

II

HIV-1/SIVcpz Complete Genomes

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Alignment of HIV-1/SIVcpz Genomes

The goal in selecting which sequences to include in the published Compendium alignment was to display, in the limited space of two pages per alignment section, a representation of the genetic variability of the HIV-1 world. The basis for this was phylogenetic trees and the removal of known duplicates and close clone sequences from the same isolates or patients, thereby creating a non-redundant set. Some effort was also put into representing geographic diversity and sampling times of each subtype. This year we have included more sequences from the more important subtypes, only one representative for each CRF (except more from CRF01 and CRF02), a few U's and URF's as well as more group N and O and CPZ sequences than last year. For URF's especially, however, there are many more variants of HIV-1 reported.

The HXB2 sequence was chosen as master sequence in this alignment. This is also the HIV Database genome coordinate standard sequence. The alignment was generated by an iterative process between automated alignment using HMMER and manual editing using MASE, BioEdit and Se-AL. As in previous years, the alignment presented is not suggested to be an "optimal alignment" with the absolute minimum number of gaps and mismatches. It is a compromise between optimal alignment, readability, and an attempt to keep insertions and deletions from altering the protein reading frame presentation. Most gaps have been introduced in multiples of 3 bases to maintain open reading frames when translated directly from the alignment.

At the bottom of the alignment, the HXB2 protein sequences are displayed; the HIV genome has many overlapping coding regions, and all are shown. For more complete annotation of functional domains, see the protein sequence alignments in Part IV.

Features of HIV-1 annotated in the alignment that follows.

DNA	Page	Protein
5' LTR U3 start	180	
TCF-1 α	184	
NF-kB-I, II	186	
Spl, II, III	186	
TATA Box	186	
5' LTR U3 end, R repeat begins	188	
mRNA start site	188	
TAR element	188	
Poly-A signal	188	
5' LTR repeat end, U5 start	188	
5' LTR U5 end	190	
Lys tRNA primer binding site	190	
Gag binding loops	192	
Packaging signal	192	
End packaging loops	194	
	194	Gag-Pol start
	202	p17 end, p24 start
	214	p24 end, p2 start
	214	p2 end, p7 (NC) start
	214	Gag-Pol TF start
	218	p7 end, p1 start
ribosome slip site	218	
	218	p1 end, p6 start
	222	gag-pol TF end, pol protease start
	222	Gag end
	222	Pol protease start
	228	protease end, p66/p51 RT start
	248	p51 RT end, p15 RNase H start
	252	p15 RNaseH end, p31 integrase start
	266	Vif start
	266	Pol end
	274	Vpr start
	274	Vif end
	278	Tat ex1 start
	278	Vpr end
	280	Rev ex1 start
	282	Tat ex1 end, Rev ex1 end
	282	Vpu start
	286	Env signal peptide start
	288	Vpu end, gp120 Env start
	302	V3 loop start, V3 tip
	304	V3 loop end
Rev resp. element start, Stem I	314	
	314	gp120 end, gp41 start
Stem IIA, IIIB, IIB', IIC, IIC', IIA', III-IV	316	
Stem III-IV', V, V', I'	318	
Stem I', Rev resp. element end	320	
	326	Tat ex2 start, Rev ex2 start
	326	Tat ex2 end
	330	Subtype C Rev ex2 end
	330	Rev ex2 end
	332	Env gp41, gp160 end
	332	Nef start
3' LTR U3 start	338	
TCF-1 α binding	344	
	344	Nef end
NF-k-BII	346	
NF-k-BI, SPI-III	346	
SP-II, SP-1	348	
TATA box	348	
poly-A signal	350	
3' LTR U3 end V repeat start	350	
3' LTR repeat end V 3' LTR U5 start	350	
3' LTR U5 end	352	

Table 1. Table of sequences included in the HIV-1/SIVcpz complete genome alignments.

Name	Accession	Country	Author	Reference
A.SN.01.DDI579	AY521629	Senegal	Meloni, ST	<i>J Virol</i> 78 (22):12438–12445 (2004)
A.SN.01.DDJ369	AY521631	Senegal	Meloni, ST	<i>J Virol</i> 78 (22):12438–12445 (2004)
A.SN.96.DDJ360	AY521630	Senegal	Meloni, ST	<i>J Virol</i> 78 (22):12438–12445 (2004)
A.ZA.04.04ZASK162B1	DQ396400	S. Africa	McKay, AR	<i>J Virol Methods</i> 136 (1-2):118–25 (2006)
A1.KE.94.Q23_17	AF004885	Kenya	Poss, M	<i>J Virol</i> 72 (10):8240–51 (1998)
A1.RU.03.03RU20_06_13	AY500393	Russia	Papuashvili, MN	<i>Infect Genet Evol</i> 5 (1):45–53 (2005)
A1.RW.93.93RW037A	AB287379	Rwanda	Tatsumi, M	Unpublished
A1.SE.94.SE7253	AF069670	Sweden	Laukkanen, T	<i>AIDS</i> 13 (14):1819–26 (1999)
A1.TZ.01.A173	AY253305	Tanzania	Herbinger, K-H	<i>ARHR</i> 20 (8):895–901 (2004)
A1.UA.00.98UA0116	AF413987	Ukraine	Masharsky, AE	<i>ARHR</i> 19 (10):933–9 (2003)
A1.UG.92.92UG037	U51190	Uganda	Gao, F	<i>J Virol</i> 70 (3):1651–67 (1996)
A1.UG.98.98UG57136	AF484509	Uganda	Harris, ME	<i>ARHR</i> 18 (17):1281–90 (2002)
A2.CD.97.97CDKFE4	AF286240	D.R.C.	Gao, F	<i>ARHR</i> 17 (8):675–88 (2001)
A2.CD.97.97CDKS10	AF286241	D.R.C.	Gao, F	<i>ARHR</i> 17 (8):675–88 (2001)
A2.CD.97.97CDKTB48	AF286238	D.R.C.	Gao, F	<i>ARHR</i> 17 (8):675–88 (2001)
A2.CY.94.94CY017_41	AF286237	Cyprus	Gao, F	<i>ARHR</i> 17 (8):675–88 (2001)
B.AR.00.ARMS008	AY037269	Argentina	Carr, JK	<i>AIDS</i> 15 (15): F41–7 (2001)
B.AU.96.MBCD36	AF042105	Australia	Oelrichs, RB	<i>ARHR</i> 14 (9):811–4 (1998)
B.CO.01.PCM074	AY561240	Colombia		
B.FR.83.HXB2	K03455	France	Wong-Staal, F	<i>Nature</i> 313 (6000):277–84 (1985)
B.GA.88.OYI	M26727	Gabon	Huet, T	<i>AIDS</i> 3 (11):707–15 (1989)
B.NL.00.671_00T36	AY423387	Netherlands	Geels, MJ	<i>J Virol</i> 77 (23):12430–12440 (2003)
B.RU.04.04RU129005	AY751406	Russia		
B.TH.90.BK132	AY173951	Thailand	Hierholzer, J	<i>ARHR</i> 18 (18):1339–1350 (2002)
B.US.90.WEAU160	U21135	U.S.A.	Tozser, J	<i>FEBS Lett</i> 281 (1-2): 77–80 (1991)
B.US.98.1058_11	AY331295	U.S.A.	Bernardin, F	<i>J Virol</i> 79 (17):11523–8 (2005)
C.AR.01.ARG4006	AY563170	Argentina	Aguayo, N	<i>ARHR</i> 20 (9):1022–5 (2004)
C.BR.92.BR025-d	U52953	Brazil	Gao, F	<i>J Virol</i> 70 (3):1651–1667 (1996)
C.BR.04.04BR013	AY727522	Brazil	Sanabani, SS	<i>ARHR</i> 22 (2):171–6 (2006)
C.BW.00.00BW07621	AF443088	Botswana	Novitsky, VA	<i>J Virol</i> 76 (11):5435–51 (2002)
C.ET.86.ETH2220	U46016	Ethiopia	Salminen, MO	<i>ARHR</i> 12 (14):1329–39 (1996)
C.IN.95.95IN21068	AF067155	India	Lole, KS	<i>J Virol</i> 73 (1):152–60 (1999)
C.IN.99.01IN565_10	AY049708	India	Khurana, S	Unpublished
C.KE.00.KER2010	AF457054	Kenya	Dowling, WE	<i>AIDS</i> 16 (13):1809–20 (2002)
C.TZ.01.BD9_11	AY253322	Tanzania	Herbinger, K-H	<i>ARHR</i> 20 (8):895–901 (2004)
C.UY.01.TRA3011	AY563169	Uruguay	Aguayo, N	<i>ARHR</i> 20 (9):1022–5 (2004)
C.ZA.04.SK164B1	AY772699	S. Africa	Kiepiela, P	<i>Nature</i> 432 (7018):769–775 (2004)
C.ZA.05.05ZASK245B1	DQ369982	S. Africa	McKay, AR	<i>J Virol Methods</i> 136 (1-2):118–25 (2006)
C.ZM.02.02ZM115	AB254148	Zambia	Tatsumi, M	Unpublished
C.ZM.96.96ZM651	AF286224	Zambia	Rodenburg, CM	<i>ARHR</i> 17 (2):161–8 (2001)
D.CD.83.ELI	K03454	D.R.C.	Alizon, M	<i>Cell</i> 46 (1):63–74 (1986)
D.CD.83.NDK	M27323	D.R.C.	Spire, B	<i>Gene</i> 81 (2):275–84 (1989)
D.CM.01.01CM_4412HAL	AY371157	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
D.KE.01.NKU3006	AF457090	Kenya	Dowling, WE	<i>AIDS</i> 16 (13):1809–20 (2002)
D.TD.99.MN012	AJ488927	Chad	Vidal, N	<i>JAIDS</i> 33 (2):239–46 (2003)
D.TZ.01.A280	AY253311	Tanzania	Herbinger, K-H	<i>ARHR</i> 20 (8):895–901 (2004)
D.UG.94.94UG114	U88824	Uganda	Gao, F	<i>J Virol</i> 72 (7):5680–98 (1998)

D.UG.99.99UGD23550	AF484485	Uganda	Harris, ME	<i>ARHR</i> 18 (17):1281–90 (2002)
D.UG.99.99UGK09958	AF484499	Uganda	Harris, ME	<i>ARHR</i> 18 (17):1281–90 (2002)
D.ZA.86.R482	AY773341	S. Africa		
F1.BE.93.VI850	AF077336	Belgium	Laukkanen, T	<i>Virology</i> 269 (1):95–104 (2000)
F1.BR.89.BZ126	AY173957	Brazil	Hierholzer, J	<i>ARHR</i> 18 (18):1339–1350 (2002)
F1.BR.93.93BR020_1	AF005494	Brazil	Gao, F	<i>J Virol</i> 72 (7):5680–98 (1998)
F1.FI.93.FIN9363	AF075703	Finland	Laukkanen, T	<i>Virology</i> 269 (1):95–104 (2000)
F1.FR.96.MP411	AJ249238	France	Peeters, M	<i>ARHR</i> 16 (2):139–51 (2000)
F2.CM.02.02CM_0016BBY	AY371158	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
F2.CM.95.MP255	AJ249236	Cameroon	Peeters, M	<i>ARHR</i> 16 (2):139–51 (2000)
F2.CM.95.MP257	AJ249237	Cameroon	Peeters, M	<i>ARHR</i> 16 (2):139–51 (2000)
F2.CM.97.CM53657	AF377956	Cameroon	Carr, JK	<i>Virology</i> 286 (1):168–81 (2001)
G.BE.96.DRCBL	AF084936	Belgium	Debyser, Z	<i>ARHR</i> 14 (5):453–9 (1998)
G.CM.01.01CM_4049HAN	AY371121	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
G.ES.99.X138	AF450098	Spain	Delgado, E	<i>JAIDS</i> 29 (5):536–43 (2002)
G.KE.93.HH8793_12_1	AF061641	Kenya	Salminen, MO	<i>ARHR</i> 8 (9):1733–42 (1992)
G.NG.92.92NG083	U88826	Nigeria	Gao, F	<i>J Virol</i> 72 (7):5680–98 (1998)
G.SE.93.SE6165	AF061642	Sweden	Laukkanen, T	<i>Virology</i> 247 (1):22–31 (1998)
H.BE.93.VI991	AF190127	Belgium	Janssens, W	<i>AIDS</i> 14 (11):1533–43 (2000)
H.BE.93.VI997	AF190128	Belgium	Janssens, W	<i>AIDS</i> 14 (11):1533–43 (2000)
H.CF.90.056	AF005496	C.A.R.	Murphy, E	<i>ARHR</i> 9 (10):997–1006 (1993)
J.SE.93.SE7887	AF082394	Sweden	Laukkanen, T	<i>ARHR</i> 15 (3):293–7 (1999)
J.SE.94.SE7022	AF082395	Sweden	Laukkanen, T	<i>ARHR</i> 15 (3):293–7 (1999)
K.CD.97.EQTB11C	AJ249235	D.R.C.	Peeters, M	<i>ARHR</i> 16 (2):139–51 (2000)
K.CM.96.MP535	AJ249239	Cameroon	Peeters, M	<i>ARHR</i> 16 (2):139–51 (2000)
U.CD.83.83CD003	AF286236	D.R.C.	Gao, F	<i>ARHR</i> 17 (12):1217–22 (2001)
U.CD.90.90CD121E12	AF457101	D.R.C.	Mokili, JLK	<i>ARHR</i> 18 (11):817–23 (2002)
U.GR.99.GR303	AY046058	Greece	Paraskevis, D	<i>J Gen Virol</i> 82 (10):2509–14 (2001)
U.NL.x.U_NL_95_H10986_D1	EF029066	Netherlands	van der Hoek, L	Unpublished
01_AE.CF.90.90CF402	U51188	C.A.R.	Gao, F	<i>J Virol</i> 70 (10):7013–29 (1996)
01_AE.CN.05.FJ051	DQ859178	China	Yan, Y	<i>Chin Med J(Engl)</i> 119 (19):1622–8 (2006)
01_AE.HK.x.HK001	DQ234790	Hong Kong		
01_AE.JP.93.93JP_NH1	AB052995	Japan	Sato, H	<i>J Virol</i> 75 (12):5604–13 (2001)
01_AE.TH.01.OUR414I	AY358050	Thailand	Tovanabuttra, S	<i>ARHR</i> 20 (5):465–75 (2004)
01_AE.TH.02.OUR769I	AY358062	Thailand	Tovanabuttra, S	<i>ARHR</i> 20 (5):465–75 (2004)
01_AE.TH.90.CM240	U54771	Thailand	Laukkanen, T	<i>J Virol</i> 70 (9):5935–43 (1996)
02_AG.CM.02.02CM_1669LE	AY371139	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
02_AG.EC.x.ECU41	AY151001	Ecuador	Carrion, G	<i>ARHR</i> 19 (4):329–32 (2003)
02_AG.FR.91.DJ264	AF063224	France	Laukkanen, T	<i>Virology</i> 247 (1):22–31 (1998)
02_AG.GH.03.GHNJ196	AB231898	Ghana	Tatsumi, M	Unpublished
02_AG.NG.x.IBNG	L39106	Nigeria	Howard, TM	<i>ARHR</i> 10 (12):1755–7 (1994)
02_AG.SN.98.MP1211	AJ251056	Senegal	Toure-Kane, C	<i>ARHR</i> 16 (6):603–9 (2000)
02_AG.UZ.02.02UZ693	AY829204	Uzbekistan	Carr, JK	<i>JAIDS</i> 39 (5):570–5 (2005)
03_AB.RU.97.KAL153_2	AF193276	Russia	Liitsola, K	<i>AIDS</i> 12 (14):1907–19 (1998)
04_cpx.CY.94.CY032	AF049337	Cyprus	Gao, F	<i>J Virol</i> 72 (12):10234–41 (1998)
05_DF.BE.x.VI1310	AF193253	Belgium	Laukkanen, T	<i>Virology</i> 269 (1):95–104 (2000)
06_cpx.AU.96.BFP90	AF064699	Australia	Oelrichs, RB	<i>ARHR</i> 14 (16):1495–500 (1998)
0708.CN.00.HH069	AP005206	China	Yang, R	<i>J Virol</i> 77 (1):685–695 (2003)
07_BC.CN.97.CN54	AX149771	China	Shao, Y	Patent: WO 0136614-A125
08_BC.CN.97.97CNGX_6F	AY008715	China	Piyasirisilp, S	<i>J Virol</i> 74 (23):11286–95 (2000)
09_cpx.GH.96.96GH2911	AY093605	Ghana	McCutchan, FE	<i>ARHR</i> 20 (8):819–26 (2004)
10_CD.TZ.96.96TZ_BF061	AF289548	Tanzania	Koulinka, IN	<i>ARHR</i> 17 (5):423–31 (2001)

11_cpx.GR.x.GR17	AF179368	Greece	Paraskevis, D	<i>ARHR</i> 16 (9):845–55 (2000)
12_BF.AR.99.ARMA159	AF385936	Argentina	Carr, JK	<i>AIDS</i> 15 (15): F41-7 (2001)
13_cpx.CM.96.1849	AF460972	Cameroon	Wilbe, K	<i>ARHR</i> 18 (12):849–856 (2002)
14_BG.ES.99.X397	AF423756	Spain	Delgado, E	<i>JAIDS</i> 29 (5):536–43 (2002)
15_01B.TH.99.99TH_MU2079	AF516184	Thailand	Viputtijul, K	<i>ARHR</i> 18 (16):1235–7 (2002)
16_A2D.KR.97.97KR004	AF286239	Korea	Gao, F	<i>ARHR</i> 17 (8):675–88 (2001)
18_cpx.CU.99.CU76	AY586540	Cuba	Thomson, M	<i>AIDS</i> 19 (11):1155–63 (2005)
19_cpx.CU.99.CU7	AY894994	Cuba	Thomson, M	<i>JAIDS</i> 40 (5):532–7 (2005)
20_BG.CU.03.CB134	DQ020274	Cuba	Perez, L	<i>ARHR</i> 22 (8):724–33 (2006)
21_A2D.KE.91.KNH1254	AY945737	Kenya	Visawapoka, U	<i>ARHR</i> 22 (7):695–702 (2006)
23_BG.CU.03.CB118	AY900571	Cuba	Perez, L	<i>ARHR</i> 22 (8):724–33 (2006)
24_BG.CU.03.CB378	AY900574	Cuba	Perez, L	<i>ARHR</i> 22 (8):724–33 (2006)
25_cpx.CM.01.101BA	DQ826726	Cameroon	Carr, JK	Unpublished
28_BF.BR.99.BREPM12609	DQ085873	Brazil	De Sa Filho, DJ	<i>ARHR</i> 22 (1):1–13 (2006)
29_BF.BR.02.BREPM119	AY771590	Brazil	Sa Filho, DJd	<i>ARHR</i> 21 (2):145–51 (2005)
31_BC.BR.02.110PA	EF091932	Brazil	Santos, AF	<i>AIDS</i> 20 (16):2011–9 (2006)
33_01B.MY.05.05MYKL007_1	DQ366659	Malaysia	Tee, KK	<i>JAIDS</i> 43 (5):523–529 (2006)
A1C.TZ.02.CO3710	AY734553	Tanzania	Arroyo, MA	<i>AIDS</i> 19 (14):1517–1524 (2005)
A1CDGKU.ZA.99.CM4	AF411964	S. Africa	Papathanasopoulos, M	<i>ARHR</i> 18 (12):879–886 (2002)
A1DHK.NO.97.97NOGIL3	AJ237565	Norway	Jonassen, TO	<i>ARHR</i> 16 (1):49–58 (2000)
A1GHU.GA.x.VI354	AF076474	Gabon	Laukkanen, T	Unpublished
A2D.KE.99.KER2003	AF457051	Kenya	Dowling, WE	<i>AIDS</i> 16 (13):1809–20 (2002)
AF2.CM.02.02CM_3163MN	AY371160	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
AGU.CM.01.01CM_0989MO	AY371166	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
AHJU.CM.01.01CM_1296NG	AY371162	Cameroon	Kijak, GH	<i>ARHR</i> 20 (5):521–30 (2004)
BC.CN.96.YNRL9607	AY967804	China	Qiu, Z	<i>ARHR</i> 21 (12):1051–6 (2005)
BC.MM.99.mIDU103	AB097873	Myanmar	Takebe, Y	<i>AIDS</i> 17 (14):2077–2087 (2003)
BF1.BR.02.02BR006	DQ358807	Brazil	Sanabani, S	<i>Infect Genet Evol</i> 6 (5):368–377 (2006)
O.BE.87.ANT70	L20587	Belgium	Vanden Haesevelde, M	<i>J Virol</i> 68 (3):1586–96 (1994)
O.CM.91.MVP5180	L20571	Cameroon	Gurtler, LG	<i>J Virol</i> 68 (3):1581–5 (1994)
O.CM.96.96CMABB637	AY169810	Cameroon	Yamaguchi, J	<i>ARHR</i> 19 (11):979–88 (2003)
O.SN.99.SEMP1300	AJ302647	Senegal	Vergne, L	<i>J Clin Microbiol</i> 38 (11):3919–25 (2000)
N.CM.02.DJO0131	AY532635	Cameroon	Bodelle, P	<i>ARHR</i> 20 (8):902–908 (2004)
N.CM.04.04CM_1015_04	DQ017382	Cameroon	Yamaguchi, J	<i>ARHR</i> 22 (1):83–92 (2006)
N.CM.04.04CM_1131_03	DQ017383	Cameroon	Yamaguchi, J	<i>ARHR</i> 22 (1):83–92 (2006)
N.CM.95.YBF30	AJ006022	Cameroon	Simon, F	<i>Nat Med</i> 4 (9):1032–7 (1998)
N.CM.97.YBF106	AJ271370	Cameroon	Ayouba, A	<i>AIDS</i> 14 (16):2623–5 (2000)
CPZ.CD.90.ANT	U42720	D.R.C.	Vanden Haesevelde, M	<i>Virology</i> 221 (2):346–50 (1996)
CPZ.CM.01.SIVcpzCAM13	AY169968	Cameroon	Nerrienet, E	<i>J Virol</i> 79 (2):1312–9 (2005)
CPZ.GA.88.GAB1	X52154	Gabon	Huet, T	<i>Nature</i> 345 (6273):356–9 (1990)
CPZ.US.85.CPZUS	AF103818	U.S.A.	Gao, F	<i>Nature</i> 397 (6718):436–41 (1999)
CPZ.CM.05.SIVcpzMB66	DQ373063	Cameroon	Keele, BF	<i>Science</i> 313 (5786):523–6 (2006)
CPZ.CM.05.SIVcpzLB7	DQ373064	Cameroon	Keele, BF	<i>Science</i> 313 (5786):523–6 (2006)
CPZ.CM.05.SIVcpzEK505	DQ373065	Cameroon	Keele, BF	<i>Science</i> 313 (5786):523–6 (2006)
CPZ.CM.05.SIVcpzMT145	DQ373066	Cameroon	Keele, BF	<i>Science</i> 313 (5786):523–6 (2006)
CPZ.TZ.01.TANI	AF447763	Tanzania	Santiago, ML	<i>J Virol</i> 77 (3):2233–2242 (2003)

Table 2. Notes on full-length HIV-1/SIVcpz complete genomes that appear in the alignment

Name	Accession	Country	Author	Reference
A1.KE.94.Q23_17	AF004885	Kenya	Poss, M	<i>J Virol</i> 72 (10):8240–51 (1998) This subtype A sequence was derived from a woman from Mombasa, Kenya, who had been recently infected with HIV-1. The blood sample was drawn in June 1994. An env gene fragment from a PCR amplification from an earlier blood sample (July 1993) was published in Poss, M., et al. (<i>ARHR</i> 13(6):493-499(1997)). Many env sequences from this same patient are available with accession numbers AF004893 and AF047979-AF048346. Sequence record updated in GenBank; revision updated in HIV database Jan 2006.
A1.RU.03.03RU200613	AY500393	Russia	Papuashvili, MN	<i>Infect Genet Evol</i> 5 (1):45–53 (2005) Sequence described by Papuashvili et al. 2005 as a typical East European subtype A1 sequence.
A1.RW.93.93RW037A	AB287379	Rwanda	Tatsumi, M	Unpublished Subtype A1 sequence from Rwanda.
A1.SE.94.SE7253	AF069670	Sweden	Laukkanen, T	<i>AIDS</i> 13 (14):1819–26 (1999) This subtype A sequence is from a 27-year-old male living in Sweden, who is thought to have been infected in Somalia via heterosexual contact. The patient was CDC stage C3 when sampled in 1994. The virus is NSI and uses the CCR5 coreceptor. The patient's CD4 count was zero. Virus was cocultured with donor PBMC before PCR amplification and direct sequencing. Genome sequence lacks part of non-coding regions.
A1.TZ.01.A173	AY253305	Tanzania	Herbinger, K-H	<i>ARHR</i> 20 (8):895–901 (2004) This sequence comes from a HIV-1-positive blood bank unit collected between October 2000 and August 2001 from Mbeya, Tanzania.
A1.UA.00.98UA0116	AF413987	Ukraine	Masharsky, AE	<i>ARHR</i> 19 (10):933–9 (2003) This sequence was derived from a 28-year-old woman from Kiev, Ukraine. She was found to be seropositive in 1998 and was presumed to be infected parenterally as an intravenous drug user. The blood sample was obtained in 2000 as a part of large-scale molecular epidemiological survey in the former Soviet countries of Ukraine, Belarus and Russia. All samples in this survey were serotyped using gp120 V3 mimicking peptides, and selected ones were genotyped by sequencing V3-V5 env and p17/p24 gag regions. According to these tests, isolate 98UA0116 belonged to subtype A, which was one of two prevalent HIV-1 variants among IDUs in the former Soviet Union. The full-length genome of this isolate was obtained by amplifying 8 overlapping subgenomic fragments from PBMC DNA using nested PCR. This is the second cloned and sequenced full-length genome of subtype A HIV-1 isolate from the former Soviet Union after isolate 97BL006 (GenBank accession# AF193275).
A1.UG.92.92UG037	U51190	Uganda	Gao, F	<i>J Virol</i> 70 (3):1651–67 (1996) This subtype A sequence is from a complete genome PCR amplified from proviral DNA. The patient was a 31-year-old ARV-naive asymptomatic female from Entebbe, Uganda. The risk factor for infection was heterosexual contact. 92UG037 is one of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. The isolate 92UG037 was established and propagated by short term cocultivation with normal donor lymphocytes; the near full length genome was PCR amplified and sequenced. There is an in-frame stop codon in pol at position 3144 in this clone. The isolate from which this sequence was derived is non-syncytium-inducing (NSI) and uses CCR5 or CCR8 (Bjorndal, A. et al., <i>J Virol</i> 71:7478 (1997) and Rucker, J., et. al., <i>J Virol</i> 71: 8999-9007 (1997). See also: Gao F. et al., <i>J Virol</i> 70: 7013-7029 (1996). The isolate 93UG037 is available from the NIH AIDS Reagent program.
A1.UG.98.98UG57136	AF484509	Uganda	Harris, ME	<i>ARHR</i> 18 (17):1281–90 (2002) One of a set of complete genomes from 46 patients from Uganda. These sequences are from volunteers from Rakai district, 37 of whom are enrolled in cohort studies; they were referred by an AIDS surveillance program or an STD clinic. Another nine sequences were obtained from anonymous discard samples. Of the set, more than half were subtype D; 15% were subtype A; and a quarter were AD recombinants with unique mosaic patterns. A few AC and CD recombinants were also found.

