   471
MM32H         ----------------------------------------------------------------------   475
MM239         -------S--------------------------------------------------------------   475
MM142         ------------------S---------------------------------------------------   471
MNE           ------------------------------------------------K-------------------   471
SMMH4         -------------G--------------------------------------------------------   434
SMMH9         ------------------------------------------------------------N-----------   437
SMMPBJ        ----------------------------------------------------------------------   437
6P6           ----------------------------------------------------------------------   437
CONSENSUS-STM HDRVVLQLKELLNNLGFSTPEEKFQKDPPFQWMGYELWPTKWKLQKIELPQRDVWTVNDIQKLVGVLNWA   456
STM           ----------------------------------------------------------------------   456
CONSENSUS-E   HDRMVVQLKDMLNNLGFSTPEDKFQREPPLKWMGYLLYPKKWKLQKIELPEKERWTVNDIQKLVGILNWA   226
PAR           ----------------------------------------------------------------------   226
CONSENSUS-B   HDrVVSQLKELLNdMGFSTPEEKFQKDPPFkWMGYELWPKkWKLQKIQlPEkEVWTVNdIQKLVGVLNWA   461
BA_7312AR     --K---------------------------Q-----------------I--R------------------   226

CONSENSUS-A   AQiYpGIKTkhLCrLIrGKMTlTEEvQWTELAEAELEEN?iILsQeQEGhYYQEEkeLEATvqKdQdnQW   547
ROD           --L-----------------------------------R--------------------------E---   521
NIHZ          ----------------------------------------R-----K----------K-------------   520
ISY           -------------K-------P-----------------K----------------------------   520
ST            ---------RN----------------------------K---------C--------------------   540
BEN           ----S---------------------------------K---------Y-----------I--S-GH--   540
CAM2          ----------------------------------------R------------------------------   520
D194          -------------K------------------------K---------S-----E------I-S-----   558
GH1           ----------------K---------------------K---------Y-----------I--N-----   540
UC2           ----------------------------------------R---D-----------------I--S-----   540
MDS           -------------------------I-------------RV-----------------------------   540
KR            ----------------------------------------K---------C--------------------   540
S52907        --L-----------------------------------R------------------------------   338
CONSENSUS-B   AQLFPGIKTRHICkLIrGKMTLTEEVQWTELAEAElQENKIILeQEQEGSYYKEgVPLEATVQKNLANQW   531
D205          ------------------------------------------------------R---------------   539
UC1           ----------------------------------------------------------------------   541
EHOACG        ----------------------------------F-----------------------------------   540
CONSENSUS-D   AQIYPGIKTKHLCRLIRGKKTLTEEVQWTEMAEAEYEENKIILSQEQEGCYYQESKPLEATVVKDQDNQW   351
FORTC2        ----------------------------------------------------------------------   351
CONSENSUS-SD  AQIYPGIKTKHLCRLIRGKMTLTEEVQWTEMAEAEYEENKIIlSQEqEGCYYQEgKPlEAtVIKsQDNQW   519
MM251         ----------------------------------------------------------------------   541
MM32H         ----------------------------------------------------------------------   545
MM239         ----------------------------------------------------------------------   545
MM142         ------------------------------------------------------S---------------   541
MNE           ------------------------------------------------------------------N-----   541
SMMH4         ------------------------------------------------------------I------------   504
SMMH9         ----------------------------------------P---P-------------P---------   507
SMMPBJ        ----------------------------------------------------------------------   507
6P6           ----------------------------------------------------------------------   507
CONSENSUS-STM AQIYPGIKTKHLCKLIRGKMALTEEVQWTEMAEAEYAENKIILSQEQEGQYYREDKPLEATVVKDQDNQW   526
STM           ----------------------------------------------------------------------   526
CONSENSUS-E   AQVYPGIKTKNLCKLIRGKMTLTEEVQWTELSEAELAENKIILSQGQEGRYYREEENLEATVLKNQDNQW   296
PAR           ----------------------------------------------------------------------   296
CONSENSUS-B   AQLFPGIKTRHICkLIrGKMTLTEEVQWTELAEAElQENKIILeQEQEGSYYKEgVPLEATVQKNLANQW   531
BA_7312AR     -------------R--K-----------------M-------G--------------------------   296
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HIV2/SIV POL

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CONSENSUS-A   tYKiHQ?ekiLKvGKyaKiKnthtngvrLLAqVVQKIGKEALVIwGRiPKFHLPVERetWEQWWDnYWQV    616