- A2.CD.97.97CDKFE4 AF286240 Congo Gao, F *ARHR* **17**(8):675–88 (2001)
This sequence was obtained from an asymptomatic pregnant woman from Kinshasa, DRC, as part of a molecular epidemiological survey conducted in April 1997. The sequence was derived from uncultured PBMCs.
- A2.CD.97.97CDKS10 AF286241 Congo Gao, F *ARHR* **17**(8):675–88 (2001)
This sample was obtained during a molecular epidemiological study survey in Kinshasa, DRC, in April 1997.
- A2.CD.97.97CDKTB48 AF286238 Congo Gao, F *ARHR* **17**(8):675–88 (2001)
This sample was obtained during a molecular epidemiological study survey in Kinshasa, DRC, in April 1997. This sequence is from a primary culture of virus obtained from a patient suffering from tuberculosis.
- A2.CY.94.94CY017_41 AF286237 Cyprus Gao, F *ARHR* **17**(8):675–88 (2001)
This sequence was obtained from a 35 year old female AIDS patient from Nicosia, Cyprus (HO17). Her husband and child and the husband's sexual partner were also infected with this strain, which may have originated in the UK. The sequence is from a primary isolate.
- A.SN.01.DDI579 AY521629 Senegal Meloni, ST *J Virol* **78**(22):12438–12445 (2004)
Nearly full length genome defined by Meloni et al. 2004 as sub-subtype A3. Sample derived from female sex worker who seroconverted in 1994.
- A.SN.01.DDJ369 AY521631 Senegal Meloni, ST *J Virol* **78**(22):12438–12445 (2004)
Nearly full length genome defined by Meloni et al. 2004 as sub-subtype A3. Sample derived from female sex worker who seroconverted in 2001.
- A.SN.96.DDJ360 AY521630 Senegal Meloni, ST *J Virol* **78**(22):12438–12445 (2004)
Nearly full length genome defined by Meloni et al. 2004 as sub-subtype A3. Sample derived from female sex worker who seroconverted in 1991.
- A.ZA.04.04ZASK162B1 DQ396400 South Africa McKay, AR *J Virol Methods* **136**(1-2); 118-25 (2006)
This subtype A1 sequence has a section of gag most closely resembling a subtype A portion of CRF01_AE. The patient from which this sequence was taken was a heterosexually-infected female of Zulu or Xhosa ethnicity and antiretroviral therapy-naive. The sequence is derived from a plasmid clone. Genome sequence lacks part of non-coding region.
- B.AR.00.ARMS008 AY037269 Argentina Carr, JK *AIDS* **15**(15); F41-7 (2001)
This sequence came from a 34 year old heterosexual female in Buenos Aires, Argentina. The sample was collected in 2000.
- B.AU.96.MBCD36 AF042105 Australia Oelrichs, RB *ARHR* **14**(9):811–4 (1998)
Sequence derived from peripheral blood sampled on 10/96 and cultured with donor PBMC. Patient was Sydney Blood Bank Cohort member D36, who was the Cohort donor (Deacon, N.J. *Science* **270**, 988-991 (1995)). Patient is a homosexual Caucasian male infected in December 1980 at age 22. He remained asymptomatic at the time of sampling in 1996. Sequence shows previously described deletions in the nef/LTR region. All other open reading frames are intact, and the nucleic acid sequence clusters within subtype B in p17, pol and env. Viral phenotype: Dual tropic.
- B.CO.01.PCM074 AY561240 Colombia
Sequence derived from heterosexual male in Medellin, Colombia.
- B.FR.83.HXB2 K03455 France Wong-Staal, F *Nature* **313**(6000):277–84 (1985)
This sequence is used as the primary reference genome for HIV-1 at the Los Alamos HIV Databases. HXB2 is a specific clone from the French isolate LAI (formerly BRU), which is also referred to as IIIB or LAV. It was one of the first published nucleotide sequences of HIV-1. The present sequence (HXB2R) is a revised version of the originally-published sequence. Since the LAI isolate is a widely-used laboratory strain, it is associated with many publications; not all of the references linked to this entry are concerned with this specific clone. This sequence contains a mutation of the vpu start codon (bases 6062–6064; ACG instead of ATG). It contains a frameshift at

5772, resulting in premature termination of Vpr. Despite these mutations, the clone corresponding to this sequence is demonstrably infectious. The database contains a number of other full-length and partial sequences derived from the same patient as the HXB2 clone. Other related clones include BH1-BH10, N1T, and PV22. The clone NL43 (or NL4-3) is spliced from the envelope of HXB2 and gag-pol from NY5. Other sequences from the same isolate as HXB2 include: PV22 (K08083), MFA (M33943), F12CG (Z11530), TH4 (L31963), MCK1 (D86068), PM213 (D86069), BH10 (M15654), and LAI (M14100, K02013, X01762). Other GenBank entries with IIIB-LAI sequences include many patent sequences and cloning vectors. Note that occasionally laboratory samples become contaminated by the LAI/HXB2 lab strain, resulting in sequences with a high degree of similarity to HXB2; such sequences may be labeled as C ('contaminant') in the HIV database 'problematic' field; however, not all such contaminants are detected and labeled. The NCBI REFSEQ for HIV-1 is also a clone of HXB2, but it lacks the first 454 bases of this sequence, and has the Vpu start codon (defective ACG in this sequence) corrected to ATG. See entries with accession numbers NC_001802 and AF033819.

- B.GA.88.OYI M26727 Gabon Huet, T *AIDS* 3(11):707–15 (1989)
 This sequence is derived from the Gabonese isolate OYI, designated elsewhere as isolate 397, which was obtained from a healthy HIV-1 infected individual presenting a typical Western Blot. This sequence is from a lambda phage clone, the cloned provirus being functionally defective. The vpu gene does not have a start codon. Phylogenetic analysis reveals that the sequence is closely related (across the genome) to the North American isolate SF2 and the European virus HAN. This was the first report of a virus from Africa that clusters with North American rather than Zairean viruses: OYI and SF2 differ by approximately 7% in envelope. The single C → S substitution at residue 22 of the OYI tat protein renders it inactive, but may not account for the avirulence of the virus. 5 sibling sequences for OYI(397), each 59 bases long, are available (see the 1989 HIV Database Compendium page I-A-181).
- B.NL.00.671_00T36 AY423387 Netherlands Geels, MJ *J Virol* 77(23):12430–12440 (2003)
 This sequence comes from a set of samples from patient H671. Patient H671 entered the Amsterdam Cohort Studies in June 1986 and tested seropositive for HIV-1-specific antibodies in March 1995, with testing every 3 months. The CD4+ cell count at the set point was 1120 cells/ml. The patient showed wild-type homozygosity for CCR2 and SDF-1, but heterozygosity for CCR5delta32. The patient was infected with an AZT-resistant virus, and has not received any antiviral treatment. This molecular clone (T36) has an aberrant 3'LTR sequence, with a duplication of another region of the LTR apparently pasted onto the very 3' end of this sequence. It is most likely a sequence data handling artifact and not actually present in infectious virus.
- B.RU.04.04RU129005 AY751406 Russia Galkin, AN *ARHR* 22(11):1192–1197 (2006)
 This sequence was derived from a study of 4 HIV-positive patients in Russia. The patient from which this sequence was derived was a 52-year-old female from Moscow; the patient was drug naive and had slow disease progression at the time of sampling. The sequence is characterized by an 18-bp in-frame insertion in the region encoding the N-terminus of the p6 Gag protein; such duplications are associated with increased infectivity and NRTI resistance.
- B.TH.90.BK132 AY173951 Thailand Hierholzer, J *ARHR* 18(18):1339–1350 (2002)
 Sequence derived from DNA from coculture of viral strain BK132. This sample originates from Thailand in 1990 and is available from the NIH AIDS Reference Reagent Program. Genome sequence lacks part of non-coding region.
- B.US.90.WEAU160 U21135 United States Tozser, J *FEBS Lett* 281(1-2): 77–80 (1991)
 Sequence kindly provided prior to publication by Sajal K. Ghosh, UAB, Birmingham. A cytopathic HIV-1 virus was cloned from an acutely infected patient in 1990. The clone WEAU 1.60 is replication competent and upon transfection produces highly cytopathic T-cell tropic virus. The clone and the viral isolate from which it was derived is syncytium-inducing (SI). The WEAU 1.60 clone was obtained from a coculture of the patient's PBMCs, first with normal donor PHA-stimulated lymphocytes for 14 days, then with the H9 T-cell line for another 14 days. The patients' blood specimen was obtained 15 days after the onset of clinical symptoms of acute (primary) infection, and 35 days after a single sexual encounter with a partner whose virus was proven phylogenetically to be responsible for the transmission. (According to Wei et al. 2003, seroconversion occurred 4 days after the 16-day sample, i.e., 20 days after the acute primary infection.) The patient is identified as "Patient #1" in *N. Engl. J. Med.* 324: 954-960 (1991) and as "WEAU 0575" in *Science* 259: 1749-1754 (1993). The patient is also discussed in Borrow et al., *Nat Med*, 3:205-11 (1997). The WEAU 1.60 clone has been completely sequenced from a plasmid. There is a deletion of a single T at position 9069, resulting in a frameshift mutation and premature termination of Nef. The frameshifting deletion in nef was not present in the patients' uncultured PBMCs, where instead there is a

- “T”. The nef gene was not interrupted in 10 of 10 clones analyzed by PCR sequencing from uncultured PBMCs. It has been sequenced in its entirety by two different labs (G. Shaw and L. Hood) with 100% concordance. This sequence has one extra base at the 3' end that has been removed from our multiple sequence alignments. Lentiviruses all end with TAGCA, but this one ends with TAGCAG, so the terminal “G” is probably vector or host genome.
- B.US.98.1058_11 AY331295 United States Bernardin, F *J Virol* **79**(17):11523–8 (2005)
Bernardin [PMID 16103205] studied 9 African-American plasma donors in San Francisco during the seroconversion period. Each was sequenced at 2 time points separated by 7–28 days. The sample from which this sequence was derived was taken during acute infection.
- C.AR.01.ARG4006 AY563170 Argentina Aguayo, N *ARHR* **20**(9):1022–5 (2004)
Sample was collected in 2001 from patient ARG4006, a 39-year-old male coinfecting with TB. Subtype C. Sample collected as part of a surveillance study of uncommon non-B/non-F subtype viruses circulating in South America [Carrion et al. 2004].
- C.BR.92.BR025-d U52953 Brazil Gao, F *J Virol* **70**(3):1651–1667 (1996)
This sequence is from a PCR clone from a primary isolate that is part of a set obtained through WHO Global Programme on AIDS (WHO Network, *ARHR* 10:1327-1344 (1994)). It is from a 23 year old male hemophilia patient from Porto Alegre, Brazil. He had seroconverted more than 1.2 months prior to the date this blood sample was collected in 1992. He was asymptomatic, and had not taken any anti-retroviral therapy prior to sampling. 92BR025 was established and propagated by short-term co-cultivation with normal donor lymphocytes, and then the near full length genome was PCR amplified and sequenced. The HIV isolate exhibited an NSI phenotype, when assayed by the WHO. The full length genome is clone 8, 92BR025.8. This clone has two inframe stop codons in pol at positions 2141, and 3115, and a frame shift mutation at position 4131. Additional env, nef and ltr region sequences are available from this isolate: U09126, U09132, U51282, and U15121. The isolate 92BR025 is available from the NIH AIDS Reagent program, and is NSI R5. A small region of Gag, beginning very near the junction of p1/p6 (position 2131 in the HXB2R K03455 genome; 1471 in this genome) and ending before the end of p6 (position 2237 in HXB2R; position 1579 in this genome) was discovered to be subtype B at the HIV Database. This region includes 3 indels that are highly indicative of either subtype B or C, that contribute to the B-like nature of this region in 92BR025, but which would be overlooked if gapstripping were used prior to bootscanning.
- C.BR.04.04BR013 AY727522 Brazil Sanabani, SS *ARHR* **22**(2):171–6 (2006)
Sanabani et al. 2006 examined subtype C and BC genomes from 3 geographically distinct regions of Brazil and concluded that subtype C viruses circulating in Brazil were likely introduced from a unique point source followed by rapid expansion. Like most subtype C isolates, this sequence contains 3 NF-kappaB binding sites.
- C.BW.00.00BW07621 AF443088 Botswana Novitsky, VA *J Virol* **76**(11):5435–51 (2002)
Genome sequence lacks part of non-coding region. Sample was collected in Gaborone, Botswana year 2000. Sequence comes from cocultured PBMC extracted DNA.
- C.ET.86.ETH2220 U46016 Ethiopia Salminen, MO *ARHR* **12**(14):1329–39 (1996)
ETH2220 is the first reported near-full-length subtype C sequence from Ethiopia. The patient sample from which this clone was obtained was taken in 1986. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF-kB instead of two. This is a feature that was preserved in other Ethiopian C subtype samples, as well as C viruses from Zambia. This sequence was cloned as a PCR amplified near full length genome, and has a defective tat gene.
- C.IN.95.95IN21068 AF067155 India Lole, KS *J Virol* **73**(1):152–60 (1999)
A small section of the 5' LTR sequence present in the 21068 virus is not included in this sequence. It is derived from primary PBMC coculture taken Feb. 1995 from a 21 year old man from Pune in Maharashtra State, India. The patient seroconverted in 1994 and his only identified risk factor for HIV infection was genital ulcer disease. This sample is available in plasmid form through the NIH AIDS Research and Reference Reagent Program and is named p95IN21068.
- C.IN.99.01IN565_10 AY049708 India Khurana, S Unpublished
Sequence from a sample obtained from 34 yr. old female probably infected during multiple transfusion 4-6 months

prior to collection of blood in August 1999; patient suffered from pulmonary tuberculosis and was on anti-tuberculosis drugs for 3 months at the time of blood collection. Additional clones from the same individual are present in GenBank (accessions AY047909 - AY047911).

- C.KE.00.KER2010 AF457054 Kenya Dowling, WE *AIDS* **16**(13):1809–20 (2002)
Sample comes from a blood bank at Kericho District Hospital, Kenya in year 2000. An erratum to the publication was published in *AIDS* 2002 16(15); 2104.
- C.TZ.01.BD9_11 AY253322 Tanzania Herbinger, K-H *ARHR* **20**(8):895–901 (2004)
This sample came from a HIV-1-positive blood bank unit collected between October 2000 and August 2001 from Mbeya, Tanzania.
- C.UY.01.TRA3011 AY563169 Uruguay Aguayo, N *ARHR* **20**(9):1022–5 (2004)
Collected in 2001 from patient TRA3011, a 25 year old male commercial sexworker. Subtype C. A premature stop in pol is due to a single base deletion around base 4032.
- C.ZA.04.SK164B1 AY772699 South Africa Kiepiela, P *Nature* **432**(7018):769–775 (2004)
Sample obtained in 2004 in Durban, South Africa as part of a large study of HIV and its interaction with the immune system. Genome sequence lacks part of non-coding region.
- C.ZA.05.05ZASK245B1 DQ369982 South Africa McKay, AR *J Virol Methods* **136**(1–2); 118–25 (2006)
The patient from which this sequence was taken from was of Zulu or Xhosa ethnicity and antiretroviral therapy naive. The sequence is derived from a plasmid clone.
- C.ZM.02.02ZM115 AB254148 Zambia Tatsumi, M Unpublished
Subtype C isolate from Lusaka, Zambia.
- C.ZM.96.96ZM651 AF286224 Zambia Rodenburg, CM *ARHR* **17**(2):161–8 (2001)
This sequence is part of an international survey of subtype C, based mostly on isolates obtained by the UNAIDS and NIAID networks for isolation and characterization of HIV. DNA was isolated from PBMC after short-term coculture. The samples included CRF07 and CRF08 BC recombinants.
- D.CD.83.ELI K03454 Congo Alizon, M *Cell* **46**(1):63–74 (1986)
This sequence is of a phage clone derived from the Zairean isolate ELI. ELI was recovered in 1983 from a 24 year old woman with AIDS. All reading frames in this sequence are intact. The complete genomic sequence and an infectious clone are available. In the 1995 Compendium (pages III-45 and III-47), ELI was listed as an unlikely D/A mosaic, with only gp41 being weakly A-like. Entry with accession number M27949 is from this same isolate.
- D.CD.83.NDK M27323 Congo Spire, B *Gene* **81**(2):275–84 (1989)
The NDK virus was isolated from a Zairean man residing in France. He had AIDS and infected his wife; she infected her lover. The cytopathicity of this virus was found not to be localized to env, and might be regulated by regions of gag, vpr and env. Kindly provided prior to publication by J.-C. Chermann, Pasteur Institute, Marseille.
- D.CM.01.01CM_4412HAL AY371157 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
A subtype D sequence from a sample obtained in Lomie, Cameroon. This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- D.KE.01.NKU3006 AF457090 Kenya Dowling, WE *AIDS* **16**(13):1809–20 (2002)
Sample was taken 2001 from a blood bank at Rift Valley Provincial Hospital, Kenya.
- D.TD.99.MN012 AJ488927 Chad Vidal, N *J Acquir Immune Defic Syndr* **33**(2):239–46 (2003)
This sample was taken from a native of Chad between 1999 and 2000 attending the National Hospital of N'Djamena, the main health center in Chad. DNA was extracted from primary PBMC.

- D.TZ.01.A280 AY253311 Tanzania Herbinger, K-H *ARHR* **20**(8):895–901 (2004)
This sample came from a HIV-1-positive blood bank unit collected between October 2000 and August 2001 from Mbeya, Tanzania.
- D.UG.94.94UG114 U88824 Uganda Gao, F *J Virol* **72**(7):5680–98 (1998)
Sample 94UG114 was obtained from an asymptomatic 31-year-old man from Butuku, Uganda as part of the WHO/UNAIDS study. He had not taken any anti-retroviral therapy prior to sampling. His risk factor for infection was heterosexual contact. The near full length genome was PCR amplified from a short term culture of a PBMC sample and sequenced. The isolate from which this sequence was derived is NSI by an MT-2 assay. This sequence was kindly made available prior to publication by Feng Gao. Biotypes were determined by MT-2 syncytium assay; however, both syncytium-inducing (SI) and non-syncytium-inducing (NSI) variants may be present in the viral “swarm” for each isolate. Recent studies indicate that NSI isolates contain predominantly CCR5-using variants while most SI isolates contain both CXCR4 (SI) and CCR5 (NSI) variants. Some SI isolates may contain dual-tropic variants that use both CXCR4 and CCR5 co-receptors. The isolate 94UG114 is available from the NIH AIDS Reagent program, and is NSI R5.
- D.UG.99.99UGD23550 AF484485 Uganda Harris, ME *ARHR* **18**(17):1281–90 (2002)
One of a set of complete genomes from 46 patients from Uganda. These sequences are from volunteers from Rakai district, 37 of whom are enrolled in cohort studies; they were referred by an AIDS surveillance program or an STD clinic. Another nine sequences were obtained from anonymous discard samples. Of the set, more than half were subtype D; 15% were subtype A; and a quarter were AD recombinants with unique mosaic patterns. A few AC and CD recombinants were also found.
- D.UG.99.99UGK09958 AF484499 Uganda Harris, ME *ARHR* **18**(17):1281–90 (2002)
One of a set of complete genomes from 46 patients from Uganda. These sequences are from volunteers from Rakai district, 37 of whom are enrolled in cohort studies; they were referred by an AIDS surveillance program or an STD clinic. Another nine sequences were obtained from anonymous discard samples. Of the set, more than half were subtype D; 15% were subtype A; and a quarter were AD recombinants with unique mosaic patterns. A few AC and CD recombinants were also found.
- D.ZA.86.R482 AY773341 South Africa
This sample from Cape Town is a representative of a small subtype D epidemic in South Africa sampled in 1984–86 and described by Loxton et al. 2005. Genome sequence lacks part of non-coding region.
- F1.BE.93.VI850 AF077336 Belgium Laukkanen, T *Virology* **269**(1):95–104 (2000)
Small sections of the 5' and 3' LTRs are not included in this sequence. This sequence was isolated from a Belgian man in 1993 whose wife was infected in Zaire (now called the Dem Rep of the Congo). This sequence was kindly provided prior to publication by J. Carr et al. This sequence was originally classified as subtype F, but because F is readily subdivided into two distinct categories, it has been reclassified as subtype F1. See Triques et al, *Virology*. 259(1):99–109 (1999).
- F1.BR.89.BZ126 AY173957 Brazil Hierholzer, J *ARHR* **18**(18):1339–1350 (2002)
Sequence derived from DNA from coculture of viral strain BZ126. This strain is available from the NIH AIDS Reference Reagent Program. Genome sequence lacks part of non-coding region.
- F1.BR.93.93BR020_1 AF005494 Brazil Gao, F *J Virol* **72**(7):5680–98 (1998)
This sequence was originally classified as subtype F, but because F is readily subdivided into two distinct categories, it has been reclassified as subtype F1. See Triques et al, *Virology*. 259(1):99–109 (1999). This sample is part of a set of sequences generated through the WHO Global Programme on AIDS (WHO Network, *ARHR* 10:1327–1344 (1994) and came from an asymptomatic HIV seropositive bisexual contact. The isolate 92BR020 was established and propagated by short term co-cultivation with normal donor lymphocytes, and then the near full length genome was PCR amplified and sequenced. The isolate 92BR020 was described as syncytium inducing (SI) using an MT-2 assay. An envelope gene sequence from this isolate is described in Gao, F., et al., *J Virol* 70:1651–1657 (1996). This sequence was kindly made available prior to publication, and was eventually published in Gao, F. et al., *J Virol* 72(7):5680–98 (1998). There were no defective genes. A summary of isolates with known co-receptor usage can be found in the HIV database reviews.

- F1.FI.93.FIN9363 AF075703 Finland Laukkanen, T *Virology* **269**(1):95–104 (2000)
The virus was isolated in 1993 from a Finnish male who claims that he was most likely infected in Finland in 1985 by a Kenyan woman, however, he had multiple partners. This sequence was originally classified as subtype F, but because F is readily subdivided into two distinct categories, it has been reclassified as subtype F1.
- F1.FR.96.MP411 AJ249238 France Peeters, M *ARHR* **16**(2):139–51 (2000)
Prior to 1999, the F subtype was made up of 3 distinctive clusters and very diverse viruses. Triques and colleagues have defined a new subtype K, and broken F into two subclusters, F1 and F2. This sequence is a complete genome reference for F1. This isolate was from a French patient who believes he was infected when deployed in Chad or Yugoslavia. Annotated as drug-naive based on Vergne et al. 2006 [PubMed 16563858].
- F2.CM.02.02CM_0016BBY AY371158 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
A subtype F2 sequence from a sample obtained from a blood bank in Yaounde, Cameroon. This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- F2.CM.95.MP255 AJ249236 Cameroon Peeters, M *ARHR* **16**(2):139–51 (2000)
Prior to 1999, the F subtype was made up of 3 distinctive clusters and very diverse viruses. Triques and colleagues have defined a new subtype K, and broken F into two subclusters, F1 and F2. This sequence is a complete genome reference for F2.
- F2.CM.95.MP257 AJ249237 Cameroon Peeters, M *ARHR* **16**(2):139–51 (2000)
Prior to 1999, the F subtype was made up of 3 distinctive clusters and very diverse viruses. Triques and colleagues have defined a new subtype K, and broken F into two subclusters, F1 and F2. This sequence is a complete genome reference for F2.
- F2.CM.97.CM53657 AF377956 Cameroon Carr, JK *Virology* **286**(1):168–81 (2001)
This sample came from a 40 year old male in Douala, a large seaport city in Cameroon. He was infected heterosexually and had a VL=307,000 RNA copies/ml.
- G.BE.96.DRCBL AF084936 Belgium Debyser, Z *ARHR* **14**(5):453–9 (1998)
Clinical details are discussed in *ARHR* 14(5):453–9 (1998), and the analysis of the complete genome is in Oelrichs et al., *ARHR* 15(6):585–9 (1999). A pregnant 26 year old woman was sampled who had lived in Zaire (now called the Dem Rep of the Congo) until 1993, then moved to Belgium. She was diagnosed with AIDS and had a low CD4 when sampled in 1996. Her G subtype virus was not detected by Amplicor Monitor or Nasba RNA kits, although she was found to have a high viral load by branched DNA. The sequence was kindly provided prior to publication by R. Oelrichs et al. This complete genome sequence shows the same pattern of phylogenetic associations as 92NG083 (U88826), HH8793 (AF061640) and SE6165 (AF061642). These four (and other subtype G sequences) form their own clade (subtype G) when the complete gag, pol or env genes are included in the analysis. However, all G subtype genomes have some ambiguous A/G regions in the central part of the genome in a phylogenetically indistinct region in the the accessory gene region from the beginning of vif to the beginning of vpu. The coordinates of this region are 5055 to 6297 on HXB2, and there are several subtypes which become difficult to resolve unambiguously in this region: A, G, and the circulating recombinant forms which resemble the prototypes AE(CM240) and AG(IbNG) (pers. comm., Jean Carr). Of particular note is that a region of gp41 from these viruses clusters with the AE and IbNG circulating recombinant forms. See J. Carr et al *Virology* 247:22–31 (1998) and F. Gao et al *J Virol* 72(7):5680–5698 (1998) for analyses of the other genomes with this pattern. At this time (Jun. 2007) it is not clear whether the AE(CM240)circulating recombinant form is AEG triple recombinant, or if the above four genomes are AEG triple recombinant, or if an evolutionary anomaly rather than recombination is the basis for this pattern. This sequence has 2 extra bases on the 3' end. Lentiviruses end with TAGCA, therefore these 2 bases must be host or cloning vector DNA.
- G.CM.01.01CM_4049HAN AY371121 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
A subtype G sequence from a sample obtained from a hospitalized patient in Ndikinimeki, Cameroon. This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.

- G.ES.99.X138 AF450098 Spain Delgado, E *J Acquir Immune Defic Syndr* **29**(5):536–43 (2002)
This sample is from a female IV drug user from Vigo, Galicia (Spain). The patient was diagnosed with HIV in 1996. The sample was taken in 1999. Genome sequence lacks part of non-coding region.
- G.KE.93.HH8793_12_1 AF061641 Kenya Salminen, MO *ARHR* **8**(9):1733–42 (1992)
Sections of the 5' and 3' LTRs are not included in this sequence. This sample was taken in Finland in June 1993 (Jean Carr, Pers. Communication)
- G.NG.92.92NG083 U88826 Nigeria Gao, F *J Virol* **72**(7):5680–98 (1998)
This sequence is from a PCR clone from a primary culture from the NSI isolate 92NG083; the sample was taken in 1992 from an AIDS patient from Jos, Nigeria. The isolate was originally called JV1083, but was renamed 92NG083 to be consistent with WHO nomenclature. The full length clone has an altered initiation codon at position 157, an in-frame stop codon at position 360 in gag, and a vpu frameshift mutation at position 5462.
- G.SE.93.SE6165 AF061642 Sweden Laukkanen, T *Virology* **247**(1):22–31 (1998)
Sections of the 5' and 3' LTRs are not included in this sequence. This patient (6165) was infected in Congo and moved to Sweden. He tested HIV positive (ELISA and Western Blot) approximately 18 months prior to infecting patient 6167 via heterosexual intercourse and 19 months prior to infecting patient 6168, also via heterosexual intercourse. He had low (35 per ul) CD4 count and dermatological problems but no AIDS defining illness at the time of sampling in 1993. The molecular epidemiology of this patient and the persons he infected was published by Leitner et al. 1995, *Virology* 209:136-146. Siblings sequences from the same blood sample: L40743, L40761, L40752 Sequences from the two female sex partners of this individual: L40744, L40745, L40753, L40754, L40762, L40763.
- H.BE.93.VI991 AF190127 Belgium Janssens, W *AIDS* **14**(11):1533–43 (2000)
This sequence was isolated from a Belgian man who lived with his Belgian wife in the DRC for 20 years. The wife died of AIDS in 1990. The route of infection was unknown for both.
- H.BE.93.VI997 AF190128 Belgium Janssens, W *AIDS* **14**(11):1533–43 (2000)
This virus was isolated from a Belgian man with multiple sexual contacts in the DRC.
- H.CF.90.056 AF005496 C.A.R. Murphy, E *ARHR* **9**(10):997–1006 (1993)
This sequence clusters with available HIV-1 subtype H sequences in phylogenetic analysis, and was the first available full length H subtype sequence. The isolate comes from Bangui, Central African Republic, and was sampled in 1990 from an ARV-naïve asymptomatic individual. The isolate had an NSI phenotype by an MT-2 assay, and the sample was obtained from the Pasteur Institute, Bangui. The isolate 90CF056 was established and propagated by short term cocultivation with normal donor lymphocytes, and then the near full length genome was PCR amplified, cloned and sequenced. The isolate was at one point designated 90CR056, but was changed to 90CF056 as CR stands for Costa Rica, and CF for Central African Republic. The first genetic characterization of this virus isolate (an env V3 sequence designated 4056, accession# L11497, Murphy et al., *ARHR* 9:997-1006 (1993)) left the subtype designation as unclassified, but a second study of this env region sequence classified it as subtype H (W. Janssens, *ARHR* 10:877-879 (1994)). This sequence was kindly made available prior to publication (Gao, F. et al., *J Virol* 72(7):5680-98 (1998)). The patient was heterosexual, asymptomatic, and the biological phenotype of the isolate was NSI. There are no defective genes in the sequence.
- J.SE.93.SE7887 AF082394 Sweden Laukkanen, T *ARHR* **15**(3):293–7 (1999)
This sequence is from a male who was infected in Sweden between 1993 and 1994. Blood for sequencing was drawn in 1994. He was asymptomatic with a CD4 count of 567. The sequence was kindly provided prior to publication by M. Salminen. This sequence is from the same individual as SE7887 described by Leitner et al. *ARHR* 11(8):995-997 (1985), see accession numbers L41176 and L41178 for env and gag genes from this individual.
- J.SE.94.SE7022 AF082395 Sweden Laukkanen, T *ARHR* **15**(3):293–7 (1999)
This sequence is from a woman who was infected in Zaïre (now called the Democratic Republic of the Congo) between 1981 and 1986. Blood for sequencing was drawn in 1993. She was asymptomatic with a CD4 count of 184. The sequence was kindly provided prior to publication by M. Salminen. This sequence is from the same

individual as SE7022 described by Leitner et al. *ARHR* 11(8):995-997 (1985), see accession numbers L41177 and L41179 for env and gag genes from this individual. Other examples of subtype J have been found in Gambia, see accession numbers U33099, U33100 and U33102.

- K.CD.97.EQTB11C AJ249235 Congo Peeters, M *ARHR* 16(2):139-51 (2000)
Prior to 1999, the F subtype was made up of 3 distinctive clusters and very diverse viruses. Triques and colleagues have defined a new subtype K, and broken F into two subclusters, F1 and F2. This sequence is a complete genome reference for subtype K.
- K.CM.96.MP535 AJ249239 Cameroon Peeters, M *ARHR* 16(2):139-51 (2000)
Prior to 1999, the F subtype was made up of 3 distinctive clusters and very diverse viruses. Triques and colleagues have defined a new subtype K, and broken F into two subclusters, F1 and F2. This sequence is a complete genome reference for subtype K.
- U.CD.83.83CD003 AF286236 Congo Gao, F *ARHR* 17(12):1217-22 (2001)
This sequence is labeled as "U" because it is nearly equidistant from all other subtypes throughout its genome. It is slightly more similar to one subtype than the others in each region, which can be interpreted as either evidence of ancient recombination events, or as unequal rates of evolution of each subtype. The degree of this unequal similarity is not greater than, and in many cases less than, the degree of unequal similarity that is found in subtypes that have been defined as non-recombinant. For example, in some regions of the genome, subtypes G and A are more similar to each other, than to the other subtypes. An env gene sequence from this same blood sample was previously sequenced and is available with accession number K03347. The sample was referred to as "Z3" in the publication describing the env gene sequence. This genome sequence was also analyzed by Mokili et al. 2002 [PMID 12167273].
- U.CD.90.90CD121E12 AF457101 Congo Mokili, JLK *ARHR* 18(11):817-23 (2002)
Although annotated in GenBank as subtype L, this sequence at this time (Jun 2007) has just one other sequence that is phylogenetically related to it (accession# AF286236 known as 83CD003 or Z3). The criterion of 3 unlinked samples for establishing subtype L from these sequence has thus not yet been met.
- U.GR.99.GR303 AY046058 Greece Paraskevis, D *J Gen Virol* 82(Pt 10):2509-14 (2001)
Although this sequence is described by the authors as being AGJKU? recombinant, it is unique enough in most regions of the genome to possibly be classified as its own sub-subtype or subtype. It is thus listed in the HIV database as "U" for unidentified at this time (Jun 2007).
- U.NL.x.U_NL_95_H10986_D1 EF029066 Netherlands van der Hoek, L Unpublished
Although the complete genomes from this patient have some regions that are more similar to one subtype or another, such that it appears to be a complex intersubtype recombinant, it is listed as "U" for unclassified so far, because it is not clear if any of the regions are truly within the "crown group" of any subtype.
- 01_AE.CF.90.90CF402 U51188 C.A.R. Gao, F *J Virol* 70(10):7013-29 (1996)
One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CF402 (previously named CAR-E 4002 or 90CR402) was obtained from a man from Bangui, Central African Republic, who had lymphadenopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. Sample 90CR402 (accession number U51188) was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. The sequence has a defective vpu due to the loss of a start codon, and a defective vif gene. The pattern of subtype AE recombination of breakpoints is shared between AE subtype sequences from Thailand and from the Central African Republic, suggesting a shared ancestral recombined virus that arose prior to the subsequent epidemics in the two areas.
- 01_AE.CN.05.FJ051 DQ859178 China Yan, Y *Chin Med J(Engl)* 119(19): 1622-8 (2006)
This sequence comes from a heterosexual male in the Fujian Province, China. At time of sampling CD4 count was 486 c/ul, and viral load 28111 c/ml.
- 01_AE.HK.x.HK001 DQ234790 Hong kong
- 01_AE.JP.93.93JP_NH1 AB052995 Japan Sato, H *J Virol* 75(12):5604-13 (2001)
The 93JP-NH1, previously named NH1, has been characterized genetically and biologically as one of five HIV-1

subtype E (CRF01-AE) sequential isolates from an intra-familial infection case in Japan (Sato, H, et al. *J. Virol.*73:3551-3559 (1999) and Sato, H, et al. *J. Virol.*74:5357-5362 (2000)). It was isolated in June 1993 from an index case (NH1) who had developed AIDS. It is sensitive to RT inhibitors (AZT, ddI, ddC, 3TC, d4T, nevirapine), as well as protease inhibitors (IDV, APV, NFV, SQV, and RTV). The 93JP-NH1 isolate was passaged in human PBMCs and MT2 cells prior to cloning with lambda phage vector. There are addition sequences for patient NH1.

- 01_AE.TH.01.OUR414I AY358050 Thailand Tovanabutra, S *ARHR* **20**(5):465–75 (2004)
This sample came from a 14 year old Thai male in Chiang Mai, Thailand.
- 01_AE.TH.02.OUR769I AY358062 Thailand Tovanabutra, S *ARHR* **20**(5):465–75 (2004)
This sample came from a 41 year old Thai male injecting drug user in Chiang Mai, Thailand.
- 01_AE.TH.90.CM240 U54771 Thailand Laukkanen, T *J Virol* **70**(9):5935–43 (1996)
Virus from which this sequence was derived is available from the NIH AIDS Reference Reagent Program. Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and clade E virus, with the gag gene (and other regions) of subtype E viral genome falling within clade A in phylogenetic analysis. This is the pattern of A/E sequences found through out Asia and Africa. No full length E subtype reference strain has been identified (as for 93TH253). Carr et al. provided detailed analysis of the breakpoints, and point out that the A/E mosaic genomes have a natural pseudotype structure where the external envelope protein spikes on the virion essentially are contributed by the E subtype, and the rest of the viral proteins have a subtype A origin. See also the env sequence from the same isolate (L14572), Mascola et al. 1993, *JID* 169:48-54.
- 02_AG.CM.02.02CM_1669LE AY371139 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
A subtype CRF02_AG sequence from a sample obtained from a healthy adult in Lomie, Cameroon. This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- 02_AG.EC.x.ECU41 AY151001 Ecuador Carrion, G *ARHR* **19**(4):329–32 (2003)
This sample came from a male in Guayaquil, Ecuador with no travel history abroad nor contacts with foreigners, but many sexual contacts. Guayaquil is the principal port in Ecuador.
- 02_AG.FR.91.DJ264 AF063224 France Laukkanen, T *Virology* **247**(1):22–31 (1998)
A small section of LTR sequence present in the DJ263 virus is not included in this file. Carr et al. states that this virus was from a French foreign legion soldier assigned to peace-keeping duties in Djibouti, referencing Louwagie et al (*J Virol* 69(1):263-271 (1995)). However the Louwagie paper does not mention the French soldiers and only states that the blood sample was from Djibouti. The sample was isolated in 1991. There are several sequences which share AG recombination breakpoints with IbNG, and are essentially the same recombinant recirculating form, CRF02_AG; IbNG is the prototype, sharing a similar structure with DJ264 and DJ263.
- 02_AG.GH.03.GHNJ196 AB231898 Ghana Tatsumi, M Unpublished
Sequence of subtype CRF02_AG from Accra, Ghana.
- 02_AG.NG.x.IBNG L39106 Nigeria Howard, TM *ARHR* **10**(12):1755–7 (1994)
HIV-1 IbNg was isolated from the PBMCs of an apparently healthy 23 year old man from Nigeria. The patient's PBMCs were cocultured with PHA-stimulated donor PBMCs from an HIV sero-negative donor. After confirming HIV infection in the culture, a mixture of cells and culture supernatant were used to infect a second culture of donor PBMCs, with fresh PHA-stimulated PBMCs added on days 4 and 6. The cultured cells were harvested on day 8 and cytoplasmic RNA was harvested. RT-PCR was used to amplify the complete HIV-1 genome in 5 overlapping segments. The partial env gene sequence (U48628) was originally designated subtype A (Howard, T., et al., *ARHR* 10:1755-1757 (1994)); as was the full length genome. The full length sequence was eventually shown to be an A/G recombinant with multiple cross-over points (Gao F, et al., (*J. Virol* 70:7013 (1996)). The breakpoints are mapped in (Robertson, D., et al., part III pages 25-30 of the 1997 compendium). The IbNg sequence has a 16 bp insertion within the Lys-tRNA primer binding site, just 3' of the 5' LTR. It also has a single nucleotide deletion in tat cds at position 5449. See also the entry with accession number U48628, which is from another isolate taken from this

same individual. There are many sequences which share recombination breakpoints with IbNG, and are essentially the same recombinant circulating form; IbNG is the prototype for CRF02_AG, and shares a similar structure with DJ264 and DJ263 (Carr et al., *Virology* 247:22-31 (1998)).

- 02_AG.SN.98.MP1211 AJ251056 Senegal Toure-Kane, *CARHR* 16(6):603–9 (2000)
This full length genome came from a study of subtype prevalence in Senegal, and CRF02_AG IbNG like strains were found to be most common.
- 02_AG.UZ.02.02UZ693 AY829204 Uzbekistan Carr, JK *J Acquir Immune Defic Syndr* 39(5):570–5 (2005)
Sample from a 19-year-old injecting drug user in Tashkent, Uzbekistan. Part of a study of HIV diversity in Uzbekistan, which found predominantly subtype A and CRF02_AG viruses.
- 03_AB.RU.97.KAL153_2 AF193276 Russia Liitsola, K *AIDS* 12(14):1907–19 (1998)
This was the first complete genome sequence of the 03_AB (A in gag; B in env) circulating recombinant form, which is common among IV drug users in the Kaliningrad region of Russia. The non-recombinant subtype A and subtype B parents of this recombinant are common in Russia and southern Ukraine. A gag gene sequence from this same patient is available with accession number AF082414. This sequence was kindly provided by Mika Salminen in 1998 as a CRF03 reference strain, prior to the published description.
- 04_cpx.CY.94.CY032 AF049337 Cyprus Gao, F *J Virol* 72(12):10234–41 (1998)
This sample, like others in this study (with subtypes A, B, C, and F) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. Patient HO31 was a 24 year old asymptomatic female known to have been HIV seropositive for at least 5 years. Patient HO32 was a 35 year old asymptomatic male, also seropositive for at least 5 years. Both were intravenous drug users who had lived in Greece and used IV drugs there, before moving to Cyprus. DNA was extracted from patient PBMCs and PCR amplified. Products were cloned and sequenced. Two env gene clones from HO32 and one from HO31 were sequenced (accession numbers U28672, U28673 and U28685). A complete genome is only available for HO32 (CY032). For patient information see Kostrikis et al. (*J Virol* 69:6122–6130 (1995)). This sequence has the same genetic recombination breakpoints as PVCH and PVMY, and 94CY032 is the prototype of the CRF04 circulating recombinant form. Gao et al. 1998 characterizes this subtype in greater detail, presenting the first published account of this full length genome. The analysis of C2-V3 env gene sequences confirmed that 94CY032.3 was closely related to sequences previously classified as subtype I. However, the remainder of its genome has various regions in which 94CY032.3 was significantly clustered with either subtype A or subtype G. Only regions in vpr, nef, and the middle portions of pol and env, formed independent lineages roughly equidistant from all other known subtypes. Since these latter regions most likely have a common origin, Gao et al. classified them all as subtype I, and report that 94CY032 represents a triple recombinant (A/G/I) with at least 11 points of recombination crossover. Since subtype I is now obsolete and has been found to consist of segments of subtype K as well as regions of unknown or undefined subtype, the designation for this CRF should be AGHKU.
- 05_DF.BE.x.VII1310 AF193253 Belgium Laukkanen, T *Virology* 269(1):95–104 (2000)
This D/F recombinant sequence is an example of the CRF05_DF circulating recombinant form. Another genome of this form is available with accession number AF076998. CRF05_DF sequences have been found in individuals with links to the Democratic Republic of the Congo; VII1310 was isolated from a woman who was infected by a man who traveled frequently in the DRC.
- 06_cpx.AU.96.BFP90 AF064699 Australia Oelrichs, RB *ARHR* 14(16):1495–500 (1998)
HIV-1 from Burkina Faso, identified in Australia. The patient is a 32 year old African male who acquired the infection heterosexually in 1991. The patient was diagnosed in August 1996 at which time he had a CD4 count of 125. This sequence was derived by PCR directly from patient PBMCs when therapy-naive. The genome of this virus is a mosaic between subtypes A, G and J. The LTR is subtype J, a segment of about 950 bp at the beginning of gag is subtype A, the remainder of gag and part of the protease sequence are subtype G. Most of the pol gene cannot be assigned to a subtype. The mid-genome accessory region is mostly subtype J. gp120 is subtype G. The 3' region of gp41, the third exons of tat and rev, and the nef gene are subtype J. The subtype G protease region clusters tightly in phylogenetic analysis, with three sequences from the Ivory Coast (accession numbers AF000482, AF000491 and AF000492), indicating that this is possibly a circulating recombinant form with 4 isolates from 2 different countries obtained to date (Aug 1999); BFP90 is now considered the prototype isolate of CRF06_cpx.

- 0708.CN.00.HH069 AP005206 China Yang, R *J Virol* **77**(1):685–695 (2003)
This sample is from an IDU in Yunnan, China. HH069 and HH086 (accession AP005207) are both described by the authors as being recombinant between CRF07_BC and CRF08_BC. The publication makes a compelling argument for the 07/08 recombination.
- 07_BC.CN.97.CN54 AX149771 China Shao, Y Patent: WO 0136614-A 125
This sequence, and the CN001 sequence with accession number AF286226, are both derived from the same blood sample.
- 08_BC.CN.97.97CNGX_6F AY008715 China Piyasirisilp, S *J Virol* **74**(23):11286–95 (2000)
This sequence is the first complete genome available for the CRF08_BC circulating recombinant form. The genome is mostly subtype C, with two regions of subtype B.
- 09_cpx.GH.96.96GH2911 AY093605 Ghana McCutchan, FE *ARHR* **20**(8):819–26 (2004)
This sequence came from a sample from a 33 year old female commercial sex worker in Ghana. She was infected before 1996. Genome sequence lacks part of non-coding region.
- 10_CD.TZ.96.96TZ_BF061 AF289548 Tanzania Koulinska, IN *ARHR* **17**(5):423–31 (2001)
This sequence was isolated from a perinatally infected infant from Dar es Salaam, Tanzania in 1996, and was part of a set of full length HIV-1 genomes characterizing CRF10_CD.
- 11_cpx.GR.x.GR17 AF179368 Greece Paraskevis, D *ARHR* **16**(9):845–55 (2000)
This subject that this sequence was isolated from was born in 1971 in Zaire, probably infected heterosexually in the DRC in 1991, and moved to in Greece in 1992. The genome is thought to be a mosaic of A/G/E/J.
- 12_BF.AR.99.ARMA159 AF385936 Argentina Carr, JK *AIDS* **15**(15):F41-7 (2001)
This sequence comes from a sample from a heterosexual 26 year old female from Argentina. She had CDC stage A2 at time of sampling in 1999 and she had a HCV coinfection. This sequence is part of a set of South American isolates from various countries. It is one of the reference strains for CRF12_BF.
- 13_cpx.CM.96.1849 AF460972 Cameroon Wilbe, K *ARHR* **18**(12):849–856 (2002)
Sample comes from a non-transmitting mother in Cameroon, taken at delivery in 1996. Viral load at sampling was 4.9 log copies/ml. The corresponding isolate was R5 tropic. This genome sequence lacks part of non-coding sequence. It has been classified by the authors as belonging to the CRF13_cpx circulating recombinant form. The authors describe the CRF13_cpx recombinant genomic structure as being derived from subtypes A, CRF01_AE, CRF11_cpx, G, J and unclassified.
- 14_BG.ES.99.X397 AF423756 Spain Delgado, E *J Acquir Immune Defic Syndr* **29**(5):536–43 (2002)
Sample from a male IDU taken 1999 in Pontevedra, Spain. Genome sequence lacks part of non-coding region. This CRF appears to be a locally circulating form in Spain (Galicia) and Portugal.
- 15_01B.TH.99.99TH_MU2079 AF516184 Thailand Viputtijul, K *ARHR* **18**(16):1235–7 (2002)
This sequence is a CRF15_01B circulating recombinant form, i.e. a recombinant between CRF01_AE (majority of genome) and subtype B (primarily in the env region). The sample was obtained in Bangkok, Thailand in 1999 from a 28 year old female sex worker who had late-stage AIDS.
- 16_A2D.KR.97.97KR004 AF286239 Korea Gao, F *ARHR* **17**(8):675–88 (2001)
This sequence is from a 1997 blood sample from Yosoo, Korea. It is sub-subtype A2 in some regions and subtype D in other regions of the genome [2]. The blood sample was from a 33 year old female sex worker who lived in Yosoo, and was first diagnosed with AIDS February 1997 with CD4+ T-cell count less than 30. She died of AIDS in October, 1997. She reported having clients from many continents, including Africa. AF457060 and AF286239 are two complete genomes representative of the CRF16_A2D circulating recombinant form.
- 18_cpx.CU.99.CU76 AY586540 Cuba Thomson, M *AIDS* **19**(11):1155–63 (2005)
Genome sequence lacks part of non-coding region. CU76 is more closely related to CU68 (ACCESSION AY894993), CM53379 (ACCESSION AF377959) and CU14 (ACCESSION AY586541) than to any subtype or CRF of HIV-1. This recombinant has been named CRF18_cpx and is comprised of subtypes A, F, G, H, K and U.

- 19_cpx.CU.99.CU7 AY894994 Cuba Thomson, M *J Acquir Immune Defic Syndr* **40**(5):532–7 (2005)
 The sample came from a homosexual/bisexual male in Havana City, Cuba. He had been diagnosed with HIV in 1997. This sequence has some regions that do not cluster with any of the major subtypes of HIV-1 M group, and thus are labeled “U” for untyped at this time. Other regions fall within the A1, D and G clades. CU7 is closely related, in at least some regions, to CU29 (AY588971), CU38 (AY588970), CU64 (AY894995) and CU67 (AY894996). This sequence is the reference sequence for recombinant CRF19_cpx.
- 20_BG.CU.03.CB134 DQ020274 Cuba Perez, L *ARHR* **22**(8):724–33 (2006)
 This sample came from a large molecular epidemiological study of HIV-1 in Cuba.
- 21_A2D.KE.91.KNH1254 AY945737 Kenya Visawapoka, U *ARHR* **22**(7):695–702 (2006)
 This sequence is one of three with similar breakpoints (KNH1254, KER2003 & KSM4001). Samples came from discarded blood units in Kericho District Hospital (KER), and Kenyatta National Hospital (KNH), Nairobi.
- 23_BG.CU.03.CB118 AY900571 Cuba Perez, L *ARHR* **22**(8):724–33 (2006)
 This sample came from a large molecular epidemiological study of HIV-1 in Cuba. Although this sequence is from Cuba, and shares some recombination breakpoints with the CRF20_BG sequences from Cuba, it has several regions which do not cluster with CRF20 sequences in phylogenetic analysis. It is B/G recombinant, and has become the reference sequence for CRF23_BG.
- 24_BG.CU.03.CB378 AY900574 Cuba Perez, L *ARHR* **22**(8):724–33 (2006)
 This sample came from a large molecular epidemiological study of HIV-1 in Cuba. Although this sequence is from Cuba, and shares some recombination breakpoints with the CRF20_BG sequences from Cuba, it has several regions which do not cluster with CRF20 sequences in phylogenetic analysis. It is B/G recombinant, and has become the reference sequence for CRF24_BG.
- 25_cpx.CM.01.101BA DQ826726 Cameroon Carr, JK Unpublished
 This genome, along with AY371169 02CM_1918LE, is defined as CRF25_cpx A1/G/U. The sequence has regions of similarity to subtypes A and G, along with a large central region that is not similar to any of the defined subtypes.
- 28_BF.BR.99.BREPM12609 DQ085873 Brazil De Sa Filho, DJ *ARHR* **22**(1):1–13 (2006)
 De Sa Filho et al. 2006 performed a study of genetic variation in HIV-1 in San Paulo, Brazil. They reported full length sequences defining two novel subtype BF circulating recombinants, CRF28_BF and CRF29_BF, with three genomes provided for each. BREPM12609 was taken in 1999 from a 32-year-old asymptomatic female with heterosexual transmission.
- 29_BF.BR.02.BREPM119 AY771590 Brazil Sa Filho, DJd *ARHR* **21**(2):145–51 (2005)
 De Sa Filho et al. 2006 performed a study of genetic variation in HIV-1 in San Paulo, Brazil. They reported full length sequences defining two novel subtype BF circulating recombinants, CRF28_BF and CRF29_BF, with three genomes provided for each. BREPM119 was taken in 2002 from a 5-year-old symptomatic female with mother-to-child transmission.
- 31_BC.BR.02.110PA EF091932 Brazil Santos, AF *AIDS* **20**(16):2011–9 (2006)
 Genome sequence lacks part of non-coding region. Santos et al. 2006 provided 3 genome sequences of a novel circulating recombinant form, CRF31_BC, identified in southern Brazil.
- 33_01B.MY.05.05MYKL007_1 DQ366659 Malaysia Tee, KK *J Acquir Immune Defic Syndr* **43**(5):523–529 (2006)
 This sample came from a Chinese, homosexual, treatment-naïve individual in Kuala Lumpur, Malaysia. This CRF was found among individuals of various risk groups, and is well spread in Malaysia. Intravenous drug users are the main infected risk group in Malaysia.
- A1C.TZ.02.CO3710 AY734553 Tanzania Arroyo, MA *AIDS* **19**(14):1517–1524 (2005)
 This sample came from an individual in Mbeya Town, Tanzania, as part of a HIV-1 diversity study. The study showed many unique recombinants as well as several subtypes.

- A1CDGKU.ZA.99.CM4 AF411964 South Africa Papathanasopoulos, MA *ARHR* **18**(12):879–886 (2002)
This sequence is from a 34 year old male AIDS patient with cryptococcal meningitis who was sampled in Johannesburg in 1999. His CD4+ T-cell count as 47 per microliter. The virus was found to be subtype ACDGK recombinant by the authors. Some regions of the genome do not cluster within the “crown group” of any of the subtypes and thus might better be considered as “untyped” in that region rather than belonging to the subtype. For example the three regions listed as subtype D, are equidistant from subtype B and subtype D sequences. Subtype B was not included in the bootscanning, only subtypes C, D, K and CRF02 (figure 3A). The viruses isolated by coculture of the patient PBMCs with donor PBMCs were assayed for coreceptor usage using U87.CD4 cells expressing either the CCR5 or CXCR4 coreceptor. The cultures were monitored for syncytia formation and for p24 antigen production. Viruses from this patient used the CCR5 coreceptor and not the CXCR4 coreceptor.
- A1DHK.NO.97.97NOGIL3 AJ237565 Norway Jonassen, TO *ARHR* **16**(1):49–58 (2000)
This sample came from one of four epidemiologically linked Norwegian individuals. The sequence involves MAL-like (recombinant of A, D and U) and subtype H-like fragments.
- A1GHU.GA.x.VI354 AF076474 Gabon Laukkanen, T Unpublished
Small sections of the 5' and 3' LTRs are not included in this sequence. This sequence is either untyped, or a complex mosaic/recombinant with regions of similarity to several other subtypes. The env V3 region seems especially similar to the entry with accession number L76899.
- A2D.KE.99.KER2003 AF457051 Kenya Dowling, WE *AIDS* **16**(13):1809–20 (2002)
This sample was part of a study revealing subtype A and A-containing recombinants in Kenya. This sample was from a blood unit collected in 1999 at Kericho District Hospital.
- AF2.CM.02.02CM_3163MN AY371160 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- AGU.CM.01.01CM_0989MO AY371166 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- AHJU.CM.01.01CM_1296NG AY371162 Cameroon Kijak, GH *ARHR* **20**(5):521–30 (2004)
This sequence was detected when designing a genotyping method for evaluation of large cohorts in West/West Central Africa. Several CRFs, subtypes and URFs were detected.
- BC.CN.96.YNRL9607 AY967804 China Qiu, Z *ARHR* **21**(12):1051–6 (2005)
The sample came from Ruili City at the epicenter of the Yunnan Province, China, epidemic. It came from an IDU who was confirmed as HIV positive in 1989. This sequence is a subtype B/C recombinant, with at least one recombination breakpoint shared with the CRF07_BC and CRF08_BC forms. The central region of this genome is subtype B and unrelated to CRF07_BC or CRF08_BC.
- BC.MM.99.mIDU103 AB097873 Myanmar Takebe, Y *AIDS* **17**(14):2077–2087 (2003)
This sample came from a study on genetic diversity in Myanmar. It is one of several different recombinants found. This sequence is mostly derived from subtype B, with a segment from subtype C in the Nef and 3'LTR region.
- BF1.BR.02.02BR006 DQ358807 Brazil Sanabani, S *Infect Genet Evol* **6**(5):368–377 (2006)
This sample came from a heterosexual female in Sao Paulo, Brazil. Many BF1 recombinants have been found in Brazil, and this is an example of one of them. Genome sequence lacks part of LTR non-coding region.
- O.BE.87.ANT70 L20587 Belgium Vanden Haesevelde, M *J Virol* **68**(3):1586–96 (1994)
ANT70 was isolated from the first O group infection discovered, and the very divergent LTR sequence was published in 1990 (de Leys, R., et al., *J Virol* 64:1207–1216 (1990)). The isolate came from CDC stage II infected 19 year old female with unusual serological reactivity, who progressed to CDC stage III before publication. She seroconverted in March 1987, and her husband was also infected with an O group HIV-1. Both the husband and wife were originally from Cameroon, and living in Belgium. The husband was CDC stage III at the time virus was isolated from the wife for sequencing. The wife had a CD4:CD8 ratio of 0.25. Supernatant from the original coculture

of wife PBMCs plus PHA-stimulated donor PBMCs, was used to infect MOLT4 clone 8cells and MT-4 cells. Syncytia were formed in both these cell lines. After several weeks culture, chronically infected cell lines were obtained that shed virus, and supernatant from these stable lines were used for viral RNA isolation. HIV-1 O group viruses have the same genetic organization as HIV-1 M group viruses. For a review see Korber, B., et al., Human Retroviruses and AIDS Database, Part III, 41-56 1996.