ROD           ------E-----------V-------I------------------------------I-----------    591
NIHZ          ---V--G-----G--IC-D-KYPYQR------------------------------D------------    590
ISY           ---V--G-------------------------------------------------------------    590
ST            ------GG----------V-------------------------------------D------------    610
BEN           ------E-------------------------------------------------------------    610
CAM2          ------E-------------H------K----------------$-------------V-----------    589
D194          A-----G-RV-------------------------------------V---------D------------    628
GH1           ------E-------------------------------------------------------------    610
UC2           ------E-------------------------------------------------------------    610
MDS           ---V--G--T--------V-------------------------------------I------D----    610
KR            ------G------------------------H------------------------------------    610
S52907        ------ED----------V-------I------------------------------I-----------    408
CONSENSUS-B   TYKIHQGnk?LKVGKYAKVKNTHTNGVRlLAHVVQKIGKEALVIWGEIPvFHLPVERETWDQWWTDYWQV    600
D205          ---------V---------------------------------------------------------    609
UC1           --------RI----------------------------------------------------------    611
EHOACG        -------D-I-----------------------------------------M--------------------    610
CONSENSUS-D   SYKIHQEDKILKVGKYAKIKNTHTNGVRLLAHVVQKIGKEAIVIWGRVPKSHLPIERDVWEQWWSDYWQV    421
FORTC2        ---------------------------------------------------------------------    421
CONSENSUS-SD  SYKIHQEDKiLKVGKFAKiKNTHTNGVrLLAHV?QKIGKEAivIWGqVPkFHLPVEr??WEQWWTDYWQV    586
MM251         ----------------------------------I------------------------DV-----------    611
MM32H         ----------------------------------I----------------------KDV-----------    615
MM239         ----------------------------------I----------------------KDV-----------    615
MM142         ----------------------------------I----------------------KDV-----------    611
MNE           ----------------------------------I----------------------KDV-----------    611
SMMH4         ---------V--------V--------------V-------L----E----------EI-----------    574
SMMH9         ----------------------------S-----V--------I------R------xEI-----------    577
SMMPBJ        ---------------------------------V---------------R-------EI-----------    577
6P6           ---------------------------------V---------------R-------EI-----------    577
CONSENSUS-STM SYKIHQEDKILKVGKFAKIKNTHTNGVRLLAHVIQKIGKEAIVIWGQIPKFHLPVEREVWEQWWADYWQV    596
STM           ---------------------------------------------------------------------    596
CONSENSUS-SO                                                                   AR?V      3
SMMLIB1                                                                          x-      2
SMMM7                                                                          --P-      4
CONSENSUS-E   SYKIHQGDRILKVGKFPQIKNTHTNGVRLLASVVQK                                     332
PAR           ----------------------------------                                       332
CONSENSUS-B   TYKIHQGnk?LKVGKYAKVKNTHTNGVRlLAHVVQKIGKEALVIWGEIPvFHLPVERETWDQWWTDYWQV    600
BA_7312AR     ---------V------------------I-------                                     332

                        Reverse Transcriptase \/ RNase H
CONSENSUS-A   TWiPdWDFvSTPPLVRLaFNLVgdPipGaETFYTDGSCNrQSkEGKAgYvTDrGrDkV?vLEqTtNQQAE    685
ROD           -------------------------------------------------------K---KK----------    661
NIHZ          -----------------------E-V-----------------------I------R-K-----------    660
ISY           ----------------------K--------------------------I----K---RI----------    660
ST            --------I---------V----K---L------------K--R------I--------RL----------    680
BEN           ----E------------T-----------------------------------K---K-----------    680
CAM2          ----------------------------T-----------------------------KI----------    659
D194          --V-E------------T----------T---------------------------R-R-----S-----    698
GH1           ----E------------T-----------------------------R----------R---R-------    680
UC2           ----E------------T----------T----------------------------R-----------    680
MDS           ----------------V----K----------------------------K-----K-----------    680
KR            ----------------------K-----E--------------------I--------RI----------    680
S52907        -------------------------------------------------------K---KK----------    478
CONSENSUS-B   TWIPEWDFVSTPPLiRLAYNLVKDPLEgvETYYTDGSCNraSKEGKAGYVTDRGKDKVKvLEQTTNQQAE    670