- O.CM.91.MVP5180 L20571 Cameroon Gurtler, LG *J Virol* **68**(3):1581–5 (1994)
This isolate was derived from a Cameroonian woman, sampled in 1991, who died of AIDS in 1992. The viral isolate MVP-5180 was grown in several human T-cell lines and the monocytic U937 line. The isolate MVP5180 is available from the NIH AIDS Reagent program, and is SI R5X4. A summary of isolates with known co-receptor usage can be found in the HIV database reviews.
- O.CM.96.96CMABB637 AY169810 Cameroon Yamaguchi, J *ARHR* **19**(11):979–88 (2003)
Genome sequence lacks part of non-coding region. Yamaguchi et al. 2003 identified 5 phylogenetic clusters of HIV-1 group O, and published 15 full length sequences. CMABB637 is associated with Cluster 5.
- O.SN.99.SEMP1300 AJ302647 Senegal Vergne, L *J Clin Microbiol* **38**(11):3919–25 (2000)
Sequence from spouse 1 of a Senegalese man (patient 98SE-42HALD) with 2 wives. The man was apparently infected by spouse 2 (isolate 99SE-MP1299), who had previously lived in Cameroon.
- N.CM.02.DJO0131 AY532635 Cameroon Bodelle, P *ARHR* **20**(8):902–908 (2004)
Genome sequence lacks part of non-coding region. This sequence is from a blood sample collected at the D'Joungolo hospital in Yaounde Cameroon in 2002, but no information on the blood donor is available. The blood was HIV-1 reactive on the 3A77 HIV immunoassay and showed reactivity to HIV-1 M and N group virus antigens in the MO2N test. HIV-1 N group seroprevalence in Cameroon is still low, as this was the only N group virus detected in 7,000 HIV-1 seropositive blood samples examined.
- N.CM.04.04CM_1015_04 DQ017382 Cameroon Yamaguchi, J *ARHR* **22**(1):83–92 (2006)
This sequence comes from an infected couple (1131 and 1015) in Yaounde, Cameroon. This patient (1015) was drug-naïve at sampling. Genome sequence lacks part of non-coding region.
- N.CM.04.04CM_1131_03 DQ017383 Cameroon Yamaguchi, J *ARHR* **22**(1):83–92 (2006)
This sequence comes from an infected couple (1131 and 1015) in Yaounde, Cameroon. This patient (1131) had received antiviral treatment. Genome sequence lacks part of non-coding region.
- N.CM.95.YBF30 AJ006022 Cameroon Simon, F *Nat Med* **4**(9):1032–7 (1998)
YBF30 was isolated from a 40 year old woman who had never traveled outside Cameroon. She presented with *Histoplasma capsulatum* infection of the colon in May, 1995 and died of AIDS (cachexia, neurological involvement and suspected disseminated histoplasmosis) in December, 1995. YBF30 was isolated from a May, 1995 blood sample and YBF31 from a December 1995 blood sample. YBF30 and YBF31 are greater than 98% identical to each other and less than 85% identical to HIV-1 M group, HIV-1 O group and SIV-CPZ sequences. The authors propose labeling this and similar viruses as N (between M and O, and also non-O non-M) group HIV-1. The N group designation is based upon sero-epidemiological surveys in Cameroon, and another sequence (YBF105 not yet submitted to the databases) which indicate that more than one patient is infected with this clade of HIV-1. 700 stored sera collected between 1988 and 1997 were serologically tested, with a peptide-based EIA. 611 (87%) were reactive with M-group. 65 (9%) were reactive with O group. 8 were indeterminate. 16 (2%) were reactive with SIV-CPZ and not M or O group, 3 of these were strongly reactive with YBF30 peptides. A partial Pol gene was sequenced for one (YBF105). YBF30 uses CCR5 as a co-receptor, and was also tested on cell lines expressing CCR2b and CCR3 and did not utilize these coreceptors. YBF30 grew on chimpanzee PBMCs, but did not replicate in T-cell lines (MT-2 and HUT78). YBF30 infection of cells was entirely blocked by RANTES alone or in combination with MIP-1alpha and MIP-1beta.
- N.CM.97.YBF106 AJ271370 Cameroon Ayouba, A *AIDS* **14**(16):2623–5 (2000)
YBF106 is from a 51 year old male patient with AIDS, from the central part of Cameroon. He was found to be HIV-seropositive in October, 1997 and died of AIDS in December, 1998.
- CPZ.CD.90.ANT U42720 Congo Vanden Haesevelde, MM *Virology* **221**(2):346–50 (1996)
CPZANT is a simian immunodeficiency virus, phylogenetically linked to HIV-1. It was isolated from a captured

wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1, after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) were isolated from chimps in Gabon. Another chimpanzee virus was sequenced in 1998, and published in 1999 with accession number AF103818 (CPZ-US). The chimpanzee viral sequences are genetically more closely related to the HIV-1 sequences derived from infected humans than are HIV-2 strains or other SIVs. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population. In 2002, B. Hahn et al reported (Science 295[5554]: 465 2002) sequencing of virus from another Pan troglodytes schweinfurthii chimp. That sequence is available with accession number AF382822, and is more closely related to this schweinfurthii sequence, than to sequences from other chimpanzees or humans. The Hahn paper labels the CPZ-ANT chimpanzee as ch-No.

- CPZ.CM.01.SIVcpzCAM13 AY169968 Cameroon Nerrienet, E *J Virol* **79**(2):1312–9 (2005)
Phylogenetic analyses by Nerrienet et al. 2005 revealed that SIVcpzCAM13 fell well within the radiation of the SIVcpzPtt group of viruses, as part of a clade including all other SIVcpzPtt strains as well as HIV-1 groups M and N. However, SIVcpzCAM13 clustered most closely with SIVcpzGAB1 from Gabon rather than with SIVcpzCAM3 and SIVcpzCAM5 from Cameroon, indicating the existence of divergent SIVcpzPtt lineages within the same geographic region. On or before Nov 1, 2003 this sequence version replaced gi:27447612, gi:27447613, gi:27447611.
- CPZ.GA.88.GAB1 X52154 Gabon Huet, T *Nature* **345**(6273):356–9 (1990)
SIV-CPZ isolate GAB1 is from a Pan troglodytes troglodytes subspecies of chimpanzee. The viruses isolated from Pan troglodytes troglodytes, such as GAB1, US, CAM3, and CAM5 are more closely related to HIV-1 M and N group viruses than are SIVs from Pan troglodytes schweinfurthii (see CPZ-ANT, accession number U42720). In at least some regions of the genome, the HIV-1 O group viruses are nearly equidistant between SIV-CPZ from troglodytes and SIV-CPZ from schweinfurthii chimpanzees. Also see CPZGAB2, U11495 for a sequence fragment from an additional chimpanzee caught in Gabon.
- CPZ.US.85.CPZUS AF103818 United States Gao, F *Nature* **397**(6718):436–41 (1999)
This full length molecular clone of a simian immunodeficiency virus, which infected an African wild-caught chimpanzee (Marilyn) who was the only chimpanzee identified as virus infected during a serosurvey of 98 chimpanzees in 1985. Marilyn had never been used in AIDS research and had not received human blood products after 1969. She died in captivity in 1985 after giving birth to stillborn twins. The complete genome was sequenced from 4 overlapped PCR fragments amplified in 1998 from spleen tissues frozen at autopsy in 1985. Recovery of infectious virus from the frozen tissue was attempted but unsuccessful. Lentivirus genomes end with TAGCA, so the extra 7 bases at the 3' end of this sequence (gtggcgc) are not included in multiple sequence alignments of genomes at the HIV Databases.
- CPZ.CM.05.SIVcpzMB66 DQ373063 Cameroon Keele, BF *Science* 2006 May 25;
This sequence comes from a wild western chimpanzee (*P. t. troglodytes*), sampled in southern Cameroon. The virus was extracted from a fecal specimen.
- CPZ.CM.05.SIVcpzLB7 DQ373064 Cameroon Keele, BF *Science* 2006 May 25;
This sequence comes from a wild western chimpanzee (*P. t. troglodytes*), sampled in southern Cameroon. The virus was extracted from a fecal specimen.
- CPZ.CM.05.SIVcpzEK505 DQ373065 Cameroon Keele, BF *Science* 2006 May 25;
This sequence comes from a wild western chimpanzee (*P. t. troglodytes*), sampled in southern Cameroon. The virus was extracted from a fecal specimen.
- CPZ.CM.05.SIVcpzMT145 DQ373066 Cameroon Keele, BF *Science* 2006 May 25;
This sequence comes from a wild western chimpanzee (*P. t. troglodytes*), sampled in southern Cameroon. The virus was extracted from a fecal specimen.
- CPZ.TZ.01.TAN1 AF447763 Tanzania Santiago, ML *J Virol* **77**(3):2233–2242 (2003)
Genome lacks part of the non-coding region; sequence is oriented in the R-U5-gag-pol-env-U3-R configuration. Distance and phylogenetic tree analyses by Santiago et al. 2003 identified TAN1 unambiguously as a member of the HIV-1/SIVcpz group of viruses, but also revealed an extraordinary degree of divergence from all previously characterized SIVcpz and HIV-1 strains. The documentation of SIVcpzTAN1 in Gombe extends the geographic range of SIVcpz from Gabon and Cameroon across equatorial Africa to Tanzania.

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A1.SE.94.SE7253	0
A1.TZ.01.A173	0
A1.UA.00.98UA0116	361
A1.UG.92.92UG037	0
A1.UG.98.98UG57136	0
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A2.CD.97.97CDKS10	0
A2.CD.97.97CDKTB48	0
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C.IN.99.01IN565_10	0
C.KE.00.KER2010	0
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C.ZM.96.96ZM651	0
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D.CD.83.NDK	0
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F1.FI.93.FIN9363	0
F1.FR.96.MP411	0
F2.CM.02.02CM_0016BBY	0
F2.CM.95.MP255	0
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F2.CM.97.CM53657	0
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K.CM.96.MP535	0

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01 AE.TH.01.0UR4141
01 AE.TH.02.0UR7691
02 AE.TH.90.CM240
02 AG.CM.02.02CM_16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SN.98.MPI211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153_2
04 CDX.CV.94.CY032
05 DF.BE.x.VII1310
06 CDX.AU.96.BFP90
07 BC.CN.97.CM54
08 BC.CN.97.97CNGX_6F
09 CDX.GH.96.96GH2911
10 CD.TZ.96.96TZ_BF061
11 CDX.GR.x.GR17
12 BF.AR.99.ARMAL159
13 CDX.CM.96.H849
14 BG.ES.99.X397
15 01B.TH.99.99TH_MU2079
16 A2D.KR.97.97KR004
18 CDX.CU.99.CU76
19 CDX.CU.99.CU77
20 BG.CU.03.CB134
21 A2D.KE.91.KNHI254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CDX.CM.x.101BA
28 BF.BR.99.BREPMI2609
29 BF.BR.02.BREPMI19
31 BC.BR.02.110PA
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U.CD.90.90CD121E12
U.GR.99.GR303
U.NL.x.U.NL.95.H10986_D1
N.CM.02.DJ00131
N.CM.04.04CM_1131_03
N.CM.95.YBF30
N.CM.97.YBF106
O.BE.87.AN170
O.CM.91.MVPS180
O.CM.96.96CMWAB637
O.SN.99.SEMPL300
CFZ.CD.90.ANT
CFZ.CM.01.SIVcpzCAM13
CFZ.CM.05.SIVcpzE4505
CFZ.CM.05.SIVcpzLB7
CFZ.CM.05.SIVcpzMB66
CFZ.CM.05.SIVcpzWTL145
CFZ.GA.88.GAB1
CFZ.TZ.01.TANI1
CFZ.US.85.CFPZUS

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01 AE.CF.90.90CF402	A---C-G	G-T	G-T	GT	T-A	A	469
01 AE.CN.05.FJ051	A-A---C-G	G-T	G-T	AGT	TT	A	446
01 AE.HK.x.HK001	A	G-T	G-T	AGT	TT	A	446
01 AE.JP.93.93JP.NH1	A	G-T	G-T	AGT	TT	A	446
01 AE.TH.01.OUR4141	A	G-T	G-T	AGT	TT	A	446
01 AE.TH.02.OUR7691	A	G-T	G-T	AGT	TT	A	446
01 AE.TH.90.CM240	A	G-T	G-T	AGT	TT	A	446
02 AG.CM.02.02CM_16691E	A	G-T	G-T	AGT	TT	A	446
02 AG.EC.x.EC041	A	G-T	G-T	AGT	TT	A	446
02 AG.FR.91.DJ264	A	G-T	G-T	AGT	TT	A	446
02 AG.GH.03.GHNJ196	A	G-T	G-T	AGT	TT	A	446
02 AG.NG.x.IBNG	A	G-T	G-T	AGT	TT	A	446
02 AG.SN.98.MP1211	A	G-T	G-T	AGT	TT	A	446
02 AG.UZ.02.02UZ693	A	G-T	G-T	AGT	TT	A	446
03 AB.RU.97.KAL153_2	A	G-T	G-T	AGT	TT	A	446
04 CPX.CV.94.CY032	A	G-T	G-T	AGT	TT	A	446
05 DF.BE.x.VII1310	A	G-T	G-T	AGT	TT	A	446
06 CPX.AU.96.BFP90	A	G-T	G-T	AGT	TT	A	446
07 BC.CN.97.CNS4	A	G-T	G-T	AGT	TT	A	446
08 BC.CN.97.97CNGX_6F	A	G-T	G-T	AGT	TT	A	446
09 CPX.GH.96.96GHD2911	A	G-T	G-T	AGT	TT	A	446
10 CD.TZ.96.96TZ_BF061	A	G-T	G-T	AGT	TT	A	446
11 CPX.GR.x.GR17	A	G-T	G-T	AGT	TT	A	446
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13 CPX.CM.96.1849	A	G-T	G-T	AGT	TT	A	446
14 BG.ES.99.X397	A	G-T	G-T	AGT	TT	A	446
15 01B.TH.99.99TH_MU2079	A	G-T	G-T	AGT	TT	A	446
16 A2D.KR.97.97KR004	A	G-T	G-T	AGT	TT	A	446
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19 CPX.CU.99.CU7	A	G-T	G-T	AGT	TT	A	446
20 BG.CU.03.CB134	A	G-T	G-T	AGT	TT	A	446
21 A2D.KE.91.KNHI254	A	G-T	G-T	AGT	TT	A	446
23 BG.CU.03.CB118	A	G-T	G-T	AGT	TT	A	446
24 BG.CU.03.CB378	A	G-T	G-T	AGT	TT	A	446
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28 BF.BR.99.BREPM12609	A	G-T	G-T	AGT	TT	A	446
29 BF.BR.02.BREPM119	A	G-T	G-T	AGT	TT	A	446
31 BC.BR.02.110PA	A	G-T	G-T	AGT	TT	A	446
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AP2.CM.02.02CM_3163MN	A	G-T	G-T	AGT	TT	A	446
AGU.CM.01.01CM_0989MO	A	G-T	G-T	AGT	TT	A	446
ARU.CM.01.01CM_1296NG	A	G-T	G-T	AGT	TT	A	446
BC.CN.96.YNRL96607	A	G-T	G-T	AGT	TT	A	446
BC.MW.99.MIDDU103	A	G-T	G-T	AGT	TT	A	446
BF1.BR.02.02BR006	A	G-T	G-T	AGT	TT	A	446
0708.CN.00.HH069	A	G-T	G-T	AGT	TT	A	446
U.CD.83.83CD003	A	G-T	G-T	AGT	TT	A	446
U.CD.90.90CD121E12	A	G-T	G-T	AGT	TT	A	446
U.GR.99.GR303	A	G-T	G-T	AGT	TT	A	446
U.NL.x.U.NL_95_H10986_D1	A	G-T	G-T	AGT	TT	A	446
N.CM.02.DJU00131	A	G-T	G-T	AGT	TT	A	446
N.CM.04.04CM_1131_03	A	G-T	G-T	AGT	TT	A	446
N.CM.95.YBF30	A	G-T	G-T	AGT	TT	A	446
N.CM.97.YBF106	A	G-T	G-T	AGT	TT	A	446
O.BE.87.ANI70	A	G-T	G-T	AGT	TT	A	446
O.CM.91.MVPS180	A	G-T	G-T	AGT	TT	A	446
O.CM.96.96CMBAB637	A	G-T	G-T	AGT	TT	A	446
O.SN.99.SEMP1300	A	G-T	G-T	AGT	TT	A	446
CPZ.CD.90.ANT	A	G-T	G-T	AGT	TT	A	446
CPZ.CM.01.SIVcpzCAM13	A	G-T	G-T	AGT	TT	A	446
CPZ.CM.05.SIVcpzEK505	A	G-T	G-T	AGT	TT	A	446
CPZ.CM.05.SIVcpzLI57	A	G-T	G-T	AGT	TT	A	446
CPZ.CM.05.SIVcpzMB66	A	G-T	G-T	AGT	TT	A	446
CPZ.CM.05.SIVcpzWT145	A	G-T	G-T	AGT	TT	A	446
CPZ.GA.88.GAB1	A	G-T	G-T	AGT	TT	A	446
CPZ.TZ.01.TANI	A	G-T	G-T	AGT	TT	A	446
CPZ.US.85.CPZUS	A	G-T	G-T	AGT	TT	A	446

HIV-1/SIVcpz complete genomes

5' LTR U3 end	+1 mRNA start site	5' LTR R repeat begin	Poly-A signal	5' LTR R repeat end	5' LTR start	
B.FR.83.HXB2	CTGTACTGGTCTCTCTCTGTAGACCAAGATCACTTGGAGCTCTCTGGCTAACT.....AGGGAACCCACTGCTTAA.CCCTCAATA.AAGCTTCCCTTGGAGTCT.TCAAGTAGTGTGGCCCGTC					568
A1.KE.94.Q23.17					38
A1.RU.03.03RU20.06.13					54
A1.RW.93.93RW037A					569
A1.SE.94.SET253					0
A1.TZ.01.A173					579
A1.UA.00.98UA0116					0
A1.UG.92.92UG037					0
A1.UG.98.98UG57136					0
A2.CD.97.97CDKFE4					0
A2.CD.97.97CDKS10					0
A2.CD.97.97CDKTB48					0
A2.CY.94.94CY017.41					0
A.SN.01.DD1579					0
A.SN.01.DD3369					0
A.SN.96.DD3360					0
A.ZA.04.04ZASK162B1					2
B.AR.00.ARMS008					0
B.AU.96.MBCD36					0
B.CO.01.PCM074					0
B.GA.88.OYI					114
B.NL.99.671					20
B.RU.04.04RU129005					54
B.TH.90.EK132					568
B.US.90.WEAU160					0
B.US.98.1058.11					0
C.AR.01.ARG4006					0
C.BR.04.04BR013					29
C.BR.92.BR0253d					0
C.BW.00.00BW07621					0
C.ET.86.ETH2220					0
C.IN.95.95IN21068					0
C.IN.99.01IN565.10					0
C.KE.00.KER2010					0
C.TZ.01.BD9.11					0
C.UY.01.TRA3011					2
C.ZA.04.SKJ64B1					2
C.ZA.05.05ZASK245B1					569
C.ZM.02.02ZM115					0
C.ZM.96.96ZM651					114
D.CD.83.ELI					112
D.CD.83.NDK					0
D.CM.01.01CM.4412HAL					0
D.KE.01.NKU3006					0
D.TD.99.MN012					0
D.TZ.01.A280					0
D.UG.94.94UG114					0
D.UG.99.99UGD23550					0
D.UG.99.99UGK09958					0
D.ZA.86.R482					0
F1.BE.93.VI850					0
F1.BR.89.BZ126					0
F1.BR.93.93BR020.1					0
F1.FI.93.FIN9363					0
F1.FR.96.MP411					0
F2.CM.02.02CM.0016BBY					0
F2.CM.95.MP255					0
F2.CM.95.MP257					0
F2.CM.97.CM53657					0
G.BE.96.DRCBL					534
G.CM.01.01CM.4049HAN					0
G.ES.99.X138					0
G.KE.93.HH8793.12.1					0
G.NG.92.92NG083					0
G.SE.93.SE6165					0
H.BE.93.VI991					0
H.BE.93.VI997					0
H.CF.90.056					0
J.SE.93.SE7887					0
J.SE.94.SE7022					0
K.CD.97.EQTB11C					0
K.CM.96.MP535					0

HIV-1/SIVcpz
complete genomes

	5' ITR US end	Lys tRNA primer binding site	
B.FR.83.HXB2	TGTT...GTCTGA.CTCTGTAACCTAGATCCCTCAGACC...CITTTAGTC...AGTGTGG...AAAATCTCTAG.CAGTGGCCCGGACAGGG...	-----	660
A1.KE.94.Q23.17	-----	AC-C-A-G-----	126
A1.RU.03.03RU20.06.13	-----	AC-C-G-----	142
A1.RW.93.93RW037A	-----	T-A-A-----	657
A1.SE.94.SE7253	-----	-----	0
A1.TZ.01.A173	-----	-----	0
A1.UA.00.98UA0116	-----	-----	667
A1.UG.92.92UG037	-----	-----	30
A1.UG.98.98UG57136	-----	-----	0
A2.CD.97.97CDKPE4	-----	-----	0
A2.CD.97.97CDKS10	-----	-----	7
A2.CD.97.97CDKTB48	-----	-----	28
A2.CY.94.94CY0117_41	-----	-----	0
A.SN.01.DDI579	-----	-----	0
A.SN.01.DDJ369	-----	-----	0
A.SN.96.DDJ360	-----	-----	0
A.ZA.04.04ZASK162B1	-----	-----	90
B.AR.00.ARMS008	-----	-----	0
B.AU.96.MBCD36	-----	-----	26
B.CO.01.PCM074	-----	-----	0
B.GA.88.OYI	-----	-----	217
B.NL.99.671	-----	-----	182
B.RU.04.04RU1129005	-----	-----	157
B.TH.90.RK132	-----	-----	22
B.US.90.WEAU160	-----	-----	671
B.US.98.1058.11	-----	-----	0
C.AR.01.ARG4006	-----	-----	0
C.BR.04.04BR013	-----	-----	132
C.BR.92.BR025.d	-----	-----	21
C.BW.00.00BW07621	-----	-----	46
C.ET.86.ETH2220	-----	-----	50
C.IN.95.95IN21068	-----	-----	49
C.IN.99.01IN565_10	-----	-----	51
C.KE.00.KER2010	-----	-----	0
C.TZ.01.BD9.11	-----	-----	0
C.UY.01.TRA3011	-----	-----	0
C.ZA.04.SK164B1	-----	-----	105
C.ZA.05.05ZASK245B1	-----	-----	672
C.ZM.02.02ZM115	-----	-----	17
C.ZM.96.96ZM651	-----	-----	0
D.CD.83.ELI	-----	-----	217
D.CD.83.NDK	-----	-----	215
D.CM.01.01CM.4412HAL	-----	-----	0
D.KE.01.NKU3006	-----	-----	0
D.TD.99.MN012	-----	-----	0
D.TZ.01.A280	-----	-----	18
D.UG.94.94UG114	-----	-----	0
D.UG.99.99UGD2550	-----	-----	0
D.UG.99.99UGK03958	-----	-----	0
D.ZA.86.R482	-----	-----	0
F1.BE.93.VI850	-----	-----	21
F1.BR.89.B2126	-----	-----	39
F1.BR.93.93BR020_1	-----	-----	17
F1.FI.93.FIN9363	-----	-----	15
F1.FR.96.MP411	-----	-----	0
F2.CM.02.02CM.0016BBY	-----	-----	0
F2.CM.95.MP255	-----	-----	0
F2.CM.95.MP257	-----	-----	0
F2.CM.97.CW53657	-----	-----	0
G.BE.96.DRCBL	-----	-----	646
G.CM.01.01CM.4049HAN	-----	-----	0
G.ES.99.X138	-----	-----	111
G.KE.93.HH8793_12_1	-----	-----	64
G.NG.92.92NG083	-----	-----	29
G.SE.93.SE6165	-----	-----	65
H.BE.93.VI991	-----	-----	49
H.BE.93.VI997	-----	-----	0
H.CF.90.056	-----	-----	18
J.SE.93.SE7887	-----	-----	0
J.SE.94.SE7022	-----	-----	0
K.CD.97.EQTB11C	-----	-----	0
K.CM.96.MP535	-----	-----	0

Extensive secondary structure in this region.

See Rizvi *J Virol* 67:2681-8 (1993)

Extensive secondary structure in this region.

See Rizvi *J Virol* 67:2681-8(1993)

5' ITR US end | - Lys tRNA primer binding site

B.FR.83.HXB2	660	CGTTGAAAGCGGAAAGTCTTAATAGGACTCG-A	ACCTGAAAG
01 AE.CF.90.90CF402	703	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
01 AE.CN.05.FU051	680	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
01 AE.HK.x.HK001	39	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
01 AE.JP.93.93JP.NH1	680	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
01 AE.TH.01.OUR414T	0		
01 AE.TH.02.OUR769T	0		
01 AE.TH.90.CM240	229	CACTGAAAGCGGAAAGTCTTAATAGGACTCG-A	
02 AG.CM.02.02CM_16691E	0		
02 AG.EC.x.EC041	0		
02 AG.FR.91.DJ264	27	GCACCCGGGAAAGTCTTAATAGGACTCG-A	
02 AG.GH.03.GHNJ196	686	ACCGG...AACTTAATAGGAC-CG-A	
02 AG.NG.x.IBNG	203	ACTTGCAC...GGTAATA.GGGACTCG-A	
02 AG.SN.98.MP1211	0		
02 AG.UZ.02.02UZ693	0		
03 AB.RU.97.KAL153_2	28	TTGAAAGTGAAGTCTTAATA.GGACTCG-A	
04 CPX.CV.94.CY032_2	47	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
05 DF.BE.x.VI1310	692	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
06 CPX.AU.96.BEP90	48		
07 BC.CN.97.CNS4	0		
08 BC.CN.97.97CNGX_6F	49	T.ACTGAAAGCGGAAAGTCTTAATAGGACTCG-A	
09 CPX.GH.96.96GH2911	691	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
10 CD.TZ.96.96TZ_BF061	48	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
11 CPX.GR.x.GR17	172	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
12 BF.AR.99.ARMAL159	28	CGT.AAAGTGAAGTAA.TAGGACTCG-A	
13 CPX.CM.96.1849	0		
14 BG.ES.99.X397	0		
15 01B.TH.99.99TH_MU2079	0		
16 A2D.KR.97.97KR004	0		
18 CPX.CU.99.CU76	0		
19 CPX.CU.99.CU77	0		
20 BG.CU.03.CB134	120	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
21 A2D.KE.91.KNH1254	0		
23 BG.CU.03.CB118	123	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
24 BG.CU.03.CB378	118	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
25 CPX.CM.x.101BA	0		
28 BF.BR.99.BREPM12609	42	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
29 BF.BR.02.BREPM119	127	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
31 BC.BR.02.110PA	48	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
33_01B.WY.05.05MYKL007_1	0		
A1.C.TZ.02.CO3710	0		
A1.CDGKU.ZA.99.CM4	672	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
A1.DHK.NO.97.97NOGL13	686	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
A1.GHU.GA.x.VI354	31	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
A2D.KE.99.KER2003	0		
AP2.CM.02.02CM_3163MN	0		
AGU.CM.01.01CM_0989MO	0		
ARU.CM.01.01CM_1296NG	0		
BC.CN.96.YNRL96607	40	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
BC.MM.99.MIDD103	576	ACCCGAAAGCGGAAAGTCTTAATAGGACTCG-A	
BF1.BR.02.02BR006	0		
0708.CN.00.HH069	169	ACCGGAAAGCGGAAAGTCTTAATAGGACTCG-A	
U.CD.83.83CD003	0		
U.CD.90.90CD121E12	0		
U.GR.99.GR303	0		
U.NL.x.U.NL_95_H10986_D1	566	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
N.CM.02.DJ00131	141	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
N.CM.04.04CM_1131_03	141	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
N.CM.95.YBF30	229	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
N.CM.97.YBF106	229	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
O.BE.87.ANI70	700	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
O.CM.91.MVPS180	674	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
O.CM.96.96CMBAB637	126	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
O.SN.99.SEMP1300	701	ACCGGAAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CD.90.ANT	13	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CM.01.SIVcpzCAM13	212	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CM.05.SIVcpzEK505	210	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CM.05.SIVcpzL17	215	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CM.05.SIVcpzMB66	218	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.CM.05.SIVcpzMT145	215	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.GA.88.GAB1	687	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.TZ.01.ITAN1	217	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	
CPZ.US.85.CPZUS	694	ACTTGAAGCGGAAAGTCTTAATAGGACTCG-A	

HIV-1/SIVcpz complete genomes

Gag p7 nucleocapsid binds these loops, see DeGuzman, *Science* 279:384-8
 - Packaging signal secondary structure, see Harrison, *J Virol* 72:5886-96

B.FR.83.HXB2	CGAAGGGAACACAGAGGAG	CTC....TCTCA.GCGAGG..ACTCGCTTGCTGAA.GCGCCACGCGAAGAGCGAGG.GGC....GG....CGA.CTGGTGAGTACG....CCAAAA	758
A1.KE.94.Q23_17	AAGCGAAAGTT	A	G-T-A-A	T
A1.RU.03.03RU20_06_13	AAGCGAAAGTT	A	G-T-A-A	T
A1.RW.93.93RW037A_13	AAGCGAAAGTT	A	G-T-A-A	T
A1.SE.94.SE7253	AAGCGAAAGTT	A	G-T-A-A	T
A1.TZ.01.A173	AAGCGAAAGTT	A	G-T-A-A	T
A1.UA.00.98UA0116	AA-CGAAAGTT	T	G-T-A-A	T
A1.UG.92.92UG037	AA-CGAAAGTT	T	G-T-A-A	T
A1.UG.98.98UG57136	AA-CGAAAGTT	T	G-T-A-A	T
A2.CD.97.97CDKPE4	AA-CGAAAGTT	T	G-T-A-A	T
A2.CD.97.97CDKSL0	AA-CGAAAGTT	T	G-T-A-A	T
A2.CD.97.97CDKTB48	AA-CGAAAGTT	T	G-T-A-A	T
A2.CY.94.94CY017_41	AA-CGAAAGTT	T	G-T-A-A	T
A.SN.01.DDH579	AA-CGAAAGTT	T	G-T-A-A	T
A.SN.01.DDH369	AA-CGAAAGTT	T	G-T-A-A	T
A.SN.96.DDH360	AA-CGAAAGTT	T	G-T-A-A	T
A.ZA.04.04ZASK162B1	AA-CGAAAGTT	T	G-T-A-A	T
B.AR.00.ARMS008	AA-CGAAAGTT	T	G-T-A-A	T
B.AU.96.MBCD36	AA-CGAAAGTT	T	G-T-A-A	T
B.CO.01.PCM074	AA-CGAAAGTT	T	G-T-A-A	T
B.GA.88.OYI	AA-CGAAAGTT	T	G-T-A-A	T
B.NL.99.671	AA-CGAAAGTT	T	G-T-A-A	T
B.RU.04.04RU129005	AA-CGAAAGTT	T	G-T-A-A	T
B.TH.90.RK132	AA-CGAAAGTT	T	G-T-A-A	T
B.US.90.WEAU160	AA-CGAAAGTT	T	G-T-A-A	T
B.US.98.1058_11	AA-CGAAAGTT	T	G-T-A-A	T
C.AR.01.ARG4006	AA-CGAAAGTT	T	G-T-A-A	T
C.BR.04.04BR013	AA-CGAAAGTT	T	G-T-A-A	T
C.BR.92.BR025_d	AA-CGAAAGTT	T	G-T-A-A	T
C.BW.00.00BW07621	AA-CGAAAGTT	T	G-T-A-A	T
C.ET.86.ETH2220	AA-CGAAAGTT	T	G-T-A-A	T
C.IN.95.95IN21068	AA-CGAAAGTT	T	G-T-A-A	T
C.IN.99.01IN565_10	AA-CGAAAGTT	T	G-T-A-A	T
C.KE.00.KER2010	AA-CGAAAGTT	T	G-T-A-A	T
C.TZ.01.BD9_11	AA-CGAAAGTT	T	G-T-A-A	T
C.UY.01.TRA3011	AA-CGAAAGTT	T	G-T-A-A	T
C.ZA.04.SK164B1	AA-CGAAAGTT	T	G-T-A-A	T
C.ZA.05.05ZASK245B1	AA-CGAAAGTT	T	G-T-A-A	T
C.ZM.02.02ZM115	AA-CGAAAGTT	T	G-T-A-A	T
C.ZM.96.96ZM651	AA-CGAAAGTT	T	G-T-A-A	T
D.CD.83.ELI	AA-CGAAAGTT	T	G-T-A-A	T
D.CD.83.NDK	AA-CGAAAGTT	T	G-T-A-A	T
D.CM.01.01CM_4412HAL	AA-CGAAAGTT	T	G-T-A-A	T
D.KE.01.NKU3006	AA-CGAAAGTT	T	G-T-A-A	T
D.TD.99.MN012	AA-CGAAAGTT	T	G-T-A-A	T
D.TZ.01.A280	AA-CGAAAGTT	T	G-T-A-A	T
D.UG.94.94UG114	AA-CGAAAGTT	T	G-T-A-A	T
D.UG.99.99UGD2550	AA-CGAAAGTT	T	G-T-A-A	T
D.UG.99.99UGK03958	AA-CGAAAGTT	T	G-T-A-A	T
D.ZA.86.K482	AA-CGAAAGTT	T	G-T-A-A	T
F1.BE.93.VI850	AA-CGAAAGTT	T	G-T-A-A	T
F1.BR.89.B2126	AA-CGAAAGTT	T	G-T-A-A	T
F1.BR.93.93BR020_1	AA-CGAAAGTT	T	G-T-A-A	T
F1.FI.93.FIN9363_1	AA-CGAAAGTT	T	G-T-A-A	T
F1.FR.96.MP411	AA-CGAAAGTT	T	G-T-A-A	T
F2.CM.02.02CM_0016BBY	AA-CGAAAGTT	T	G-T-A-A	T
F2.CM.95.MP255	AA-CGAAAGTT	T	G-T-A-A	T
F2.CM.95.MP257	AA-CGAAAGTT	T	G-T-A-A	T
F2.CM.97.CW53657	AA-CGAAAGTT	T	G-T-A-A	T
G.BE.96.DRCHL	AA-CGAAAGTT	T	G-T-A-A	T
G.CM.01.01CM_4049HAN	AA-CGAAAGTT	T	G-T-A-A	T
G.ES.99.X138	AA-CGAAAGTT	T	G-T-A-A	T
G.KE.93.HH8793_12_1	AA-CGAAAGTT	T	G-T-A-A	T
G.NG.92.92NG083	AA-CGAAAGTT	T	G-T-A-A	T
G.SE.93.SE6165	AA-CGAAAGTT	T	G-T-A-A	T
H.BE.93.VI991	AA-CGAAAGTT	T	G-T-A-A	T
H.BE.93.VI997	AA-CGAAAGTT	T	G-T-A-A	T
H.CF.90.056	AA-CGAAAGTT	T	G-T-A-A	T
J.SE.93.SE7887	AA-CGAAAGTT	T	G-T-A-A	T
J.SE.94.SE7022	AA-CGAAAGTT	T	G-T-A-A	T
K.CD.97.EQTB11C	AA-CGAAAGTT	T	G-T-A-A	T
K.CM.96.MP535	AA-CGAAAGTT	T	G-T-A-A	T

Gag p7 nucleocapsid binds these loops, see DeGuzman, *Science* 279:384-8
 - Packaging signal secondary structure, see Harrison, *J Virol* 72:5886-96

B_FR_83_HXB2	CGAAGGGAACACAGAGGAG	CTC.....TCTCGA.CGCAGG..ACTCGCTTCTGTA.....A.GCCGCACCGAAGAGGCGAGG.GGC.....GG....CGA.CTGGTGAGTACG.....CCAAAA	758
01_AE_CF_90_90CF402	AAGCGAAAGTTG-T-A-A-A	800
01_AE_CN_05_FU051	AAGCGAAGTTA	774
01_AE_HK_x_HK001	AAGCGAAGTTG	135
01_AE_JP_93_93JP_NH1	AAGCGAAGTTA	775
01_AE_TH_01_0UR4141	0
01_AE_TH_02_0UR7691	0
01_AE_TH_90_CM240	A.GCGAAAGTTG-T-A-A-A	324
02_AG_CM_02_02CM_16691EA	0
02_AG_EC_x_EC041	0
02_AG_FR_91_DJ264	A.GCGAAAGTTG-T-A-A-A	123
02_AG_GH_03_GHNJ196	AAGCGAAGTTG-T-A-A-A	781
02_AG_NG_x_IBNG	A.GCGAAAGTTA-G	299
02_AG_SN_98_MP1211	0
02_AG_UZ_02_02UZ693	0
03_AB_RU_97_KAL153_2	A.GCGAAAGTTG-T-A-A-A	124
04_CFX_CV_94_CV032	A.AG-TA	134
05_DF_BE_x_VII1310	AAGCGAAGTTG-T-A-A-A	786
07_BC_CN_97_CNS4A	134
08_BC_CN_97_97CNGX_6F	0
09_CFX_GH_96_96GHD2911G.CA	136
10_CD_TZ_96_96TZ_BF061G	773
11_CFX_GR_x_GR17A-G	778
12_BF_AR_99_ARMAL159G	134
13_CFX_CM_96_1849	A.GCGAAAGTTG-T-A-A-A	208
14_BG_ES_99_X397	A.GCGAAAGTTG-T-A-A-A	166
15_01B_TH_99_99TH_MU2079	A.GCGAAAGTTG-T-A-A-A	123
16_A2D_KR_97_97KR004	A.GCGAAAGTTG-T-A-A-A	75
18_CFX_CU_99_CU76A	0
19_CFX_CU_99_CU7	AAGCGAAGTTG-T-A-A-A	217
20_BG_CU_03_CBI34A	0
21_A2D_KE_91_KNH1254	AAGCGAAGTTG-T-A-A-A	220
23_BG_CU_03_CBI18	AAGCGAAGTTG-T-A-A-A	215
24_BG_CU_03_CBI38A	0
25_CFX_CM_x_101BA	128
28_BF_BR_99_BREPM12609	0
29_BF_BR_02_BREPM119	0
31_BC_BR_02_110PA	213
33_01B_WY_05_05MYKL007_1	AAGCGAAGTTG-T-A-A-A	144
A1C_TZ_02_C03710	0
A1CDGKU_ZA_99_CM4	758
A1DHU_NO_97_97NOGLI3G	774
A1GHU_GA_x_VI354	ATG-T-A-A-A	127
A2D_KE_99_KER2003A	0
AP2_CM_02_02CM_3163MN	0
AGU_CM_01_01CM_0989MO	0
ARU_CM_01_01CM_1296NG	0
BC_MM_99_mIDDU103A	126
BF1_BR_02_02BR006G	663
0708_CN_00_HH069G	0
U_CD_83_83CD003G	256
U_CD_90_90CD121E12G	0
U_GR_99_GR303ACGGGTC	44
U_NL_x_U_NL_95_H10986_D1A	652
N_CM_02_DJ00131C	224
N_CM_04_04CM_1131_03C	225
N_CM_95_YBF30C	312
N_CM_97_YBF106C	313
O_BE_87_ANI70A	787
O_CM_91_MVPS180A	762
O_CM_96_96CMWAB637A	214
O_SN_99_SEMP1300A	789
CPZ_CD_90_ANTA	95
CPZ_CM_01_SIVcpzCAM13A	296
CPZ_CM_05_SIVcpzEK505A	294
CPZ_CM_05_SIVcpzL17A	303
CPZ_CM_05_SIVcpzMB66A	305
CPZ_CM_05_SIVcpzWT145A	304
CPZ_GA_88_GAB1A	771
CPZ_TZ_01_TAN1A	296
CPZ_US_85_CFPZUSA	777

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

end packaging loops - | / Gag and Gag-Pol_CDS start

A.....TTTTGACTAGCGGA...GGCTAGAAAG.....GAGAGAG..ATGGGTCCGAGAGCGTCAGTATTAGCGGGGAGAAATTAGATCGATCGGAAAAAATTCGGT 850

.....T.....A.....C.....GC.....G..... 314

.....T.....G.....A.....GC.....G..... 333

-AT..T.....A.....AC.....G.....A-C 849

.....T.....A.....GC.....G..... 57

.....A.....T.....A.....G.....GC.....G..... 55

GA..T.....A.....GC.....G..... 858

.....T.....T.....A.....GC.....G..... 220

.....T.....A.....GCG.....G..... 55

..... 0

.....G.....C.....A.....AGCT.....G..... 197

.....A.....A.....AAG.....G..... 219

.....A.....A.....GC.....G..... 57

.....A.....AAG.....G..... 57

.....A.....AAG.....G..... 57

-AT..T.....A.....TC.....G.....C..... 282

.....AA.....AA.....G..... 55

.....A.....A.....A.....G..... 205

.....CAA.....AA..... 55

.....AA.....AA..... 396

.....A.....CAA.....G..... 378

.....A.....CAA.....G..... 336

.....C.....A.....G..... 201

.....G.....A.....G..... 849

.....A.....AC.....G..... 49

.....A.....C.....A.....ACT.....G.....AA 55

.....C.....A.....A.....ACT.....G.....A 311

.....A.....A.....GCT.....G.....AA 200

TT..TTA.....A.....A.....AA.....A..... 227

TT..TTA.....A.....C.....A.....GCC.....AA 230

T.....TA.....A.....AA.....A..... 228

.....A.....A.....AA.....A..... 231

.....A.....A.....GC.....A.....A 55

.....A.....A.....AC.....A.....A 55

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.....A.....A.....AC.....A.....A 285

.....A.....A.....CAA.....A.....A 285

.....TTTA.....A.....AA.....A.....A 853

T.....TTA.....A.....AA.....A.....A 197

.....A.....AA.....A.....G..... 396

T.....A.....A.....G.....G..... 394

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.....T.....A.....GA.....G..... 68

.....A.....GA.....G.....G..... 55

.....C.....GC.....G..... 199

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.....T.....C.....GA.....G..... 55

.....CTA-CGGA.....G..... 111

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.....A.....A.....GCT.....A.....A 193

.....A.....C.....GC.....G..... 191

.....A.....GC.....G.....-A 61

.....A.....GC.....G..... 55

.....A.....GC.....G..... 61

.....A.....GAT-T..... 55

.....A.....GCT.....G..... 835

.....A.....TCT..... 55

.....A.....GC..... 300

.....S-S.....GC.....SC 252

.....A.....TCT..... 216

.....C.....GCT..... 253

-TTTTTA.....A.....GCT.....G..... 236

-TTTTTA.....CG.....ACT-T.....G..... 177

T.....G.....GCT.....G..... 197

-T..AT.....A.....T.....A.....GAT..... 173

-T..ATT.....A.....T.....A.....CGAT..... 174

.....A.....CAA.....A.....A.....G..... 61

.....A.....A.....A.....GC.....G..... 61

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A1.UG.92.92UG037

A1.UG.98.98UG57136

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A2.CD.97.97CDKS10

A2.CD.97.97CDKTB48

A3.CY.94.94CY017.41

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A.SN.96.DDQ360

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B.NL.99.671

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B.US.98.1058.11

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C.BR.92.BR025.d

C.BW.00.00BW07621

C.ET.86.ETH220

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C.IN.99.01IN565.10

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C.UY.01.TRA3011

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C.ZA.05.05ZASK245B1

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C.ZM.96.96ZM651

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D.TZ.01.A280

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D.UG.99.99UGK09958

D.ZA.86.86Z82

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F1.BR.93.93BR020.1

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F2.CM.95.MP255

F2.CM.95.MP257

F2.CM.97.CM53657

G.BE.96.DRCBL

G.CM.01.01CM.4049HAN

G.ES.99.X138

G.KE.93.HH8793.12.1

G.NG.92.92NG083

G.SE.93.SE6165

H.BE.93.VI991

H.BE.93.VI997

H.CF.90.056

J.SE.93.SE7887

J.SE.94.SE7022

K.CD.97.EQTB11C

K.CM.96.MP535

B.FR.83.HXB2	A.....TTTTGACTAGCGGA...GGCTAGTAGAG.....	end packaging loops - / Gag and Gag-Pol CDS startGAGAGAG-ATGGGTCGAGAGCGTCAGTATTAGCCGGGGGAGAAATTAGATCGATCGGAAAAAATTCGGT	850
01 AE.CF.90.90CF402A.....	T-A-A-GC-G-C	856
01 AE.CN.05.FJ051A.....	T-A-A-GC-G-C	862
01 AE.HK.x.HK001A.....	T-A-A-GC-G-C	866
01 AE.JP.93.93JP.NH1A.....	T-A-A-GC-G-C	872
01 AE.TH.01.0UR4141A.....	T-A-A-GC-G-C	878
01 AE.TH.02.0UR7691A.....	T-A-A-GC-G-C	884
02 AE.TH.90.CM240A.....	T-A-A-GC-G-C	890
02 AG.CM.02.02CM_16691EA.....	T-A-A-GC-G-C	896
02 AG.EC.x.EC041A.....	T-A-A-GC-G-C	902
02 AG.FR.91.DJ264A.....	T-A-A-GC-G-C	908
02 AG.GH.03.GHNJ196A.....	T-A-A-GC-G-C	914
02 AG.NG.x.IBNGA.....	T-A-A-GC-G-C	920
02 AG.SN.98.MP1211A.....	T-A-A-GC-G-C	926
02 AG.UZ.02.02UZ693A.....	T-A-A-GC-G-C	932
03 AB.RU.97.KAL153.2A.....	T-A-A-GC-G-C	938
04 CDX.CV.94.CY032A.....	T-A-A-GC-G-C	944
05 DF.BE.x.VII1310A.....	T-A-A-GC-G-C	950
06 CDX.AU.96.BFP90A.....	T-A-A-GC-G-C	956
07 BC.CN.97.CM54A.....	T-A-A-GC-G-C	962
08 BC.CN.97.97CNGX_6FA.....	T-A-A-GC-G-C	968
09 CDX.GH.96.96GH2911A.....	T-A-A-GC-G-C	974
10 CD.TZ.96.96TZ_BF061A.....	T-A-A-GC-G-C	980
11 CDX.GR.x.GR17A.....	T-A-A-GC-G-C	986
12 BF.AR.99.ARMA159A.....	T-A-A-GC-G-C	992
13 CDX.CM.96.H1849A.....	T-A-A-GC-G-C	998
14 BG.ES.99.X397A.....	T-A-A-GC-G-C	1004
15 01B.TH.99.99TH_MU2079A.....	T-A-A-GC-G-C	1010
16 A2D.KR.97.97KR004A.....	T-A-A-GC-G-C	1016
18 CDX.CU.99.CU76A.....	T-A-A-GC-G-C	1022
19 CDX.CU.99.CU7A.....	T-A-A-GC-G-C	1028
20 BG.CU.03.CB134A.....	T-A-A-GC-G-C	1034
21 A2D.KR.91.KNH1254A.....	T-A-A-GC-G-C	1040
23 BG.CU.03.CB118A.....	T-A-A-GC-G-C	1046
24 BG.CU.03.CB378A.....	T-A-A-GC-G-C	1052
25 CDX.CM.x.101BAA.....	T-A-A-GC-G-C	1058
28 BF.BR.99.BREPM12609A.....	T-A-A-GC-G-C	1064
29 BF.BR.02.BREPM119A.....	T-A-A-GC-G-C	1070
31 BC.BR.02.110PAA.....	T-A-A-GC-G-C	1076
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N.CM.04.04CM_1131_03A.....	T-A-A-GC-G-C	1190
N.CM.95.YBF30A.....	T-A-A-GC-G-C	1196
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O.BE.87.ANT70A.....	T-A-A-GC-G-C	1208
O.CM.91.MVP5180A.....	T-A-A-GC-G-C	1214
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CPZ.CM.90.ANTA.....	T-A-A-GC-G-C	1232
CPZ.CM.01.SIVcpzCAM13A.....	T-A-A-GC-G-C	1238
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CPZ.CM.05.SIVcpzWT145A.....	T-A-A-GC-G-C	1262
CPZ.GA.88.GAB1A.....	T-A-A-GC-G-C	1268
CPZ.TZ.01.TAN1A.....	T-A-A-GC-G-C	1274
CPZ.US.85.CPZUSA.....	T-A-A-GC-G-C	1280
Gag p17A.....	T-A-A-GC-G-C	1286

HIV-1/SIVcpz complete genomes

M G A R A S V L S G G E L D R W E K I R
 ^ Gag, Gag-Pol, Gag p17 Matrix start

HIV-1/SIVcpz complete genomes

Table with columns for accession numbers (e.g., B.FR.83.HXB2, A1.KE.94.Q23.17), sequence alignments (nucleotide strings), and corresponding positions (e.g., 980, 444, 463, 979, 187, 185, 988, 350, 185, 0, 0, 327, 349, 187, 187, 187, 412, 185, 335, 185, 526, 508, 466, 331, 979, 179, 185, 441, 330, 357, 360, 358, 361, 185, 185, 415, 983, 327, 526, 524, 185, 185, 198, 175, 329, 185, 185, 241, 335, 345, 323, 321, 191, 185, 191, 185, 965, 185, 430, 382, 346, 383, 366, 307, 327, 303, 304, 191, 191).

HIV-1/SIVcpz
complete genomes

B.FR.83.HXB2
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 A1.RU.03.03RU20_06_13
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 A1.SE.94.SE7253
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 A.SN.96.DDJ360
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 D.UG.99.99UGK09958
 D.ZA.86.R482
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 F1.BR.93.93BR020_1
 F1.FI.93.FIN9363_1
 F1.FR.96.MP411
 F2.CM.02.02CM_0016BBY
 F2.CM.95.MP255
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 G.BE.96.DRCLB
 G.CM.01.01CM_4049HAN
 G.ES.99.X138
 G.KE.93.HH8793_12_1
 G.NG.92.92NG083
 G.SE.93.SE6165
 H.BE.93.VI991
 H.BE.93.VI997
 H.ICF.90.056
 J.SE.93.SE7887
 J.SE.94.SE7022
 K.CD.97.EQTB11C
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 A-T-CA A-A A-T T-A C-A C-T A-A-GATA 574
 T-G-T-CA A-A-G T-A CAC-TG C-T A-C-TA 593
 T-G-T-CA A-A C-C C-T A-A-ATA 1109
 G-TG-CA A-A A-C C-T A-A-ATA 317
 A-T-CA A-A C-C T-G T-A-ATA 1118
 T-G-T-CAGA A-A C-A C-TG C-T A-GATA 480
 G-TT-CA A-A C-A C-TG C-T A-CFA 315
 G-T-CG A-A GT-T A-G T-A C-T-A 457
 G-T-C A-A GT-T A-G T-A C-T-A 479
 G-T-CA A-A G-T A-G T-G C-T-A 317
 T-G-T-CA A-A G C C-T A-A-ATA 317
 G-T-CA A-A G C C-T A-A-ATA 317
 G-T-CA A-A G C C-T A-A-ATA 542
 C-A C-A GT-T A-G T-A C-T 315
 G-C C-A GT-T A-G T-A C-T 465
 A-A GT-T A-G T-A C-T 315
 A-A GT-T A-G T-A C-T 656
 G-A 88.OYI T-T GC A-G T-A C-T 638
 T-T-R A-A T GC A-G T-G C-T 596
 A-G T-A A-A A-G T-G C-T 461
 TGT T-T A-G T-G T-T 1109
 T-A A-A T-G A-G T-T 309
 T-T A-GC-AA C-A C-T A-A 315
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 A-A G A-TG-CG C-A A-C 460
 A-A A-A A-TG-CG G-A C-A 487
 A-G T-T A-A C-A C-T A-A 490
 A-G T-T A-A GC-G-AG-C T-A 488
 A-A A-T-A-A GC-G-AG-C T-C 491
 A-A A-T-A-A GC-G-AG-C T-C 315
 A-A GC-GA-C-G C-G C-T 315
 A-A A-A A-TG C-C A-A 545
 A-A G-G C-G C-C A-A 545
 A-A A-GAC-G-C C-C A 1113
 A-G-G-G C-G C-C A 457
 A-A G-A-TG C-G A-A 656
 A-A G-A-TG C-G A-A 654
 A-A G-A-TG C-G A-A 475
 A-A G-A-TG C-G A-A 453
 A-A G-A-TG C-G A-A 451
 A-A G-A-TG C-G A-A 321
 A-A C-A-TG C-G A-A 315
 A-A A-TG C-G A-A 321
 A-A A-TG C-G A-A 321
 A-A A-TG C-G A-A 315
 A-A A-TG C-G A-A 1095
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 A-A A-TG C-G A-A-GATA 513
 A-A A-TG C-G A-A-GATA 496
 A-A A-TG C-G A-A-GATA 437
 A-A A-TG C-G A-A-GATA 457
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01 AE.TH.90.CM240
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02 AG.GH.03.GHNU196
02 AG.NG.x.IBNG
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08 BC.CN.97.97CNGX_6F
09 CPX.GH.96.96GH2911
10 CD.TZ.96.96TZ_BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMA159
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14 BG.ES.99.X397
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16 AZD.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
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23 BG.CU.03.CB118
24 BG.CU.03.CB378
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CFZ.CM.88.GHAB1
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CFZ.UY.85.CPZUS
Gag p17

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	CAAAACAAA.....AGTAAAG.....AAAAA.....GCACAGCAAGCAGCAGCT.....GACACAGGA.....	1158
A1.KE.94.Q23_17	A---T-G---C---G---A---A-G---A---G---GACACAGGA.....	622
A1.RU.03.03RU20_06_13	---TG-G---AC---C-G---A-C-A-G---A---G---G	641
A1.RW.93.93RW037A_1	---T-G---C---G---A---A-G---G---G---GCAGCT.....	1157
A1.SE.94.SE7253	---G-G---C---G---A---A-G---G---G	365
A1.TZ.01.A173	---T-G---C---G---A---A-G---G---G	363
A1.UA.00.98UA0116	---TG-G---AC---C-G---A-C-A-G---A---G---G	1163
A1.UG.92.92UG037	---G---C---G---A---A-G---G---G	528
A1.UG.98.98UG57136	---T---C---C---G---A---A-G---A---G---G	363
A2.CD.97.97CDKFE4	0
A2.CD.97.97CDKS10	0
A2.CD.97.97CDKTB48	---T-C---C-G-G---A---G---G---G	505
A3.CY.94.94CY017_41	---G---C-G-G---A---T---G---G	521
A.SN.01.DDI1579	---T-G---AC---C-G---A---G---A---G	368
A.SN.01.DDJ369	---G-GG---CAC---C---G---A---G---A---GCT.....	365
A.SN.96.DDJ360	---AGGG.....C---G---A---G---G	365
A.ZA.04.04ZASK162B1	---T-G---C---C---G---A---G---C---AGCCAGGCAGCA.....GCT.....A	605
B.AR.00.ARMS008	---A.....-G---GCT.....	366
B.AU.96.MBCD36	---T---A.....-G---G	513
B.CO.01.PCM074	---G.....-A-C---A---G	363
B.GA.88.OYI-A---A---G	704
B.NL.99.671	---AAACGGCAC-GC---G	695
B.RU.04.04RU129005	---G---G---A---G---G	644
B.TH.90.BK132	---G---G---A---A---A	509
B.US.90.WEAU160	---C---G---G	1157
B.US.98.1058_11	---GAGCT.....-A	363
C.AR.01.ARG4006	---G-A---C---C---G---A---G---GCT---A	366
C.BR.04.04BR013	---C---CT---A-T---G---A---G---GCT---A	622
C.BR.92.BR025_d	---C---C---A---G---A---G---GCT---A	511
C.BW.00.00BW07621	---C---C---G---A---G---GCT---AA	535
C.ET.86.ETH2220	---G---C---C---G---G---A---GCT---G	541
C.IN.95.95IN21068	---T---C---A---G---NA-AG---GMT---G	536
C.IN.99.01IN565_10	---T---C---A---A---G---AA-GG---GCT---G	549
C.KE.00.KER2010	---C---C---G---G---AA-G---GCT---T	375
C.TZ.01.BD9_11	---C---C---G---G---AA-G---GCT---G	354
C.UY.01.TRA3011	---G---G---G---A---AA-G---GCT---A	593
C.ZA.04.SK164B1	---C---C---G---AA-G---GCT---A	593
C.ZA.05.05ZASK245B1	---C---A---G---T-AG-G---GCT---G	593
C.ZM.02.02ZM115	---C---C---G---A---G---GCT---G	1161
C.ZM.96.96ZM651	---T-C---AT---AA-A-CAGCAA.....GCGGCT.....	511
D.CD.83.ELIG	704
D.CD.83.NDKG	696
D.CM.01.01CM_4412HAL	---A---T.....-T.....	363
D.KE.01.NK03006	---C---A---A---AA	376
D.TD.99.MN012	---C---A---A---AA	353
D.TZ.01.A280	---G---A---A---A	507
D.UG.94.94UG114	---GC---C---G---A---A	363
D.UG.99.99UGD23550	---C---C---A---A---A	357
D.UG.99.99UGK0958	---C---C---A---A---A	422
D.ZA.86.R482	---AAG---AAG---AG---G	513
F1.BE.93.VI850	---C---C---G---A---G---G	523
F1.BR.89.BZ126	---A-C---C---G---A---G---G	501
F1.BR.93.93BR020_1	---G-CG---A---G---GA-T---A-G	505
F1.FI.93.FIN9363	---C---C---G---A---G---GCAGCT---A-G	369
F1.FR.96.MPA411	---G-C---C---G---A---G---A	363
F2.CM.02.02CM_0016BBY	---G---TA-C---A---A-C-G---T-A-G	369
F2.CM.95.MP255	---G-T---C---C---G---A---A-AG-G---A-G	369
F2.CM.95.MP257	---G---C---C---A---A---A-G---A-G	369
F2.CM.97.CM53657	---G---C---C---A---A---C---G---A-G	363
G.BE.96.DRCEL	---G-G---C---C---G---GA-AAC	1122
G.CM.01.01CM_4049HAN	---G-G---CC---AT---G---AGA	363
G.ES.99.X138	---G---C---CA---G---ATG	608
G.KE.93.HH8793_12_1	---G---C---AT---G---ATG	560
G.NG.92.92NG083	---G-C---AT---G---AAG	524
G.SE.93.SE6165	---G---C---AT---G---ATG	561
H.BE.93.VI991	---G-T-G---AC---C---G---A---G-CC-A	550
H.BE.93.VI997	---GC---C---A---A---A	485
H.CF.90.056	---C---C---A---A---A	505
J.SE.93.SE7887	---G---AC-A---C-GC-G---A---A-A	481
J.SE.94.SE7022	---AC-A---C-GC-G---A---A-A	482
K.CD.97.EQTB11C	---G---C---C---G---G-AG	369
K.CM.96.MP535	---G---C---C---G---A---A---G	369

Table with columns for sample ID, sequence, and position. Includes sample names like B.FR.83.HXB2, 01.AE.CF.90.90CF402, and various other identifiers. The table shows the alignment of HIV-1/SIVcpz complete genomes.