D205          ----------------------------R-----------T-----------------------------    679
UC1           --------------V------------K-------------------------------------------    681
EHOACG        ----------------------------------------K-------------------P----------    680
CONSENSUS-D   TWIPEWDFVSTPPLVRLVFNLVKEPLEKTETFYVDGSCHRQSKEGKAGYVTDRDREKTKALQQTTNQQAE    491
FORTC2        ---------------------------------------------------------------------    491
CONSENSUS-SD  TWIPeWDF?STPPLVRLVFNLVK?PIqG?ET?YvDgSCn?QS?EGKAGY?TDRG?dKvK?LEQTTNQQAE    647
MM251         --------I--------------D--E-E--Y-T-----K--K------I----K----V----------    681
MM32H         --------I--------------D--K-E--Y-T-----K--K------I----K----V----------    685
MM239         --------I--------------D--E-E--Y-T-----K--K------I----K----V----------    685
MM142         --------I--------------D--E-E--Y------SK--K------I----K----V----------    681
MNE           ----K---I--------------D--K-E--Y-------K--K------I----K----V----------    681
SMMH4         ----D---V--------------E----A--F-------R--R------V----R--A-L----------    644
SMMH9         --------V--------------E----A--F---R---R--R------V----RG-T-L----------    647
SMMPBJ        --------V--------------E----A--F-------R--R------V----R--A-L----------    647
6P6           --------V--------------E----A--F-------R--R------V----R--A-L----------    647
CONSENSUS-STM TWIPEWDFVSTPPLVRLVFNLVKEPLEGTETFYVDGSCNRQSKEGKAGYITDRGKNKVKALEQTTNQQAE    666
STM           ---------------------------------------------------------------------    666
CONSENSUS-SO  ???P????ISTPPLVRLVFNLVK?P?????TFYVDGSCN??SK?GKAGYITDR?R?K?K?LEQTTNQ?AE     52
SMMLIB1       TWI-EW#F---------------E-L#GVE---------RE--V---------G-D-V-A-------K--     70
SMMM7         IRP-#CSR---------------D-IEEIG---------KQ--E---------R-S-I-F-------R--     73
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CONSENSUS-A   LEaFaMaltDSGPKvNIiVDSQYvMGIvagQPtESEsriVNqIIEeMIKKEaiYVAWvPAHKGIGGNQEv   755
ROD           ---------------------------S-S-------K--------------------------------   731
NIHZ          --------------A---------------------N--------------------------------   730
ISY           -------V---------V----------T---A--------K--------------------------I   730
ST            -------V------A----------------------K--------------------------------   750
BEN           --V-R---A---------------------------N---------------V-----------------   750
CAM2          --------------A---------------------N--------------------------------   729
D194          --------A---------------------------N--------D------V-----------------   768
GH1           ------T---------------------V---------------D------V-----------------   750
UC2           --------A--------------------S---------------D------V----I------------   750
MDS           --------------A-------------V-------N--------------------------------   750
KR            --------------A----------------------KL------------TL-----------------   750
FA                                   x----V-------N--------D-----------------------    47
5132P1                               x-------------K-------D------V----------------I    47
S52907        ----------------------------S-------K--------------------------------   548
CONSENSUS-B   LEAFALALqDSgPQVNIIVDSQY?MGI?AgQPTETESPiVnkIIEEMIKKEaiYVGWVPAHkGLGGNQEV   738
D205          --------T--E-----------V---I-A----------A-----------V-----------------   749
UC1           -----------------------V---V----------L--Q-------------------R--------   751
EHOACG        -----------------------V---V-A----------RE---------K------------------   750
JA                                   x---I-------------------------------------------    47
ON                                   x---I-------------------------------------------    47
CONSENSUS-C                          xLGIIAGQPTETESPLVNRIIEELIRKEAVYISWVPAHKGLGGNQEV    47
POLB7                                ----------------------------------------------    47
CONSENSUS-D   LEAFLLALQDSGPKANIIVDSQY??GIVAGQPTESESKLVNQIIEEMIKKEAIYIAWVPAHK?IGGNQEV   558
FORTC2        -----------------------VM-------------------------------------R-------   561
POLC12                               xI-------------------------------------G-------    47
CONSENSUS-SD  LEAF??ALaDSGPKaNIIVDSQYVMGIi?G?PTESESRLVNQIIEeMIKKe?IYVAWVPAHKgIGgNQE?   711
MM251         ----LM--T-----T-------------T-C-------------------SE-----------------I   751
MM32H         ----LM--T-------------------T-C-------------------SE-----------------I   755
MM239         ----LM--T-------------------T-C-------------------SE-----------------I   755
MM142         ----LM--T-------------------T-C-------------------TE-----------------I   751
MNE           ----LM----------------------T-C-------------------TE-----------------I   751
SMMH4         ----YL----------------------A-Q-------------------A-----------------V   714
SMMH9         ----YL----------------------VA-Q--------------K-----A----------x--E---V   717
SMMPBJ        ----YL----------------------VA-Q-------------------A-----------------V   717
6P6           ----YL----------------------VA-Q-------------------A-----------------V   717
CONSENSUS-STM LEAFAMALADSGPKANIVVDSQYVMGIITGQPTESESKLVNQIIEEMIKKEAIYVAWVPAHKGIGGNQEV   736
STM           ------------------------------------------------------------------------   736
CONSENSUS-SO  LEAFLMA??DSG?EANIIVDSQYVMGIV??QPTESE???VNQIIEEMIKKTA?YV??VPAHKG?G?NQE?   108
SMMLIB1       -------MQ---P---------------AG------NNL-------------I--AW------I-G---V   140
SMMM7         -------VT---A---------------TR------SKI-------------V--T$------L-R---I   142
CONSENSUS-B   LEAFALALqDSgPQVNIIVDSQY?MGI?AgQPTETESPiVnkIIEEMIKKEaiYVGWVPAHkGLGGNQEV   738
BA_7312AI                            x---V-------------------------------------------    47
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HIV2/SIV POL

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                 RNase H \/ Integrase
CONSENSUS-A   DHLVSQGIRQVLflEkIEPAQEEHeKYHsn?KEL?HKFgiPqLVARQIVNtCaqcQQKGEAIHGQVnAel    823
ROD           ------------------------------V---S------N--------S-------------------    801
NIHZ          ------------------------------I---S------K-----------HV---------------    800
ISY           ---------------R--------G-----V---A----L-N----------------------------    800
ST            ------------------------------V---S----L-K----------T-----------------    820
BEN           ------------------------------II---T------L--------S------------------I    820
CAM2          ----------------------------T-V---C---D---------------Y--------------V    799
D194          ------------------------------I---T----------------------------------I    838
GH1           ---------------R--------------M---T----------------------------------I    820
UC2           ------------------------------I---I----------------------------------I    820
MDS           ------------------------------V---S----L----------------------------D-    820
KR            ------------------------------V---S----L-K------------------------D---    820
FA            ---------------R--------------I---T----------------------------------I    117
5132P1        ---------------N--------------I---T---A-------------TK----------------    117
S52907        ------------$$                                                           560
CONSENSUS-B   DHLVSQGIRQvLFLEKIEPAQEEHEKYHgNVKELVHKFGipqLVAkQIVNSCDKCQQKGEAvHGQVNaeL    808
D205          ------------------------------------------------------------I------D-    819
UC1           ---------------------------------------L------------------------------    821
EHOACG        ----------I-----------------N----------------R---------------I-----S--    820
JA            ----------------------------------------HS----------------------------    117
ON            ------------------------------------------------------------------------    117
CONSENSUS-C   DHLVSQGIRQVLFLEKIEPAQEEHERFHSNAKELTHKFGIPNLVAKQIVNTCHVCQQKGEAIHGQVNADL    117
POLB7         ------------------------------------------------------------------------    117
CONSENSUS-D   DHLVSQGIRQVLFLEKIEPAQEDHEKYHSNIKELVFKFGLPKLVARQIIDTCDKCHRKGEAIHGQVNAEL    628
FORTC2        ------------------------------------------------------------------------    631
POLC12        ------------------------------------------------------------------------    117
CONSENSUS-SD  DHLVSQgIRQVLFLeKIEPAQEEHeKYHSNvKeLVFKFgLPRlVAkQIVDTCDKCHqKGEaIHGQvNsdL    781
MM251         ------------------------D-----------------I--R------------------------    821
MM32H         ------------------------D-----------------I--R------------------------    825
MM239         ------------------------D-----------------I--R-------------------A----    825
MM142         ------------------------S-----I------------------------------------    821
MNE           ------------------------D------------------------------------------    821
SMMH4         --------------K-----------------------------------------------------AE-    784
SMMH9         ------E-------------------------K-----x-----------------L---x------xx-    787
SMMPBJ        ------------------------------------------------------------------AE-    787
6P6           ------------------------------------------------------------------AE-    787
CONSENSUS-STM DHLVSQGIRQVLFLEKIEPAQEEHEKYHSNVKELVFKFGIPRLVAKQIVDTCDKCHQKGEAIHGQVNAEL    806