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

Accession	Genome Sequence	Position
B.FR.83.HXB2CAGCAATCAG.....	1223
A1.KE.94.Q23_17	A---GCA-T	687
A1.RU.03.03RU20_06_13	AG---GCA	706
A1.RW.93.93RW037A_1	A---GCA	1222
A1.SE.94.SE7253	A---GCA	430
A1.TZ.01.A173	A---GCA	428
A1.UA.00.98UA0116	AG---GCA	1228
A1.UG.92.92UG037	AGT---GCA	593
A1.UG.98.98UG57136	A---T-GCA	428
A2.CD.97.97CDKFE4C	52
A2.CD.97.97CDKS10	AG---GCA	588
A2.CD.97.97CDKTB48	A---GCA	580
A3.CY.94.94CY017_41	A---GCA	430
A.SN.01.DD1579	AG---GA	433
A.SN.01.DDQ369	A---GA	430
A.SN.96.DDQ360	A---GC	670
A.ZA.04.04ZASK162B1	A---A-C	431
B.AR.00.ARMS008	A---GC	578
B.AU.96.MBCD36	AGT-A-GC	437
B.CO.01.PCM074GCCAAA	769
B.GA.88.OYI	A---GC	760
B.NL.99.671	A-A-A-C-C	709
B.RU.04.04RU129005	A---GC	574
B.TH.90.BK132	A---GC	1222
B.US.90.WEAU160	A---A-C	428
B.US.98.1058_11	A---GC	422
C.AR.01.ARG4006	A---A	422
C.BR.04.04BR013	A---T	678
C.BR.92.BR025_d	A---T	567
C.BW.00.00BW07621	A---T	591
C.ET.86.ETH2220	A---T	597
C.IN.95.95IN21068	A---T	592
C.IN.99.01IN565_10	A---T	622
C.KE.00.KER2010	A---T	419
C.TZ.01.BD9_11	A---T	431
C.UY.01.TRA3011	A---T	410
C.ZA.04.SK164B1	A---T	649
C.ZA.05.05ZASK245B1	A---A	649
C.ZM.02.02ZM115	A---T	1217
C.ZM.96.96ZM651	A---T	567
D.CD.83.ELI	A---A-GC	769
D.CD.83.NDK	GC	758
D.CM.01.01CM_4412HAL	G-A-A	428
D.KE.01.NK03006	AG-GC	441
D.TD.99.MN012	A---GC	418
D.TZ.01.A280	AG-GC	572
D.UG.94.94UG114	A---GC	428
D.UG.99.99UGD23550	A---GC	422
D.UG.99.99UGK09958	A---GC	487
D.ZA.86.R482	A---G	566
F1.BE.93.VI850	A---A	576
F1.BR.89.B2126	A---A	554
F1.BR.93.93BR020_1	A---A	558
F1.FI.93.FIN9363_1	A---A	422
F1.FR.96.MP411	A---A	416
F2.CM.02.02CM_0016BBY	A---A	422
F2.CM.95.MP255	A---A	434
F2.CM.95.MP257	A---A	416
F2.CM.97.CM53657	GTCAGT-AAGGG	1187
G.BE.96.DRCEL	AG---GC-A	428
G.CM.01.01CM_4049HAN	G---C-A	673
G.ES.99.X138	A---A-GC-A	625
G.KE.93.HH8793_12_1	A---GC-A	589
G.NG.92.92NG083	A---T-C-A	626
G.SE.93.SE6165	A---C-A	615
H.BE.93.VI991	A-GGA-GCA	550
H.BE.93.VI997	AGGA-CA	570
H.CF.90.056	A-AGA-CA	546
J.SE.93.SE7887	G-A-G	547
J.SE.94.SE7022	G-A-G	422
K.CD.97.EQTB11C	T	422
K.CM.96.MP535	T	422

	gag p17 Matrix end \	gag p24 Capsid start	
B.FR.83.HXB2GTCACGCCAAATTACCTTATAGTCAGAAATCCAGGGGCAAAATGGTACATCAGTCACGCCAAATTACCTTATAGTCAGAAATCCAGGGGCAAAATGGTACATCA	1223
01 AE.CF.90.90CF402AGGCA AA-TGCA A	1265
01 AE.CN.05.FU051AGGCA AA-TTCA A	1239
01 AE.HK.x.HK001AGGCA AA-TGCA A	600
01 AE.JP.93.93JP.NH1AGGCA AA-TGCA A	1240
01 AE.TH.01.0UR414TAGGCA AA-TGCA A	428
01 AE.TH.02.0UR769TAGGCA AA-TGCA A	428
01 AE.TH.90.CM240AGGCA AA-TGCA A	788
02 AG.CM.02.02CM_1669LEAGGCA AA-TGCA A	419
02 AG.EC.x.EC041AGGCA AA-TGCA A	325
02 AG.FR.91.DJ264AGGCA AA-TGCA A	578
02 AG.GH.03.GHNJ196AGGCA AA-TGCA A	1255
02 AG.NG.x.IBNGAGGCA AA-TGCA A	754
02 AG.SN.98.MPI211AGGCA AA-TGCA A	426
02 AG.UZ.02.02UZ693AGGCA AA-TGCA A	419
03 AB.RU.97.KAL153_2AGGCA AA-TGCA A	455
04 CPX.CV.94.CY032AGGCA AA-TGCA A	589
05 DF.BE.x.VII1310AGGCA AA-TGCA A	602
06 CPX.AU.96.BFP90AGGCA AA-TGCA A	1248
07 BC.CN.97.CM54AGGCA AA-TGCA A	591
08 BC.CN.97.97CNGX_6FAGGCA AA-TGCA A	421
09 CPX.GH.96.96GH2911AGGCA AA-TGCA A	434
10 CD.TZ.96.96TZ_BF061AGGCA AA-TT A	602
11 CPX.GR.x.GR17AGGCA AA-TGCA A	534
12 BF.AR.99.ARMA159AGGCA AA-TGCA A	1231
13 CPX.CM.96.1849AGGCA AA-TGCA A	601
14 BG.ES.99.X397AGGCA AA-TGCA A	631
15 01B.TH.99.99TH_MU2079AGGCA AA-TGCA A	584
16 A2D.KR.97.97KR004AGGCA AA-TGCA A	619
18 CPX.CU.99.CU76AGGCA AA-TGCA A	400
19 CPX.CU.99.CU77AGGCA AA-TGCA A	672
20 BG.CU.03.CB134AGGCA AA-TGCA A	540
21 A2D.KE.91.KNH1254AGGCA AA-TGCA A	449
23 BG.CU.03.CB118AGGCA AA-TGCA A	682
24 BG.CU.03.CB378AGGCA AA-TGCA A	431
25 CPX.CM.x.101BAAGGCA AA-TGCA A	685
28 BF.BR.99.BREPM12609AGGCA AA-TGCA A	680
29 BF.BR.02.BREPM119AGGCA AA-TGCA A	431
31 BC.BR.02.110PAAGGCA AA-TGCA A	592
33_01B.MY.05.05MYKL007_1AGGCA AA-TGCA A	400
A1C.TZ.02.CO3710AGGCA AA-TGCA A	672
A1CDGKU.ZA.99.CM4AGGCA AA-TGCA A	601
A1DHK.NO.97.97NOGL13AGGCA AA-TGCA A	422
A1GHU.GA.x.VI354AGGCA AA-TGCA A	1239
A2D.KE.99.KER2003AGGCA AA-TGCA A	592
AF2.CM.02.02CM_3163MNAGGCA AA-TGCA A	428
AGU.CM.01.01CM_0989MOAGGCA AA-TGCA A	419
ARJU.CM.01.01CM_1296NGAGGCA AA-TGCA A	428
BC.CN.96.YNRL9607AGGCA AA-TGCA A	425
BC.MM.99.MIDDU103AGGCA AA-TGCA A	601
BF1.BR.02.02BR006AGGCA AA-TGCA A	1128
0708.CN.00.HH069AGGCA AA-TGCA A	425
U.CD.83.83CD003AGGCA AA-TGCA A	721
U.CD.90.90CD121E12AGGCA AA-TGCA A	425
U.GR.99.GR303AGGCA AA-TGCA A	512
U.NL.x.U.NL.95.H10986_D1AGGCA AA-TGCA A	1111
N.CM.02.DJ00131AGGCA AA-TGCA A	708
N.CM.04.04CM_1131_03AGGCA AA-TGCA A	700
N.CM.95.YBF30AGGCA AA-TGCA A	787
N.CM.97.YBFI106AGGCA AA-TGCA A	788
O.BE.87.ANT70AGGCA AA-TGCA A	1269
O.CM.91.MVPS180AGGCA AA-TGCA A	1244
O.CM.96.96CMBAB637AGGCA AA-TGCA A	692
O.SN.99.SEMPI1300AGGCA AA-TGCA A	1271
CPZ.CD.90.ANTAGGCA AA-TGCA A	635
CPZ.CM.01.SIVcpzCAM13AGGCA AA-TGCA A	800
CPZ.CM.05.SIVcpzE505AGGCA AA-TGCA A	771
CPZ.CM.05.SIVcpzL57AGGCA AA-TGCA A	769
CPZ.CM.05.SIVcpzMB66AGGCA AA-TGCA A	766
CPZ.CM.05.SIVcpzWTL14AGGCA AA-TGCA A	762
CPZ.GA.88.GAB1AGGCA AA-TGCA A	1284
CPZ.TZ.01.TANIAGGCA AA-TGCA A	855
CPZ.US.85.CPZUSAGGCA AA-TGCA A	1271
gag p17/p24V S O N Y P I V O N I O G O M V H QV S O N Y P I V O N I O G O M V H Q	Gag

B.FR.83.HXB2	GGCCATATCACCTAGAACCTTTAAATGCATGGTAAAGTAGTAGAGAGAGAGGCTTTTCACCCACAGAGGTTACACCCAGACCCACCAGAGTATTAAACACCATGCCTA	1352	1353
01 AE.CF.90.90CF402	-T-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.CN.05.FJ051	-C-TC-T-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.HK.x.HK001	-T-TT-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.JP.93.93JP.NH1	-C-TT-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.TH.01.OUR4141	-C-TT-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.TH.02.OUR7691	-C-TG-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
01 AE.TH.90.CM240	-C-TT-G-G-T-A-A-C-C	-G-T-A-A-C-C	-T-TG-C
02 AG.CM.02.02CM.16691E	-C-C-G-G-G-C-A-A-A-A	-G-C-A-A-A-A	-T-TG-C
02 AG.EC.x.EC041	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
02 AG.FR.91.DJ264	-C-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
02 AG.GH.03.GHNU196	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
02 AG.NG.x.IBNG	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
02 AG.SN.98.MP1211	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
02 AG.UZ.02.02UZ693	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
03 AB.RU.97.KAL153.2	-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
04 CPX.CV.94.CV032	-AG-T-G-G-G-G-A-A-A-A	-G-G-A-A-A-A	-T-TG-C
05 DF.BE.x.Vil1310	-C-C-G-C-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
06 CPX.BU.96.BFP90	-C-C-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
07 BC.CN.97.CNE4	-C-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
08 BC.CN.97.97CNGX.6F	-C-C-R-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
09 CPX.GH.96.96GHZ911	-C-C-T-A-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
10 CD.TZ.96.96TZ.BF061	-C-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
11 CPX.GR.x.GR17	-C-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
12 BF.AR.99.ARMAL159	-T-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
13 CPX.CM.96.1849	-C-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
14 BG.ES.99.X397	-C-TG-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
15 01B.TH.99.99TH.MU2079	-AA-T-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
16 A2D.KR.97.97KR004	-T-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
18 CPX.CU.99.CU76	-C-C-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
19 CPX.CU.99.CU7	-C-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
20 BG.CU.03.CB134	A-G-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
21 A2D.KR.91.KNH1254	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
23 BG.CU.03.CB118	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
24 BG.CU.03.CB378	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
25 CPX.CM.x.101BA	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
28 BF.BR.99.BREPM12609	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
29 BF.BR.02.BREPM119	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
31 BC.BR.02.110PA	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
33 01B.WV.05.05MYKL007_1	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
A1C.TZ.02.C03710	-C-C-A-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
A1CDGK.ZA.99.CM4	-C-C-A-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
A1LHK.NO.97.97NOGLI3	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
A1LGHU.GA.x.VI354	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
A2D.KE.99.KER2003	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
AF2.CM.02.02CM.3163MN	-T-TT-G-G-G-G-G-G	-G-G-A-A-A-A	-T-TG-C
AGU.CM.01.01CM.0989MO	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
AHJU.CM.01.01CM.1296NG	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
BC.CN.96.YNPL9607	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
BC.MM.99.mIU103	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
BF1.BR.02.02BR006	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
0708.CN.00.HH069	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
U.CD.83.83CD003	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
U.CD.90.90CD121E12	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
U.GR.99.GR303	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
U.NL.x.U.NL.95.H10986_D1	-G-G-G-G-G-G-A-G	-A-A-G-G-G-G	-T-TG-C
N.CM.02.DJ00131	-C-GC-GA-C-C-T-T	-G-G-G-G-G-G	-G-A-A-CGC-C-T-T
N.CM.04.04CM.1131_03	-C-GC-GA-C-C-T-T	-G-G-G-G-G-G	-G-A-A-CGC-C-T-T
N.CM.95.YBF30	-C-GC-GA-C-C-T-T	-G-G-G-G-G-G	-G-A-A-CGC-C-T-T
N.CM.97.YBF106	-C-GC-GA-C-C-T-T	-G-G-G-G-G-G	-G-A-A-CGC-C-T-T
O.BE.87.ANT70	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
O.CM.91.WP5180	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
O.CM.96.96CMBB637	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
O.SN.99.99SEMP1300	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.CO.90.ANT	-C-AC-GA-A-C-C	-G-GTGT-G-G	-G-G-T-T-G-G
CPZ.CO.01.SIVcpzCAM13	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.CO.05.SIVcpzE505	-C-GC-GA-C-C-T-T	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.CO.05.SIVcpzLB7	-C-C-C-G-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.CO.05.SIVcpzMB66	-C-C-C-G-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.CO.05.SIVcpzMT145	-C-C-C-G-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.GA.88.GAB1	-C-C-C-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.TZ.01.TAN1	-C-T-T-C-G-G	-G-G-G-G-G-G	-G-G-G-G-G-G
CPZ.US.85.CPZUS	-A-G-T-T-C-C	-G-G-G-G-G-G	-G-G-G-G-G-G
Gag p24	A_I_S_P_R_T_L_N_A_W_V_K_V_E_K_A_F_S_P_E_V_I_P_M_F_S_A_L_I_S_E_G_A_T_P_Q_D_L_N_T_M_L		

Table with columns for accession numbers (e.g., B.FR.83.HXB2, O1.AE.CF.90.90CF402), sequence alignments (conserved regions and variable regions), and Gag p24 protein amino acid sequences (e.g., N_T_V_G_G_H_Q_A_A_M_Q_M_L_K_E_T_I_N_E_E_A_A_E_W_D_R_V_H_P_V_H_A_G_P_I_A_P_G_Q_M_R_E_P).

HIV-1/SIVcpz complete genomes

Accession ID	Genomic Coordinates	Sequence
B. FR. 83. HXB2	GGGGAAGTCATGACATGACATGACCTTCAGGAAACAATAGGATGGATGACA.....AAATAATCACCTTCACCCAGTAGGAGAAATTTTATAAAGATGGATATCCTGGGATTAAATAA	1604
01 AE. CF. 90. 90CF402	-----GC-----T-----G-----GC-----C-----T-----G-----AG-----	1646
01 AE. CN. 05. FJ051	-----A-----A-----A-----G-----G-----C-----C-----C-----C-----	1620
01 AE. HK. x. HK001	C-----A-----A-----G-----C-----C-----C-----C-----T-----	981
01 AE. JP. 93. 93JP. NH1	-----A-----A-----C-----A-----C-----C-----C-----C-----	1621
01 AE. TH. 01. OUR4141	-----T-----A-----A-----G-----C-----C-----C-----C-----G-----	809
01 AE. TH. 02. OUR7691	-----A-----A-----A-----A-----C-----G-----C-----C-----C-----	809
01 AE. TH. 90. CM240	-----A-----A-----A-----A-----C-----C-----C-----C-----C-----	1169
02 AG. CM. 02. 02CM_16691E	-----GCA-----G-----C-----A-----GGC-----G-----C-----C-----G-----	800
02 AG. EC. x. EC041	-----A-----A-----A-----G-----GC-----C-----C-----C-----C-----	706
02 AG. FR. 91. DJ264	-----A-----A-----A-----G-----GC-----C-----C-----C-----C-----	959
02 AG. GH. 03. GHNJ196	-----A-----A-----A-----G-----GC-----C-----C-----C-----C-----	1636
02 AG. NG. x. IBNG	-----A-----A-----A-----G-----GC-----C-----C-----C-----C-----	1135
02 AG. SN. 98. MP1211	-----A-----A-----A-----G-----GC-----C-----C-----C-----C-----	807
02 AG. UZ. 02. 02UZ693	-----C-----A-----A-----G-----C-----C-----C-----C-----C-----	800
03 AB. RU. 97. KAL153_2	-----G-----G-----A-----A-----GC-----C-----C-----C-----C-----	836
04 CPX. CV. 94. CV032	-----T-----C-----C-----C-----T-----GC-----C-----C-----C-----	970
05 DF. BE. x. VIL1310	-----T-----T-----C-----C-----C-----C-----T-----C-----A-----	983
06 CPX. AU. 96. BFP90	-----T-----T-----C-----C-----C-----C-----T-----C-----A-----	1629
07 BC. CN. 97. CNE4	-----A-----A-----A-----A-----G-----C-----C-----G-----T-----T-----	972
08 BC. CN. 97. 97CNGX_6F	-----T-----G-----A-----A-----G-----C-----C-----C-----C-----	802
09 CPX. GH. 96. 96GH2911	-----T-----G-----A-----A-----G-----C-----C-----C-----C-----	815
10 CD. TZ. 96. 96TZ_BF061	-----T-----G-----A-----A-----G-----C-----C-----C-----C-----	983
11 CPX. GR. x. GR17	-----T-----A-----G-----A-----A-----G-----GC-----C-----C-----G-----	915
12 BF. AR. 99. ARMA159	-----T-----T-----G-----C-----A-----CA-----GC-----C-----C-----	1612
13 CPX. CM. 96. 1849	-----T-----T-----G-----C-----G-----AC-----C-----C-----C-----	982
14 BG. ES. 99. X397	-----T-----T-----G-----C-----A-----A-----G-----GC-----C-----C-----	1051
15 01B. TH. 99. 99TH_MU2079	-----T-----T-----G-----C-----A-----A-----G-----GC-----C-----C-----	1012
16 A2D. KR. 97. 97KR004	-----T-----T-----A-----A-----A-----G-----GC-----C-----C-----	965
18 CPX. CU. 99. CU76	-----T-----T-----A-----A-----A-----G-----GC-----C-----C-----	921
19 CPX. CU. 99. CU7	-----C-----T-----T-----A-----A-----G-----GC-----C-----C-----	830
20 BG. CU. 03. CBL134	-----C-----T-----T-----A-----A-----G-----GC-----C-----C-----	1063
21 A2D. KE. 91. KMH1254	-----C-----T-----T-----A-----A-----G-----GC-----C-----C-----	812
23 BG. CU. 03. CBL118	-----C-----T-----T-----A-----A-----G-----GC-----C-----C-----	1066
24 BG. CU. 03. CB378	-----C-----T-----T-----A-----A-----G-----GC-----C-----C-----	1061
25 CPX. CM. x. 101BA	-----T-----T-----C-----A-----A-----G-----GC-----C-----C-----	812
28 BF. BR. 99. BREPM12609	-----T-----T-----C-----A-----A-----G-----GC-----C-----C-----	973
29 BF. BR. 02. BREPM119	-----T-----T-----C-----A-----A-----G-----GC-----C-----C-----	781
31 BC. BR. 02. 110PA	-----C-----C-----C-----A-----C-----A-----G-----GC-----C-----	1053
33 01B. WY. 05. 05MYKL007_1	-----C-----C-----C-----A-----A-----G-----GC-----C-----C-----	989
A1C. TZ. 02. C03710	-----C-----C-----C-----A-----A-----G-----GC-----C-----C-----	803
A1CDGKU.ZA.99.CM4	-----C-----C-----C-----A-----A-----G-----GC-----C-----C-----	1603
A1DHK.NO.97.97NOGLI3	-----C-----C-----C-----A-----A-----G-----GC-----C-----C-----	1620
A1GHU.GA.x.VI354	-----T-----T-----AC-----A-----A-----GC-----C-----C-----	973
A2D.KE.99.KER2003	-----T-----T-----AC-----A-----A-----GC-----C-----C-----	809
AF2.CM.02.02CM.3163MN	-----T-----T-----G-----C-----T-----G-----GC-----C-----C-----	800
AGU.CM.01.01CM_0989MO	-----AT-----T-----G-----C-----A-----A-----GC-----C-----C-----	809
AHJU.CM.01.01CM_1296NG	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	806
BC.CN.96.YNRL9607	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	982
BC.MM.99.mtIU103	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	1509
BF1.BR.02.02BR006	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	806
0708.CN.00.HH069	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	1102
U.CD.83.83CD003	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	806
U.CD.90.90CD121E12	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	887
U.GR.99.GR303	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	1492
U.NL.x.U.NL.95.H10986_D1	-----T-----T-----G-----C-----A-----A-----GC-----C-----C-----	1492
N.CM.02.DJ00131	-----A-----C-----T-----G-----A-----G-----G-----G-----G-----	1089
N.CM.04.04CM_1131_03	-----A-----C-----T-----G-----A-----G-----G-----G-----G-----	1081
N.CM.95.YBF30	-----A-----A-----C-----T-----G-----A-----G-----G-----G-----	1168
N.CM.97.YBF106	-----A-----A-----C-----T-----G-----A-----G-----G-----G-----	1169
O.BE.87.ANT70	CA-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1653
O.CM.91.WPES180	CA-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1628
O.CM.96.96CMAB8637	CA-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1076
O.SN.99.SEMP1300	CA-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1655
CPZ.CD.90.ANT	CA-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1025
CPZ.CM.01.SIVCPZCAM13	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1181
CPZ.CM.05.SIVCPZE505	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1152
CPZ.CM.05.SIVCPZL87	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1150
CPZ.CM.05.SIVCPZMB66	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1147
CPZ.CM.05.SIVCPZMT145	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1143
CPZ.GA.88.GABI	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1665
CPZ.TZ.01.TANI	CA-----GGCA-----T-----T-----G-----C-----A-----A-----G-----G-----	1245
CPZ.US.85.CPZUS	-----T-----T-----A-----A-----C-----A-----G-----A-----G-----	1652
Gag p24	R_G_S_D_I_A_G_T_T_S_T_L_Q_E_Q_I_G_W_M_T_.....N_N_P_P_I_P_V_G_E_I_Y_K_R_W_I_I_L_G_L_N_K	Gag



HIV-1/SIVcpz
complete genomes

AANTAGTAAGATTGTATAGCCCTTACAGCAITTTGACGACATGAGACTATGTAGACGCTTTATATAAACCTTAAGACGCCGAGCAAGCTTCCACAGGAGGTTAAAAAAT	1734
A1.KE.94.Q23_17	1198
A1.RU.03.03RU20_06_13	1217
A1.RW.93.93RW037A_	1733
A1.SE.94.SE7253	941
A1.TZ.01.A173	939
A1.UA.00.98UA0116	1739
A1.UG.92.92UG037	1104
A1.UG.96.96UG57136	939
A2.CD.97.97CDKFE4	563
A2.CD.97.97CDKS10	1099
A2.CD.97.97CDKTB48	1091
A2.CY.94.94CY017_41	941
A.SN.01.DDI579	944
A.SN.01.DDJ369	944
A.SN.96.DDJ360	941
A.ZA.04.04ZASK1.62B1	1181
B.AR.00.ARMS008	942
B.AU.96.MBCD36	1089
B.CO.01.PCM074	948
B.GA.88.OYI	1280
B.NL.99.671	1271
B.RU.04.04RU129005	1220
B.TH.90.BK132	1085
B.US.90.WEAU160	1733
B.US.98.1058_11	939
C.AR.01.ARG4006	933
C.BR.04.04BR013	1189
C.BR.92.BR025_d	1078
C.BW.00.00BW07621	1102
C.ET.86.ETH2220	1108
C.IN.95.95IN21068	1103
C.IN.99.01INS65_10	1133
C.KE.00.KER2010	930
C.TZ.01.BD9_11	942
C.UY.01.TRA3011	921
C.ZA.04.SK164B1	1160
C.ZA.05.05ZASK245B1	1178
C.ZM.02.02ZM115	1078
C.ZM.96.96ZM651	1280
D.CD.83.ELI	1269
D.CD.83.NDK	939
D.CM.01.01CM_4412HAL	939
D.KE.01.NK03006	952
D.TD.99.MN012	929
D.TZ.01.A280	1083
D.UG.94.94UG114	933
D.UG.99.99UGD23550	933
D.UG.99.99UGK09958	933
D.ZA.86.R482	998
F1.BE.93.VI850	1077
F1.BR.89.B2126	1087
F1.BR.93.93BR020_1	1065
F1.FI.93.FIN9363_1	1069
F1.FR.96.MP411	933
F2.CM.02.02CM_0016BBY	927
F2.CM.95.MP255	933
F2.CM.95.MP257	945
F2.CM.97.CM53657	927
G.BE.96.DRCEL	1698
G.CM.01.01CM_4049HAN	939
G.ES.99.X138_	1184
G.NG.93.HH8793_12_1	1136
G.NG.92.92NG083_	1100
G.SE.93.SE6165	1137
H.BE.93.VI991	1126
H.BE.93.VI997	1061
H.CF.90.056	1081
J.SE.93.SE7887	1057
J.SE.94.SE7022	1058
K.CD.97.EQTB11C	933
K.CM.96.MP535	933