STM           ------------------------------------------------------------------------    806
CONSENSUS-SO  DHLVSQ?IRQVLFLEKIEPAQEEHEKYHSN?KELVFK??IPRLVAKQIVDTCDKC?QKGEAIH?QVN?EL    171
SMMLIB1       ------G------------------------I------YG----------------H-------G---A--    210
SMMM7         ------R------------------------V------FR----------------Q-------R---T--    212
CONSENSUS-B   DHLVSQGIRQvLFLEKIEPAQEEHEKYHgNVKELVHKFGipqLVAkQIVNSCDKCQQKGEAvHGQVNaeL    808
BA_7312AI     ------------------------------------------------------------------------    117
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CONSENSUS-A   GtWQMDcTHLeGKiIIVAVHVASGFIEAeVIPQesgRQTALFLLKLASRWPITHLHTDNGaNFTSQEVKM    893
ROD           ------------------------------------------------------------------------    871
NIHZ          -------------V----------------------------------------------------------    870
ISY           ------------------------------------------------------------------------    870
ST            ------------------------------------------------------------------------    890
BEN           -V----Y-------------------------------------------------------P---------    890
CAM2          ------------------------------------------------------------------------    869
D194          -V----------------------------------------------------------P---------    908
GH1           -V----------------------------------------------------------S---------    890
UC2           -V----------------------------------------------------------P---------    890
MDS           -------------V--------------------T-----------------------------------    890
KR            -------------------------------------T----------------------------------    890
FA            -V--------------------------K----K-E------------------------S---------    187
5132P1        -V--------G-----------------------------------------------S---------    187
CONSENSUS-B   GTWQMDCTHLEGKvIIVAVHVASGFIEAEVIPQETGRQTALFLLKLASRWPITHLhTDNGANFTSqdVKM    878
D205          -------------I-----------------------------------------------------PS---    889
UC1           ------------------------------------------------------------------------    891
EHOACG        ------------------------------------------------------------------------    890
JA            ------------------------------------------------------------------------    187
ON            -------------I-----------------------------------------R--------------    187
CONSENSUS-C   GTWQMDCTHLEGKVIIVAVHVASGFIEAEVIPQETGRQTALFLLKLAARWPITHLHTDNGANFTSQEVKM    187
POLB7         ------------------------------------------------------------------------    187
CONSENSUS-D   GTWQMDCTHLEGKV?IVAVHVASGFI?AEVIPQETGRQTALFLLKLASRWPITHLHTDNGANFTSQEVKM    696
FORTC2        --------------T-----------x                                               658
POLC12        --------------I-----------E-----------------------------------------    187
CONSENSUS-SD  GTWQMDCTHLEGKIiIVAVHVaSGFIEAEVIPqETGRQTALFLLKLAsRWPITHLHTDNGANF?SQEVKM    850
MM251         --------------V-------------------------------G---------------A------    891
MM32H         ----------------------------------------------G---V-----------A------    895
MM239         ----------------------------------------------G---------------A------    895
MM142         --------------V-------------------------------------------------A------    891
MNE           ----------------------------------------------------------------A------    891
SMMH4         ----------------------------------------------G---------------T------    854
SMMH9         --------------------G----------x-----------------------------T------    857
SMMPBJ        ----------------------------------------------------------------T------    857
6P6           ----------------------------------------------------------------T------    857
CONSENSUS-STM GTWQMDCTHLEGKIIIVAVHVASGFIEAEVIPQETGRQTALFLLKLASRWPVTHLHTDNGANFTSQEVKM    876
STM           ------------------------------------------------------------------------    876
CONSENSUS-SO  ??WQ?DCTHLEGK??IVAVHVASGFIEAEVIPQETGRQTALFLLKL?SRWPITHLHTDNGANF?SQEVKM    234
SMMLIB1       GT--M--------II------------------------------V----------------T------    280
SMMM7         RI--I--------VV------------------------------A----------------A------    282
CONSENSUS-B   GTWQMDCTHLEGKvIIVAVHVASGFIEAEVIPQETGRQTALFLLKLASRWPITHLhTDNGANFTSqdVKM    878
BA_7312AI     ------------------------------------------------------------------------    187
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HIV2/SIV POL

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CONSENSUS-A   VAWWiGIEQsFGVPYNPQSQGVVEAMNHHLKNQIsrIReQANT?ETIVLmAvHCMNFKRRGGIGDMTPaE    962
ROD           ----------------------------------------I-------I----------------S-    941
NIHZ          ----V----T------------------------D--------V-----------------------    940
ISY           ----V----------------------------E--------M------------------------V-    940
ST            ------------------------------------------V--------------------------    960
BEN           ----V-------------------------------------I--------------------------    960
CAM2          ----V----T--------------------------------V-----------------------S-    939
D194          ------------------------------------------I--------------------------    978
GH1           ------------------------------------------I--------------------------    960
UC2           ----V-------------------------------------V--------------------------    960
MDS           --------------------------------------D----V------------------------S-    960
KR            ----T-----------------------------------M--------------------------    960
FA            ---------T---------------------------------I-----x                      237
5132P1        -----------------------------------K-------I-----x                      237
CONSENSUS-B   vAWWvGIEqTFGVPYNPqSQGVVEAMNHHLKNQIDRiRDQAVSiETVVL?AtHCMNFKRRGGIGDMTPAE    947
D205          -------------------------------------L------------M--------------------    959
UC1           A---I-------------------------------------------M-A------------------    961
EHOACG        A---I------------E------------------------------M--------------------    960
JA            --------R-------------------------------------x                          237
ON            ------------------------------------------L-----x                          237
CONSENSUS-C   VAWWVGVEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANTMETIVLx                          237
POLB7         ---------------------------------------------------                        237
CONSENSUS-D   VAWWVGIEQTFGVPYNPQSQGVVEAMNHHLKNQIDKIRDQANSVETIVLx                          746
POLC12        ---------------------------------------------------                        237
CONSENSUS-SD  VAWWAgIE?TFgVPYNPQSQgVVEAMNHHLK?QIDRIREQANSietIVLMAvHCmNFKRRGGIGDMTPAE    918
MM251         --------H----------------------N-----------V--------------------------    961
MM32H         --------H----------------------N-----------V--------------------------    965
MM239         --------H----------------------N-----------V--------------------------    965
MM142         --------H----------------------N-----------V--------------------------    961
MNE           --------H----------------------N-----------M--------------------------    961
SMMH4         --------Q----------------------T--------------------------------------    924
SMMH9         -----x--Q--x--------x----------T-------------------I--I---------------    927
SMMPBJ        --------Q----------------------T--------------------------------------    927
6P6           --------Q----------------------T------------VS------------------------    927
CONSENSUS-STM VAWWAGIEQTFGVPYNPQSQGVVEAMNHHLKTQIDRIRDQANTVETVVLMAVHCMNFKKRGGLGDMTPAE    946
STM           ------------------------------------------------------------------------    946
CONSENSUS-SO  VA?WA?IE?TF?VPYNPQSQ?VVEAMNHHLK?QI??IR?QANS?ETIVLMA?HCMNFKRRGGIGDMTPAE    293
SMMLIB1       --W--N--Q--G--------G----------T--DK--D----I-------T------------------    350
SMMM7         --$--D--H--K--------R----------N--ER--E----V-------V------------------    351
CONSENSUS-B   vAWWvGIEqTFGVPYNPqSQGVVEAMNHHLKNQIDRiRDQAVSiETVVL?AtHCMNFKRRGGIGDMTPAE    947
BA_7312AI     ---------------------------------------------------x                        237

CONSENSUS-A   RliNMiTtEQEIQFLqaKNSklknFrVYfREGRdQLWkGPGELLWKGdGAViVKVGtdIKvvPRRKAKII   1032
ROD           -----------------------D-----------------------E---L---------II--------   1011
NIHZ          -I-------------------------------------------------------E-------------   1010
ISY           --V------------------------------N---Q-----------------------I--------   1010
ST            -----V-A--------------Q--------------------------------A---II--------   1030
BEN           ----------------R---NF---Q--Y------------------E----------------------   1030
CAM2          ------------------------------------------------------------II--------   1009
D194          ----------------R---NF-K-Q--Y---------------------------A-------------   1048
GH1           ----------------R---NF---Q--Y---------------------------A----I--------   1030
UC2           ----------------R---NF-K-Q--Y------------------E--------A-------------   1030
MDS           ------------------------------------------------------------I---------   1030