B.F.R. 83.HXB2
01 AE.CF.90.90CF402
01 AE.CN.05.FJ051
01 AE.HK.x.HK001
01 AE.JP.93.93JP.NH1
01 AE.TH.01.OUR4141
01 AE.TH.02.OUR7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM.16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153.2
04 CPX.CV.94.CY032
05 DF.BE.x.VI1310
06 CPX.AU.96.BFP90
07 BC.CN.97.CNE4
08 BC.CN.97.97CNGX.6F
09 CPX.GH.96.96GHZ911
10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMAL159
13 CPX.CM.96.1849
14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 A2D.KE.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPM12609
29 BF.BR.02.BREPM119
31 BC.BR.02.110PA
33 01B.WY.05.05MYKL007_1
A1C.TZ.02.C03710
A1CDGKU.ZA.99.CM4
A1DHK.NO.97.97NOGLI3
A1GHU.GA.x.VI354
A2D.KE.99.KER2003
AF2.CM.02.02CM.3163MN
AGU.CM.01.01CM.0989MO
AHJU.CM.01.01CM.1296NG
BC.CN.96.YNRL9607
BC.MM.99.mINDU103
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O.CM.96.96CMWAB637
O.SN.99.SEMPL300
CPZ.CD.90.ANT
CPZ.CM.01.SIVCPZCAM13
CPZ.CM.05.SIVCPZEK505
CPZ.CM.05.SIVCPZL87
CPZ.CM.05.SIVCPZMB66
CPZ.CM.05.SIVCPZMT145
CPZ.GA.88.GAN1
CPZ.TZ.01.TAN1
CPZ.US.85.CPZUS
Gag p24

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	TGGATGACAGAACCTTTGGTCCAAATGCGAACCCAGATTGTGTAAGACTATTTAAAGCAATTTGGACACCGGCTACACTAGAGAAATGATGACAGCATCTCAGGGAGTAGGAGACCCGGCCATA	1864
A1.KE.94.Q23.17	...C-A-AC-A-T-T-C-G-A-G-A-T-T-G-A-T-T-G-G-T-T-C-G...	1328
A1.RU.03.03RU20.06.13	...C-C-A-T-T-A-T-T-A-T-T-G-A-T-T-C-T-T-T-T-G-G-T-T-C-G...	1347
A1.RW.93.93RW037A_13	...C-C-A-T-T-A-T-T-A-T-T-G-A-T-T-C-T-T-T-T-G-G-T-T-C-G...	1863
A1.SE.94.SE7253	...A-AC-A-T-T-T-C-T-G-A-G-T-T-G-T-T-G-T-T-G-T-T-G-A...	1071
A1.TZ.01.A173	...A-T-T-T-T-C-C-A-T-T-C-T-T-T-T-T-T-G-T-T-C-G-T-T-G...	1069
A1.UA.00.98UA0116	...C-C-A-G-T-T-AG-T-T-AG-C-T-T-AG-C-T-T-AG-C-T-T-AG-C...	1869
A1.UG.92.92UG037	...G-AC-A-T-T-AT-C-CC-G-A-T-G-G-T-T-G-T-T-G-T-T-G-T-T-A...	1234
A1.UG.96.98UG57136	...C-C-C-T-T-T-C-CC-G-A-T-G-G-T-T-G-T-T-G-T-T-G-T-T-G-G...	1069
A2.CD.97.97CDKFE4AT-A-CC-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	693
A2.CD.97.97CDKSI0AT-A-CC-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1229
A2.CD.97.97CDKTIB48AT-A-CC-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1221
A2.CY.94.94CY017_41	...G-C-C-GAT-C-C-G-G-A-T-T-C-G-CT-T-T-T-T-T-T-T-T-T-T-T...	1071
A.SN.01.DDI579	...T-C-T-T-C-G-A-T-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1074
A.SN.01.DDJ369	...T-C-T-T-C-G-A-T-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1071
A.SN.96.DDJ360	...C-C-T-T-C-G-A-T-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1071
A.ZA.04.04ZASK162B1	...G-T-AC-T-T-C-CAG-T-T-C-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T...	1311
B.AR.00.ARMS008	...A-T...	1072
B.AU.96.MBCD36	...G-C-C-G-G-A-T...	1219
B.CO.01.PCM074	...G-C-C-G-G-A-T...	1078
B.GA.88.OYI	...A-T...	1410
B.NL.99.671	...T-T...	1401
B.RU.04.04RU129005	...A-C-R-R-R-GA-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1350
B.TH.90.BK132	...T-T...	1215
B.US.90.WEAU160	...T-T...	1863
B.US.98.1058_11	...-T-G-C-T...	1069
C.AR.01.ARG4006	...G-C-C-G-G-A-T...	1063
C.BR.04.04BR013	...G-C-C-G-G-A-T...	1319
C.BR.92.BR025_d	...T-T...	1208
C.BW.00.00BW07621	...-A-C-C-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1232
C.ET.86.ETH2220	...C-C-A-C-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1238
C.IN.95.95IN21068	...C-T...	1233
C.IN.99.01IN565_10	...C-C-A-C-T...	1263
C.KE.00.KER2010	...C-C-G-G-A-T...	1060
C.TZ.01.BD9_11	...C-G-G-A-T...	1072
C.UY.01.TRA3011	...T-T...	1051
C.ZA.04.SK164B1	...C-C-G-G-A-T...	1290
C.ZA.05.05ZASK245B1	...C-C-G-G-A-T...	1290
C.ZM.02.02ZM115	...A-C-C-C-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1858
C.ZM.96.96ZM651	...C-C-C-C-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1208
D.CD.83.ELI	...A-C-C-C-A-T...	1410
D.CD.83.NDK	...A-C-C-C-A-T...	1399
D.CM.01.01CM.4412HAL	...T-T...	1069
D.KE.01.NKU3006	...C-A-C-C-G-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1069
D.TD.99.MN012	...A-A-C-C-G-G-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1082
D.TZ.01.A280	...T-T...	1059
D.UG.94.94UG114	...A-C-C-C-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1213
D.UG.99.99UGD23550	...T-T...	1069
D.UG.99.99UGK0958	...T-T...	1063
D.ZA.86.R482	...-T...	1128
F1.BE.93.VI850	...C-C-A-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1207
F1.BR.89.B2126	...C-C-A-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1217
F1.BR.93.93BR020_1	...C-C-C-G-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1195
F1.FI.93.FIN9363_1	...C-C-C-G-G-G-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1199
F1.FR.96.MP411	...-G-C-G-T...	1063
F2.CM.02.02CM.0016BBY	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1057
F2.CM.95.MP255	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1063
F2.CM.95.MP257	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1075
F2.CM.97.CM53657	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1057
G.BE.96.DRCBL	...C-C-A-A-T...	1828
G.CM.01.01CM.4049HAN	...C-C-A-A-T...	1069
G.ES.99.X138	...T-T...	1314
G.KE.93.HH8793_12_1	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1266
G.NG.92.92NG083	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1267
G.SE.93.SE61165	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1256
H.BE.93.VI991	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1191
H.BE.93.VI997	...C-C-C-C-C-C-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T...	1211
H.CF.90.056	...T-T...	1187
J.SE.93.SET7887	...T-T...	1188
J.SE.94.SET022	...T-T...	1063
K.CD.97.EQTB11C	...-C-C-C-C-A-T...	1063
K.CM.96.MP535	...-C-C-C-C-A-T...	1063

HIV-1/SIVcpz Complete Genomes

B.F.R. 83_HXB2
TGGATCAGAAACCTTGGTCCAAAATGGAAACCCAGATTGTAAAGCACTATTTAAAGCAATGGACCCGGCTACACTAGAGAATAATGATGACAGCATCTCAGGAGTAGGAGACCACCGGCCATA
1864
1906 T-C-A-A-T-C-C-A-A-A-G-T-T-C-C-A-A-G-T-T-C-G-T-A-
1880 1AE.CF.90.90CF402 T-T-C-C-A-AT-GA-T-T-C-C-A-AT-GA-T-T-C-G-T-A-
1241 C-A-G-T-C-A-G-GA-TT-T-T-C-C-A-G-GA-TT-T-C-G-T-A-
1881 C-A-A-A-GA-T-T-C-T-C-A-A-GA-T-T-C-G-T-A-
1069 C-A-T-C-T-C-T-C-A-CT-T-T-C-T-C-A-A-GA-CT-T-G-TA-
1069 C-A-T-C-T-C-T-C-A-A-GA-T-T-C-T-C-A-A-GA-T-T-C-G-TA-
1429 C-A-C-T-T-C-T-C-A-GA-T-T-C-T-C-A-A-GA-T-T-C-G-TA-
1060 C-C-C-T-T-C-G-G-T-T-G-G-T-T-G-G-T-T-C
966 C-C-G-A-G-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-C
1219 C-C-G-A-G-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-C
1896 C-T-T-C-T-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1395 C-G-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1067 T-T-T-C-G-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1096 C-T-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1230 C-A-T-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1243 C-A-A-A-GA-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1889 C-A-A-A-GA-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1232 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1062 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1075 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1243 -A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1175 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1872 C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1242 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1311 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1272 A-C-A-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1225 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1181 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1090 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1323 -C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1072 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1326 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1321 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1072 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1233 C-T-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1041 C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1313 T-A-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1249 -G-AC-A-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1063 A-I.C.TZ.02.CO3710 T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1863 A-I.CDGKU.ZA.99.CM4 T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1880 A-I.DHK.NO.97.97NOGLI3 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1233 A-I.GHU.GA.x.VI354 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1069 A-F2.KE.99.KER2003 T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1060 A-F2.CM.02.02CM.3163MN T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1069 A-A-GU.CM.01.01CM.0989MO T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1066 A-BC.CN.96.YNPL9607 T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1242 A-BC.MM.99.mINDU103 T-C-C-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1769 A-BF1.BR.02.02BR006 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1066 U.0708.CN.00.HH069 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1362 U.CD.83.83CD003 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1066 U.CD.90.90CD12LE12 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1147 U.GR.99.GR303 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1752 U.NL.x.U.NL.95.H10986_D1 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1349 N.CM.02.DJ00131 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1341 N.CM.04.04CM.1131_03 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1428 N.CM.95.YBF30 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1429 N.CM.97.YBF106 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1913 O.BE.87.ANT70 T-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1888 O.CM.91.MVPE180 T-C-A-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1336 O.CM.96.96CMWAB637 T-CAC-T-T-G-C-T-T-Y-ACAA-C-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1915 O.SN.99.SEMP1300 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1285 CPZ_CD.90.ANT CPZ_CD.90.ANT T-C-A-C-C-C-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1441 CPZ_CM.01.STVCPZCAM13 CPZ_CM.01.STVCPZCAM13 T-G-AC-CC-C-C-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1412 CPZ_CM.05.STVCPZE505 CPZ_CM.05.STVCPZE505 T-C-AC-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1410 CPZ_CM.05.STVCPZL87 CPZ_CM.05.STVCPZL87 T-C-T-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1407 CPZ_CM.05.STVCPZMB66 CPZ_CM.05.STVCPZMB66 T-C-T-A-G-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1403 CPZ_CM.05.STVCPZMT145 CPZ_CM.05.STVCPZMT145 T-C-A-C-C-C-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1925 CPZ_TZ.01.TFAN1 CPZ_TZ.01.TFAN1 T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1505 CPZ_US.85.CPZUS CPZ_US.85.CPZUS T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T-T
1912 Gag p24 W M T E L L V Q N A N P D C K T I L K A L G P A A T L E E M M T A C Q G V G G P G H

HIV-1/SIVcpz complete genomes

**HIV-1/SIVcpz
complete genomes**

	Gag p24 AGCCRAGAGTTTTGCTGAGCAATG	Gag p22 start GAGTCTGAGCAATG	Gag p2 end GCTACTATA	Gag-Pol fusion TF protein start Nucleocapsid (NC) start ATGATGACAGAGGCAAT	
B.FR.83.HXB2	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1961
A1.KE.94.Q23_17	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1419
A1.RU.03.03RU20_06_13	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1438
A1.RW.93.93RW037A	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1954
A1.SE.94.SE7253	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1165
A1.TZ.01.A173	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1160
A1.UA.00.98UA0116	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1960
A1.UG.98.98UG0537	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1325
A1.UG.98.98UG057136	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1166
A2.CD.97.97CDKPE4	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	790
A2.CD.97.97CDK510	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	0
A2.CD.97.97CDKTB48	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1320
A2.CY.94.94CY0117_41	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1318
A.SN.01.DDI579	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1162
A.SN.01.DDU369	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1165
A.SN.96.DDU360	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1162
A.ZA.04.04ZASK162B1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1405
B.AR.00.ARM5008	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1166
B.AU.96.MBCD36	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1316
B.CO.01.PCM074	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1175
B.GA.88.OYI	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1504
B.NL.99.671	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1495
B.RU.04.04RU129005	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1447
B.TH.90.RK132	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1312
B.US.90.WEAU160	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1960
B.US.98.1058_11	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1160
C.AR.01.ARG4006	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1157
C.BR.04.04BR013	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1413
C.BR.92.BR025_d	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1302
C.BW.00.00BW07621	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1325
C.ET.86.ETH2220	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1332
C.IN.95.95IN21068	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1324
C.IN.99.01IN565_10	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1354
C.KE.00.KER2010	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1154
C.TZ.01.BD9_11	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1163
C.UY.01.TRA3011	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1145
C.ZA.04.SK164B1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1384
C.ZA.05.05ZASK245B1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1381
C.ZM.02.02ZM115	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1952
C.ZM.96.96ZM651	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1302
D.CD.83.ELI	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1510
D.CD.83.NDK	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1499
D.CM.01.01CM_4412HAL	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1172
D.KE.01.NKU3006	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1169
D.TD.99.MN012	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1182
D.TZ.01.A280	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1159
D.UG.94.94UG114	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1313
D.UG.99.99UGD2550	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1169
D.UG.99.99UGK03958	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1163
D.ZA.86.R482	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1228
F1.BE.93.VI850	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1298
F1.BR.89.B2126	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1311
F1.BR.93.93BR020_1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1289
F1.FI.93.FIN9363_1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1290
F1.FR.96.MPA11	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1157
F2.CM.02.02CM_0016BBY	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1151
F2.CM.95.MP255	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1157
F2.CM.95.MP257	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1169
F2.CM.97.CM53657	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1151
G.BE.96.DRCHL	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1928
G.CM.01.01CM_4049HAN	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1166
G.ES.99.X138	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1408
G.KE.93.HH8793_12_1	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1366
G.NG.92.92NG083	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1333
G.SE.93.SE6165	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1367
H.BE.93.VI991	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1356
H.BE.93.VI997	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1291
H.CF.90.056	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1311
J.SE.93.SE7887	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1281
J.SE.94.SE7022	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1282
K.CD.97.EQTB11C	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1157
K.CM.96.MP535	A-G-G-G	T-C-C-A	A-G-G-G	A-G-G-G	1157

HIV-1/SIVcpz Complete Genomes

Table with columns for strain name, Gag p24 Capsid end, Gag p2 start, Gag p2 end, Gag p2 end / Nucleocapsid (NC) start, Gag-Pol fusion TF protein start, and a numerical column on the right. The table lists various HIV-1 and SIVcpz strains such as B.F.83.HXB2, 01.AE.CF.90.90CF402, and many others, providing detailed sequence alignment markers for each.

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	GTGTTTCAATTGTGGCAAGAAGGGCCACACAGCCAGAAATTTGGAGGAGGAGACCAAAATGAAAGATTGTACT	2076
A1.KE.94.Q23_17T-----G-----G-----A-----	1534
A1.RU.03.03RU20_06_13G-----A-----T-----C-----C-----	1553
A1.RW.93.93RW037AC-----G-----A-----C-----T-----	2069
A1.SE.94.SE7253T-----C-----G-----G-----G-----	1280
A1.TZ.01.A173A-----G-----A-----G-----G-----	1275
A1.UA.00.98UA0116A-----C-----T-----C-----T-----	2075
A1.UG.92.92UG037A-----T-----A-----G-----G-----	1440
A1.UG.98.98UG57136A-----A-----C-----G-----A-----	1281
A2.CD.97.97CDKFE4A-----A-----C-----C-----C-----	905
A2.CD.97.97CDKS10A-----A-----C-----C-----C-----	1435
A2.CD.97.97CDKTB48A-----A-----C-----C-----C-----	1433
A2.CY.94.94CY017_41A-----A-----C-----C-----C-----	1277
A.SN.01.DDI579A-----A-----C-----C-----C-----	1280
A.SN.01.DDJ369A-----A-----C-----C-----C-----	1277
A.SN.96.DDJ360A-----A-----C-----C-----C-----	1277
A.ZA.04.04ZASK162B1A-----A-----C-----C-----C-----	1520
B.AR.00.ARMS008A-----A-----C-----C-----C-----	1281
B.AU.96.MBCD36A-----A-----C-----C-----C-----	1431
B.CO.01.PCM074A-----A-----C-----C-----C-----	1290
B.GA.88.OYIA-----A-----C-----C-----C-----	1619
B.NL.99.671A-----A-----C-----C-----C-----	1610
B.RU.04.04RU129005A-----A-----C-----C-----C-----	1562
B.TH.90.BK132A-----A-----C-----C-----C-----	1427
B.US.90.WEAU160A-----A-----C-----C-----C-----	2075
B.US.98.1058_11A-----A-----C-----C-----C-----	1275
C.AR.01.ARG4006A-----A-----C-----C-----C-----	1272
C.BR.04.04BR013A-----A-----C-----C-----C-----	1528
C.BR.92.BR025_dA-----A-----C-----C-----C-----	1417
C.BW.00.00BW07621A-----A-----C-----C-----C-----	1441
C.ET.86.ETH2220A-----A-----C-----C-----C-----	1447
C.IN.95.95IN21068A-----A-----C-----C-----C-----	1439
C.IN.99.01INS65_10A-----A-----C-----C-----C-----	1469
C.KE.00.KER2010A-----A-----C-----C-----C-----	1269
C.TZ.01.BD9_11A-----A-----C-----C-----C-----	1278
C.UY.01.TRA3011A-----A-----C-----C-----C-----	1260
C.ZA.04.SK164B1A-----A-----C-----C-----C-----	1499
C.ZA.05.05ZASK245B1A-----A-----C-----C-----C-----	1496
C.ZM.02.02ZM115A-----A-----C-----C-----C-----	2067
C.ZM.96.96ZM651A-----A-----C-----C-----C-----	1417
D.CD.83.ELIA-----A-----C-----C-----C-----	1625
D.CD.83.NDKA-----A-----C-----C-----C-----	1614
D.CM.01.01CM_4412HALA-----A-----C-----C-----C-----	1287
D.KE.01.NK03006A-----A-----C-----C-----C-----	1284
D.TD.99.MN012A-----A-----C-----C-----C-----	1297
D.TZ.01.A280A-----A-----C-----C-----C-----	1274
D.UG.94.94UG114A-----A-----C-----C-----C-----	1428
D.UG.99.99UGD23550A-----A-----C-----C-----C-----	1284
D.UG.99.99UGK09958A-----A-----C-----C-----C-----	1278
D.ZA.86.R482A-----A-----C-----C-----C-----	1343
F1.BE.93.VI850A-----A-----C-----C-----C-----	1413
F1.BR.89.BZ126A-----A-----C-----C-----C-----	1426
F1.BR.93.93BR020_1A-----A-----C-----C-----C-----	1404
F1.FI.93.FIN9363_1A-----A-----C-----C-----C-----	1405
F1.FR.96.MP411A-----A-----C-----C-----C-----	1272
F2.CM.02.02CM_0016BBYA-----A-----C-----C-----C-----	1266
F2.CM.95.MP255A-----A-----C-----C-----C-----	1272
F2.CM.95.MP257A-----A-----C-----C-----C-----	1284
F2.CM.97.CM53657A-----A-----C-----C-----C-----	1266
G.BE.96.DRCBLA-----A-----C-----C-----C-----	2043
G.CM.01.01CM_4049HANA-----A-----C-----C-----C-----	1281
G.ES.99.X138A-----A-----C-----C-----C-----	1523
G.NG.93.HH8793_12_1A-----A-----C-----C-----C-----	1481
G.NG.92.92NG083A-----A-----C-----C-----C-----	1448
G.SE.93.SE6165A-----A-----C-----C-----C-----	1482
H.BE.93.VI991A-----A-----C-----C-----C-----	1471
H.BE.93.VI997A-----A-----C-----C-----C-----	1406
H.CF.90.056A-----A-----C-----C-----C-----	1426
J.SE.93.SE7887A-----A-----C-----C-----C-----	1396
J.SE.94.SE7022A-----A-----C-----C-----C-----	1397
K.CD.97.EQTB11CA-----A-----C-----C-----C-----	1272
K.CM.96.MP535A-----A-----C-----C-----C-----	1272

B.FR.83.HXB2	GTGTTTCAATTGTGGCAAGGACACACAGCCAGAAATTTGAGGGCCCTAGGAAAGGGCTGTTGAAATGTGGAAAGGAGACACCAAAATGAAGATTGTACT	2076
01 AE.CF.90.90CF402GAGAGA.....	2112
01 AE.CN.05.FJ051A.....	2086
01 AE.HK.x.HK001C.....	1447
01 AE.JP.93.93JP.NH1T.....	2084
01 AE.TH.01.OUR4141C.....	1275
01 AE.TH.02.OUR7691T.....	1275
01 AE.TH.90.CW240C.....	1635
02 AG.CM.02.02CM_16691ET.....	1266
02 AG.EC.x.EC041G.....	1172
02 AG.FR.91.DJ264A.....	1425
02 AG.GH.03.GHNJ196G.....	2102
02 AG.NG.x.IBNGT.....	1601
02 AG.SN.98.MP1211G.....	1273
02 AG.UZ.02.02UZ693A.....	1263
03 AB.RU.97.KAL153_2G.....	1445
04 CPX.CV.94.CY032C.....	1458
05 DF.BE.x.Vil1310G.....	2098
06 CPX.AU.96.BFP90T.....	1438
07 BC.CN.97.CNE54A.....	1268
08 BC.CN.97.97CNGX_6FT.....	1281
09 CPX.GH.96.96GH2911G.....	1458
10 CD.TZ.96.96TZ_BF061T.....	1381
11 CPX.GR.x.GR17A.....	2081
12 BF.AR.99.ARMAL159G.....	1460
13 CPX.CM.96.1849A.....	1520
14 BG.ES.99.X397T.....	1478
15 01B.TH.99.99TH.MU2079G.....	1439
16 A2D.KR.97.97KR004C.....	1387
18 CPX.CU.99.CU76A.....	1305
19 CPX.CU.99.CU7T.....	1532
20 BG.CU.03.CB134A.....	1287
21 A2D.RE.91.KNH1254T.....	1544
23 BG.CU.03.CB118G.....	1536
24 BG.CU.03.CB378T.....	1287
25 CPX.CM.x.101BAA.....	1442
28 BF.BR.99.BREPM12609G.....	1250
29 BF.BR.02.BREPM119A.....	1522
31 BC.BR.02.110PAT.....	1455
33 01B.MV.05.05MYKL007_1G.....	1272
A1C.TZ.02.C03710T.....	2078
A1CDGKU.ZA.99.CM4A.....	2086
A1DHK.NO.97.97NOGLI3C.....	1439
A1GHU.GA.x.VI354T.....	1284
A2D.KE.99.KER2003A.....	1269
AF2.CM.02.02CM.3163MNG.....	1284
AGU.CM.01.01CM_0989MOC.....	1272
AHJU.CM.01.01CM.1296NGA.....	1454
BC.MM.99.mINDU103T.....	1981
BF1.BR.02.02BR006A.....	1272
0708.CN.00.HH069T.....	1568
U.CD.83.83CD003G.....	1275
U.CD.90.90CD121E12T.....	1353
U.GR.99.GR303R.....	1961
U.NL.x.U.NL.95.H10986_D1G.....	1567
N.CM.02.DJ00131T.....	1559
N.CM.04.04CM_1131_03A.....	1649
N.CM.95.YBF30G.....	1647
N.CM.97.YBF106T.....	2143
O.BE.87.ANT70C.....	1515
O.CM.91.WPE180A.....	1659
O.CM.96.96CMWAB637G.....	1624
O.SN.99.SEMP1300T.....	1622
CPZ.CO.90.ANTA.....	1613
CPZ.CO.01.SIVcpzCAM13G.....	1624
CPZ.CO.05.SIVcpzEK505T.....	1622
CPZ.CO.05.SIVcpzL87A.....	1622
CPZ.CO.05.SIVcpzMB66G.....	1613
CPZ.CO.05.SIVcpzMT145T.....	1624
CPZ.GA.88.GAB1A.....	1729
CPZ.TZ.01.TAN1G.....	2130
CPZ.US.85.CPZUST.....	Gag p7

Gag-Pol -1 ribosomal slip site
 Gag p7 Nucleocapsid end / p1 start
 ...CAG...GCTAAATTTTAGGAGATCTGG...CCTTCCTACAG...GGA...AGCCAGGAATTTCTTCAGAGACA...
 Gag p1 end / Gag p6 start

B.FR.83.HXB2
 A1.KE.94.Q23.17
 A1.RU.03.03RU20.06.13
 A1.RW.93.93RW037A
 A1.SE.94.SE7253
 A1.TZ.01.A173
 A1.UA.00.98UA0116
 A1.UG.92.92UG0537
 A1.UG.98.98UG57136
 A2.CD.97.97CDKFE4
 A2.CD.97.97CDKSL0
 A2.CD.97.97CDKTB48
 A2.CY.94.94CY017_41
 A.SN.01.DDH579
 A.SN.01.DDJ369
 A.SN.96.DDJ360
 A.ZA.04.04ZASK162B1
 B.AR.00.ARMS008
 B.AU.96.MBCD36
 B.CO.01.PCM074
 B.GA.88.OYI
 B.NL.99.671
 B.RU.04.04RU129005
 B.TH.90.RK12
 B.US.90.WEAU160
 B.US.98.1058.II
 C.AR.01.ARG4006
 C.BR.04.04BR013
 C.BR.92.BR025_d
 C.BW.00.00BW07621
 C.ET.86.ETH2220
 C.IN.95.95IN21068
 C.IN.99.01IN565_10
 C.KE.00.KER2010
 C.TZ.01.BD9_11
 C.UY.01.TRA3011
 C.ZA.04.SK164B1
 C.ZA.05.05ZASK245B1
 C.ZM.02.02ZM115
 C.ZM.96.96ZM651
 D.CD.83.ELI
 D.CD.83.NDK
 D.CM.01.01CM.4412HAL
 D.KE.01.NKU3006
 D.TD.99.MN012
 D.TZ.01.A280
 D.UG.94.94UG114
 D.UG.99.99UGD2550
 D.UG.99.99UGK03958
 D.ZA.86.R482
 F1.BE.93.VI850
 F1.BR.89.B2126
 F1.BR.93.93BR020_1
 F1.FI.93.FIN9363_1
 F1.FR.96.MP411
 F2.CM.02.02CM.0016BBY
 F2.CM.95.MP255
 F2.CM.95.MP257
 F2.CM.97.CM53657
 G.BE.96.DRCHL
 G.CM.01.01CM.4049HAN
 G.ES.99.X138
 G.KE.93.HH8793_12_1
 G.NG.92.92NG083
 G.SE.93.SE6165
 H.BE.93.VI991
 H.BE.93.VI997
 H.CF.90.056
 J.SE.93.SE7887
 J.SE.94.SE7022
 K.CD.97.EQTB11C
 K.CM.96.MP535

2145
 1603
 1622
 2138
 1349
 1344
 2144
 1509
 1350
 974
 0
 1504
 1502
 1346
 1349
 1346
 1589
 1350
 1500
 1359
 1688
 1679
 1631
 1496
 2144
 1344
 1341
 1600
 1486
 1510
 1516
 1508
 1538
 1338
 1347
 1329
 1568
 1565
 2139
 1486
 1694
 1683
 1356
 1353
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 1482
 1495
 1473
 1474
 1341
 1335
 1341
 1353
 1335
 2112
 1350
 1592
 1549
 1517
 1551
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 1475
 1495
 1465
 1466
 1341
 1341

Genomic coordinates and sequence alignments for Gag p7, Gag p1, Gag p6, and Gag Pol. Includes labels like 'Gag p7 Nucleocapsid end', 'Gag p1 end', and 'Gag p6 start'.