KR            ---------------H-------------------------------------------I---------   1030
CONSENSUS-B   RlVNMITTEQEIQFfQaKNLKFQNFqVYYREGRDQLWKGPGeLLWKGEGAViIKVGTEIKViPRRKAKII   1017
D205          ------------------------------------------------------------V--------   1029
UC1           ---------------------------------------------------L------------------   1031
EHOACG        -I------------L-T--------R---------------D----------------------------   1030
CONSENSUS-SD  RLvNMITTEQEIQFQQSKNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAViLKVGT?IKVVPRRKAKII    987
MM251         --I-------------------------------------------------------D------------   1031
MM32H         --I-------------------------------------------------------D------------   1035
MM239         --I-------------------------------------------------------D------------   1035
MM142         --I-------------------------------------------------------D------------   1031
MNE           --L---------------------------------------------V-----D------------   1031
SMMH4         ------------------------------------------------------------E------------    994
SMMH9         ------------------------------------------------------------E------------    997
SMMPBJ        ------------------------------------------------------------E------------    997
6P6           ------------------------------------------------------------E------------    997
CONSENSUS-STM RLVNMITTEQEIQFQQSKNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVIVKVGTDIKVVPRRKAKII   1016
STM           ------------------------------------------------------------------------   1016
CONSENSUS-SO  RL?NMITTEQEIQFQQSKNSKFKNFRVY?REGRDQLWKGPGELL?KGEGA                          340
SMMLIB1       --V-------------------------Y---------------x                              395
SMMM7         --I-------------------------F---------------W-----                          401
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                              Integrase \
CONSENSUS-A   rDYGgRqe?DS?shLEGaRE?dGEvA?PCQVPEIQNKRPRGGALCSPPQGGMGMVDLQQGNIPTTRKKSS   1098
ROD           --------M--G--------.---M-                                                1036
NIHZ          K-------M--G--------.---M-                                                1035
ISY           ----P---M--G--------.---M-                                                1035
ST            K-------M--G-N------.-----                                                1055
BEN           --------L--SP-------.---M-C-------------------------------------------    1099
CAM2          --------L--S--------.N----                                                1034
D194          --------L--S--------.-----                                                1073
GH1           --------L--.--------E-----                                                1055
UC2           --------L--SP-------.-----$                                               1055
MDS           -------DM--GP----T--.-----$                                               1055
KR            ------R-V--S-----T--.-----$                                               1055
CONSENSUS-B   RhYGGGKeLDCsaDmEDTrQ.AREmAQS??VPEA                                        1048
D205          -------G------------.-------D                                             1057
UC1           -----------GT-------.-------GQ----                                        1064
EHOACG        -N------------V---M-.---V---N$                                            1058
CONSENSUS-SD  KDYGGGKElDS?SH?EDTGE.AREVA$                                               1010
MM251         --------V--S--M-----.-----                                                1056
MM32H         --------V--S--M-----.-----                                                1060
MM239         --------V--S--M-----.-----                                                1060
MM142         --------M--S--M-----.-----                                                1056
MNE           --------V--S--M-----.-----                                                1056
SMMH4         -----------G--L-----.-----                                                1019
SMMH9         -----------G--L-----.-----                                                1022
SMMPBJ        -----------G--L-----.-----                                                1022
6P6           -----------G--L-----.------                                               1022
CONSENSUS-STM KDYGGGKEVDSGSHLEDTRE.AGEVA                                                1041
STM           --------------------.-----                                                1041
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