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

B.FR.83.HXB2CCAGGCGCAACAGCC.....CCACCCAGAA.....GAGAGCTTCAGGTCCTGGG.....GTAGAGACACAACTCCCTCAGAA	2213
A1.KE.94.Q23_17TG-A-T.....C.....C-GTG-ATG.....A.....	1668
A1.RU.03.03RU20_06_13R-R-T.....C.....A-R-TG-ATGR.....A-T-CC-CT-TG.....	1687
A1.RW.93.93RW037A_1G.....C.....CT-TG-ATG.....A-T-G-CT-C-T-G.....	2203
A1.SE.94.SE7253G.....C.....CTT-TG-ATG.....A-T-G-CT-C-T-G.....	1414
A1.TZ.01.A173G.....C.....CTT-TG-ATG.....A-T-G-CT-C-TT-G.....	1409
A1.UA.00.98UA0116-T.....C.....AGA-TG-AGG.....A-T-CC-C-TG.....	2209
A1.UG.92.92UG037TG-G.....C.....CAGAGA-TTTGGAT-AGG-A.....T-GTCT-C-T-G.....	1577
A1.UG.98.98UG57136TG-G.....C.....CTG-TG-ATG.....A-T-CT-C-T-G.....	1415
A2.CD.97.97CDKFE4A.....C.....GA-TG-AATG.....A.....	1025
A2.CD.97.97CDKS10A.....C.....A.....A.....	1554
A2.CD.97.97CDKTB48A.....C.....A-G-AATG.....A-T-CT-T-C-T.....	1567
A2.CY.94.94CY017_41A.....C.....TCT-C-GG-ATG-A.....A-T-CT-T-C-C.....	1411
A.SN.01.DDI579A.....C.....CT-C-TG-AGG.....A-T-CT-T-C-C.....	1414
A.SN.01.DDJ369A.....C.....TCT-C-GG-ATG-A.....A-T-CT-T-C-C.....	1411
A.SN.96.DDJ360TG.....C.....G-ATG-ATG.....A-T-CT-C-A-AG.....	1654
A.ZA.04.04ZASK162B1G.....C.....C-T.....GG.....	1418
B.AR.00.ARMS008T.....C.....AG-A.....A.....	1568
B.AU.96.MBCD36AG-G-CTA.....G.....GAGCCAACAGCC.....AG.....	1430
B.CO.01.PCM074C.....C.....G.....A.....	1756
B.GA.88.OYICCTTTTTCAGAGACAGCCAGCCAGCC.....R-C.....T.....A.....	1777
B.NL.99.671A-T.....C.....T.....AG-G-G.....	1717
B.RU.04.04RU129005G.....C.....T.....A.....	1564
B.TH.90.BK132T-A.....C.....TCA.....A.....	2212
B.US.90.WEAU160T.....C.....T.....T.....	1412
B.US.98.1058_11C.....C.....T.....AG.....	1403
C.AR.01.ARG4006C.....C.....TC-A.....AG.....	1403
C.BR.04.04BR013A.....C.....TC-C.....AG.....	1683
C.BR.92.BR025_dC.....C.....T.....A.....	1554
C.BW.00.00BW07621C.....C.....-A-TC-A.....AG.....	1572
C.ET.86.ETH2220T.....C.....TC-A.....A.....	1611
C.IN.95.95IN21068C.....C.....TC-A.....AG.....	1570
C.IN.99.01INS65_10C.....C.....TC-A.....AG.....	1600
C.KE.00.KER2010C.....C.....TC-A.....AG.....	1400
C.TZ.01.BD9_11C.....C.....TC-A.....AG.....	1427
C.UY.01.TRA3011T.....C.....TC-AA.....AG.....	1391
C.ZA.04.SK164B1T.....C.....TC-A.....AG.....	1630
C.ZA.05.05ZASK245B1G.....C.....TC-A.....AG.....	1648
C.ZM.02.02ZM115A.....C.....TC-A.....AG.....	2201
C.ZM.96.96ZM651C.....C.....TC-A.....AG.....	1548
D.CD.83.ELIC.....C.....G-T.....A.....	1759
D.CD.83.NDKG-T.....C.....G-T.....AG-T.....	1748
D.CM.01.01CM_4412HALC.....C.....G-TC.....AG-T.....	1421
D.KE.01.NK03006C.....C.....G-T.....AG-T.....	1418
D.TD.99.MN012C.....C.....G-T.....A.....	1431
D.TZ.01.A280G.....C.....T-G-T.....AG-T.....	1408
D.UG.94.94UG114G.....C.....-T-G-A-TA.....AG-T.....	1568
D.UG.99.99UGD23550G.....C.....T.....AG-T.....	1418
D.UG.99.99UGK09958G.....C.....G-T.....A.....	1412
D.ZA.86.R482G-G-T.....C.....G-T.....G.....	1477
F1.BE.93.VI850G-TC-A-A.....AG-T.....G-TC-A-A.....AG-T.....	1547
F1.BR.89.B2126G-TC-A-A.....AG-T.....G-TC-A-A.....AG-T.....	1560
F1.BR.93.93BR020_1GT.....C.....TC.....AG-T.....	1538
F1.FI.93.FIN9363_1C-G-ATCA-A.....A-GT.....C-G-ATCA-A.....A-GT.....	1539
F1.FR.96.MP411G-CG.....C.....G-TCAAA.....AG-A-T.....	1406
F2.CM.02.02CM_0016BBYG-C.....C.....G-TC-A.....A.....	1400
F2.CM.95.MP255G-A.....C.....TC-A.....AG-G-T.....	1406
F2.CM.95.MP257G-T.....C.....G-T.....AG-T.....	1418
F2.CM.97.CM53657A.....C.....TC-A.....AG-T.....	1400
G.BE.96.DRCBLA.....C.....G-TC.....AG-T.....	2177
G.CM.01.01CM_4049HANG-AGTC-A.....AG-T.....G-AGTC-A.....AG-T.....	1415
G.ES.99.X138C.....C.....TC-A.....AG-T.....	1657
G.KE.93.HH8793_12_1C.....C.....TC-A.....AG-A-T.....	1614
G.NG.92.92NG083A.....C.....G-A-TC-A.....AG-T.....	1582
G.SE.93.SE6165A.....C.....-A-C-G-TC-A.....AG-T.....	1616
H.BE.93.VI991T.....C.....G-TC-A.....AG-TC.....	1605
H.BE.93.VI997A.....C.....TC.....AG-TG.....	1540
H.CF.90.056A.....C.....G-TC-A.....AG-TG.....	1560
J.SE.93.SE7887C-G-CTC-A.....AG-TC.....C-G-CTC-A.....AG-TC.....	1528
J.SE.94.SE7022C-G-TC-A.....AG-TC.....C-G-TC-A.....AG-TC.....	1560
K.CD.97.EQTB11CTG-TC.....AG-T.....TG-TC.....AG-T.....	1406
K.CM.96.MP535G.....C.....G.....C.....	1406

B.FR.83.HXB2
 01 AE.CF.90.90CF402
 01 AE.CN.05.FU051
 01 AE.HK.x.HK001
 01 AE.JP.93.93JP.NH1
 01 AE.TH.01.OUR4141
 01 AE.TH.02.OUR7691
 01 AE.TH.90.CM240
 02 AG.CM.02.02CM_16691E
 02 AG.EC.x.EC041
 02 AG.FR.91.DU264
 02 AG.GH.03.GHNJ196
 02 AG.NG.x.IBNG
 02 AG.SN.98.MP1211
 02 AG.UZ.02.02UZ693
 03 AB.RU.97.KAL153_2
 04 CPX.CV.94.CV032
 05 DF.BE.x.VI11310
 06 CPX.AU.96.BFP90
 07 BC.CN.97.CNE54
 08 BC.CN.97.97CNGX_6F
 09 CPX.GH.96.96GH2911
 10 CD.TZ.96.96TZ_BF061
 11 CPX.GR.x.GR17
 12 BF.AR.99.ARMAL159
 13 CPX.CM.96.1849
 14 BG.ES.99.X397
 15 01B.TH.99.99TH_MU2079
 16 A2D.KR.97.97KR004
 18 CPX.CU.99.CU76
 19 CPX.CU.99.CU7
 20 BG.CU.03.CB134
 21 A2D.KR.91.KNH1254
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 CPX.CM.x.101BA
 28 BF.BR.99.BREPM12609
 29 BF.BR.02.BREPM119
 31 BC.BR.02.110PA
 33 01B.WV.05.05MYKL007_1
 A1.C.TZ.02.C03710
 A1CDGKU.ZA.99.CM4
 A1DHK.NO.97.97NOGLI3
 A1GHU.GA.x.VI354
 A2D.KR.99.KBR2003
 A2F.CM.02.02CM_3163MN
 AGU.CM.01.01CM_0989MO
 AHJU.CM.01.01CM_1296NG
 BC.CN.96.YNPL9607
 BC.MM.99.mIDU103
 BF1.BR.02.02BR006
 0708.CN.00.HH069
 U.CD.83.83CD003
 U.CD.90.90CD121E12
 U.GR.99.GR303
 U.NL.x.U.NL.95.H10986_D1
 N.CM.02.DJ00131
 N.CM.04.04CM_1131_03
 N.CM.95.YBF30
 N.CM.97.YBF106
 O.BE.87.ANT70
 O.CM.91.WVPE180
 O.CM.96.96CMWAB637
 O.SN.99.SEMPL300
 CPZ.CD.90.ANT
 CPZ.CM.01.SIVcpzCAM13
 CPZ.CM.05.SIVcpzEK505
 CPZ.CM.05.SIVcpzL87
 CPZ.CM.05.SIVcpzMB66
 CPZ.CM.05.SIVcpzMT145
 CPZ.GA.88.GAB1
 CPZ.TZ.01.TAN1
 CPZ.US.85.CPZUS
 Gag_p6
 Gag-Pol_TF
 CCACGAGCAAGCC CCACGAGAA GAGAGCTTCAGGTCTGGG...GTAGAGACAACACTCCCTCCAGAA 2213
 2246ATGATCTTC-C
 2220TA-A-GGAAATGAATC-T-AAT
 1572TTA-A-GGATCT-TTA-T
 2218A-A-GGG-ATGATCT-TTA-C
 1409G-CA-A-GGG-ATGATCT-A-T
 1769CA-A-GGG-ATGATGGGGAAG-T
 1400CG-ATG-AAATCT-T-T
 1306G-ATG-ATGATCT-C
 1559G-AGG-ATGATCT-C
 2236G-ATG-ATGATG-CT-AA-C-C
 1735G-ATG-ATGATT-C-CAC
 1407G-ATG-ATGATCT-T-C-C
 1397AA-G-GG-ATGATCT-T-C-C
 1436A-A-TG-ATGATC-T-T-T
 1579AT-AGA-AGGAAAAGTCT-T-T
 1592G-C-CGAGTG-CT-T-C
 2232G-TTC-AAGTG-C-T-C-C
 1575GAATCAT
 1399G-T-AAGTC-AG-C
 1415G-TG-ATGAAGTC-AG-C
 1592G-TAG-TACT-T-YR
 1515G-TGAG-TATA-T
 2215G-TG-TC-AAG-TAT-C-C
 1624G-TG-TC-AAG-TAT-C-C
 1654G-TG-TC-AAG-TAT-C-C
 1609A-GGG-ATGATCT-TTA-T
 1573GA-TG-AATGAGTC-TTG-
 1521G-TG-TC-AAG-TAG-C-T-C-C
 1439G-TAG-A-TGTG-CT-T-C
 1660GGAG-TATG-CT-T-C
 1421G-TAATC-T
 1678G-A-TC-AAG-TATG-C-T-C-C
 1655TAAG-TATG-C-T-C-C
 1421G-TAAG-TAT-C-C
 1576TC-AAG-TAT-C-C
 1384T-AAG-TAT-C-C
 1653TC-AAG-TAT-C-C
 1592TAAGTCAGT
 1403TC-AAGTC-AG-C
 1591G-TAAG-TC-AG-C
 2115G-T-C-AAGTC-T-C
 1403G-T-C-AAGTC-AG-C
 1702G-T-C-AAGTC-T-G-C
 1412G-T-C-AAG-AGTC-T-G-C
 1487G-T-C-AAG-TGTC-T-C-C
 2095G-T-C-AAG-TT-C-T-C
 1710AT-ATGCAAG-GGGCA-A-AGGG
 1699T-ATGCAAG-GGGCA-A-AGAGA
 1789T-ATGCAAG-AGGCA-A-AGGG
 1787T-ATGCAAG-AGGCA-A-AGGGA
 2250GAGCAAGT-
 2225GAGCAAGT-
 1673GAGCAAGT-
 2249AC-GAGGAA-T
 1640T-ATCAAGC
 1778T-ATG-ACCAAAGGAGA-G
 1770T-ATG-A-CAAG-AGCA-A-AGGG-C
 1753T-GTCACCA-ACA-AGA-AC
 1747T-GTCAAG-GAC-G-AGA-G
 1752ATCG-A-T-CAAG-AGAAGT-AGG..G
 2265AAAG-AGAG
 1876TTGGTGA-A-AG..G
 2273GATG-A-CAAGTGA-A-AG..G
 P E P T A P P E E S F R S G V E T T P O K Gag
 T R A N S R E L Q V W G R D N N S P S E Gag-Pol

HIV-1/SIVcpz
complete genomes

Accession	Genome Sequence	Position
B.FR.83.HXB2CAGGAG...CCGATAGAC...AAG...GAACTGTAT.....	2292
A1.KE.94.Q23.17A-A-A-A-A-GCCCAA.....AA-A-GCCCAA.....	1750
A1.RU.03.03RU20.06_13A-A-A-A-A-AAGC-CCT.....AA-AAGC-CCT.....	1769
A1.RW.93.93RW037A_1A-A-A-A-A-CACCCA.....AA-A-CACCCA.....	2285
A1.SE.94.SE7253A-A-A-A-A-CTCA.....AA-A-CTCA.....	1496
A1.TZ.01.A173A-A-A-A-A-GTCCA.....AA-A-GTCCA.....	1491
A1.UA.00.98UA0116A-A-A-A-A-C-CCT.....AA-A-C-CCT.....	2291
A1.UG.92.92UG037A-A-A-A-A-C-A-CCA.....AA-A-C-A-CCA.....	1659
A1.UG.98.98UG57136A-A-A-A-A-G-A-CTCA.....AA-A-G-A-CTCA.....	1497
A2.CD.97.97CDKFE4A-A-A-A-A-C-C-ACT.....AA-A-C-C-ACT.....	1097
A2.CD.97.97CDKS10AAAC.....G-C-CCACC.....AA-A-G-C-CCACC.....	1630
A3.CY.94.94CY0117_41A-T-GAGAC.....G-C-CRAT.....AA-A-G-C-CRAT.....	1649
A.SN.01.DDI1579A-A-A-G.....G-C-C.....AA-A-G-C-C.....	1490
A.SN.01.DDU369A-A-A-G.....AACC.....AA-A-AACC.....	1493
A.SN.96.DDU360A-A-A-G.....C-GT.....AA-A-C-GT.....	1490
A.ZA.04.04ZASK162B1A-A-C.....G-A-CC.....AA-A-G-A-CC.....	1733
B.AR.00.ARMS008T...C.....GAA.....AA-A-GAA.....	1497
B.AU.96.MBCD36T...A.....G.....AA-A-G.....	1647
B.CO.01.PCM074T...A.....G.....AA-A-G.....	1509
B.GA.88.OYIA-A-A-A-A-G.....AA-A-G.....	1835
B.NL.99.671A-A-C.....G-A.....AA-A-G-A.....	1856
B.RU.04.04RU129005A-A-C.....G-A.....AA-A-G-A.....	1796
B.TH.90.BK132A-A-A.....G.....AA-A-G.....	1643
B.US.90.WEAU160A-A-A.....G.....AA-A-G.....	2291
B.US.98.1058_11A-A-A.....G.....AA-A-G.....	1482
C.AR.01.ARG4006C-A-R.....G.....AA-A-G.....	1476
C.BR.04.04BR013C-B-R.....G.....AA-A-G.....	1756
C.BR.92.BR025_dC-B-R.....G.....AA-A-G.....	1630
C.BW.00.00BW07621C-B-W.....G.....AA-A-G.....	1645
C.ET.86.ETH220C-E-T.....G-C.....AA-A-G-C.....	1684
C.IN.95.95IN21068C-I-N.....G.....AA-A-G.....	1643
C.IN.99.01IN565_10C-I-N.....G.....AA-A-G.....	1673
C.KE.00.KER2010C-K-E.....G.....AA-A-G.....	1473
C.TZ.01.BD9_11C-T-Z.....G.....AA-A-G.....	1500
C.UY.01.TRA3011C-U-Y.....G.....AA-A-G.....	1464
C.ZA.04.SK164B1C-Z-A.....G.....AA-A-G.....	1703
C.ZA.05.05ZASK245B1C-Z-A.....G.....AA-A-G.....	1721
C.ZM.02.02ZM115C-Z-M.....G.....AA-A-G.....	2286
C.ZM.96.96ZM651C-Z-M.....G.....AA-A-G.....	1621
D.CD.83.ELIA-A-A.....AA.....AA-A.....	1838
D.CD.83.NDKA-A-A.....AA.....AA-A.....	1827
D.CM.01.01CM_4412HALA-A-A.....AA.....AA-A.....	1506
D.KE.01.NK03006GA.....AA-T.....AA-A.....	1497
D.TD.99.MN012A-A-A.....G.....AA-A.....	1516
D.TZ.01.A280A-A-A.....G.....AA-A.....	1493
D.UG.94.94UG114A-A-A.....G.....AA-A.....	1647
D.UG.99.99UGD2550G.....AA-A.....AA-A.....	1497
D.UG.99.99UGK09958G.....AA-A.....AA-A.....	1491
D.ZA.86.R482A-A-A.....T-C.....AA-A.....	1556
F1.BE.93.VI850A-A-A.....GG.....CCCT.....AA-A.....	1629
F1.BR.89.B2126A-A-A.....G.....CCCT.....AA-A.....	1642
F1.BR.93.93BR020_1A-A-A.....G.....CCCT.....AA-A.....	1620
F1.FI.93.FIN9363_1A-A-A.....G.....CCCT.....AA-A.....	1621
F1.FR.96.MPA11A-A-A.....G.....CCCT.....AA-A.....	1494
F2.CM.02.02CM_0016BBYA-A-A.....G.....CCCT.....AA-A.....	1482
F2.CM.95.MP255A-A-A.....G.....CCCT.....AA-A.....	1488
F2.CM.95.MP257A-A-A.....G.....CCCT.....AA-A.....	1500
F2.CM.97.CM53657A-A-A.....G.....CCCT.....AA-A.....	1482
G.BE.96.DRCLA-A-A.....G.....CCCT.....AA-A.....	2256
G.CM.01.01CM_4049HANA-A-A.....G.....CCCT.....AA-A.....	1494
G.ES.99.X138A-A-A.....G.....CCCT.....AA-A.....	1733
G.KE.93.HH8793_12_1A-A-A.....G.....CCCT.....AA-A.....	1661
G.NG.92.92NG083A-A-A.....G.....CCCT.....AA-A.....	1689
G.SE.93.SE6165A-A-A.....G.....CCCT.....AA-A.....	1681
H.BE.93.VI991A-A-A.....G.....CCCT.....AA-A.....	1616
H.BE.93.VI997A-A-A.....G.....CCCT.....AA-A.....	1639
H.CF.90.056A-A-A.....G.....CCCT.....AA-A.....	1607
J.SE.93.SE7887A-A-A.....G.....CCCT.....AA-A.....	1606
J.SE.94.SE7022A-A-A.....G.....CCCT.....AA-A.....	1488
K.CD.97.EQTB11CA-A-A.....G.....CCCT.....AA-A.....	1488
K.CM.96.MP535A-A-A.....G.....CCCT.....AA-A.....	1488

B.FR.83.HXB2	GAG-Pol TF end \ Pol Protease start	Gag end \	2292
01 AE.CF.90.90CF402 CAGGAG... CCGATAGAC... AAG... GAACCTGTAT CCTTTAACTTCCCTCAGTCTCAGTCTTTTGGCAACGACCCCTCGTCAATAA
01 AE.CN.05.FU051	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
01 AE.HK.x.HK001	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
01 AE.JP.93.93JP.NH1	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
01 AE.TH.01.0UR4141	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
01 AE.TH.02.0UR7691	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AE.TH.90.CM240	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.CM.02.02CM.16691E	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.EC.x.EC041	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.FR.91.DJ264	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.GH.03.GHNJ196	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.NG.x.IENG	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.SN.98.MPI2111	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
02 AG.UZ.02.02UZ693	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
03 AB.RU.97.KAL153.2	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
04 CDX.CV.94.CY032	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
05 DF.BE.x.VII1310	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
06 CDX.AU.96.BFP90	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
07 BC.CN.97.CM54	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
08 BC.CN.97.97CNGX.6F	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
09 CDX.GH.96.96GH2911	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
10 CD.TZ.96.96TZ.BF061	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
11 CDX.GR.x.GR17	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
12 BF.AR.99.ARMAL159	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
13 CDX.CM.96.1849	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
14 BG.ES.99.X397	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
15 01B.TH.99.99TH.MU2079	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
16 A2D.KR.97.97KR004	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
18 CDX.CU.99.CU76	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
19 CDX.CU.99.CU76	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
20 BG.CU.03.CB134	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
21 A2D.KR.91.KNH1254	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
23 BG.CU.03.CB118	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
24 BG.CU.03.CB378	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
25 CDX.CM.x.101BA	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
28 BF.BR.99.BREPM12609	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
29 BF.BR.02.BREPM119	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
31 BC.BR.02.110PA	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
33_01B.WY.05.05MYKL007_1	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
A1C.TZ.02.CO3710	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
A1CDGKU.ZA.99.CM4	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
A1DHK.NO.97.97N0GLL3	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
A1DGHU.GA.x.VI354	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
A2D.XE.99.KER2003	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
AF2.CM.02.02CM.3163MN	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
AGU.CM.01.01CM.0989MO	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
ARJU.CM.01.01CM.1296NG	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
BC.CN.96.YNRL9607	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
BC.MM.99.MIDDU103	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
BF1.BR.02.02BR006	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
0708.CN.00.HH069	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
U.CD.83.83CD003	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
U.CD.90.90CD121E12	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
U.GR.99.GR303	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
U.NL.x.U.NL.95.H10986_D1	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
N.CM.02.DJ00131	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
N.CM.04.04CM.1131_03	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
N.CM.95.YBF30	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
N.CM.97.YBF106	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
O.BE.87.ANT70	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
O.CM.91.MVPS180	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
O.CM.96.96CMWAB637	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
O.SN.99.SEMPL1300	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CD.90.ANT	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CM.01.SIVcpzCAM13	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CM.05.SIVcpzE505	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CM.05.SIVcpzL187	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CM.05.SIVcpzMB66	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.CM.05.SIVcpzW1145	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.GA.88.GAB1	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.TZ.01.TAN1	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
CPZ.US.85.CPZUS	-A-A-A-AGC-G-.....	AA-A-C-CC-.....	AA-A-C-CC-.....
Gag p6
Gag-Pol TF/Pol Protease

Gag-Pol TF end \ Pol Protease start
 complete genomes
 HIV-1/SIVcpz

B.FR.83.HXB2	CTTCTGGGAAGTTCAATTAGGAATACACATCCCGCAGGTTAAAGAAAGAAAAATCAGTAAACAGTACTGGATGGTGGTGGATGCATATTTTTTCAGTTCCTCCCTTAGATGAAGACTTCAGGAAGTATACTGCA	2936
01 AE.CF.90.90CF402	T-T-A-TC-A-A-C-T-T-G-T-A	2972
01 AE.CN.05.FJ051	T-T-A-TC-A-A-C-T-T-G-T-A	2972
01 AE.HK.x.HK001	T-T-A-TC-A-A-C-T-T-G-T-A	2946
01 AE.JP.93.93JP.NH1	T-T-A-TC-A-A-C-T-T-G-T-A	2946
01 AE.TH.01.OUR4141	T-T-A-TC-A-A-C-T-T-G-T-A	2938
01 AE.TH.02.OUR7691	T-T-A-TC-A-A-C-T-T-G-T-A	2132
01 AE.TH.90.CM240	T-T-A-TC-A-A-C-T-T-G-T-A	2135
02 AG.CM.02.02CM_16691E	T-T-A-TC-A-A-C-T-T-G-T-A	2510
02 AG.EC.x.EC041	T-T-A-TC-A-A-C-T-T-G-T-A	2126
02 AG.FR.91.DJ264	T-T-A-TC-A-A-C-T-T-G-T-A	2032
02 AG.GH.03.GHNJ196	T-T-A-TC-A-A-C-T-T-G-T-A	2285
02 AG.NG.x.IBNG	T-T-A-TC-A-A-C-T-T-G-T-A	2965
02 AG.SN.98.MP1211	T-T-A-TC-A-A-C-T-T-G-T-A	2461
02 AG.UZ.02.02UZ693	T-T-A-TC-A-A-C-T-T-G-T-A	2133
03 AB.RU.97.KAL153_2	T-T-A-TC-A-A-C-T-T-G-T-A	2123
04 CPX.CV.94.CY032	T-T-A-TC-A-A-C-T-T-G-T-A	2162
05 DF.BE.x.VI11310	T-T-A-TC-A-A-C-T-T-G-T-A	2302
06 CPX.AU.96.BFP90	T-T-A-TC-A-A-C-T-T-G-T-A	2318
07 BC.CN.97.CNE4	T-T-A-TC-A-A-C-T-T-G-T-A	2964
08 BC.CN.97.97CNGX_6F	T-T-A-TC-A-A-C-T-T-G-T-A	2298
09 CPX.GH.96.96GHX2911	T-T-A-TC-A-A-C-T-T-G-T-A	2116
10 CD.TZ.96.96TZ_BF061	T-T-A-TC-A-A-C-T-T-G-T-A	2138
11 CPX.GR.x.GR17	T-T-A-TC-A-A-C-T-T-G-T-A	2315
12 BF.AR.99.ARMAL159	T-T-A-TC-A-A-C-T-T-G-T-A	2238
13 CPX.CM.96.1849	T-T-A-TC-A-A-C-T-T-G-T-A	2941
14 BG.ES.99.X397	T-T-A-TC-A-A-C-T-T-G-T-A	2341
15 01B.TH.99.99TH.MU2079	T-T-A-TC-A-A-C-T-T-G-T-A	2377
16 A2D.KR.97.97KR004	T-T-A-TC-A-A-C-T-T-G-T-A	2335
18 CPX.CU.99.CU76	T-T-A-TC-A-A-C-T-T-G-T-A	2299
19 CPX.CU.99.CU7	T-T-A-TC-A-A-C-T-T-G-T-A	2241
20 BG.CU.03.CB134	T-T-A-TC-A-A-C-T-T-G-T-A	2162
21 A2D.KE.91.KNH1254	T-T-A-TC-A-A-C-T-T-G-T-A	2374
23 BG.CU.03.CB118	T-T-A-TC-A-A-C-T-T-G-T-A	2141
24 BG.CU.03.CB378	T-T-A-TC-A-A-C-T-T-G-T-A	2392
25 CPX.CM.x.101BA	T-T-A-TC-A-A-C-T-T-G-T-A	2369
28 BF.BR.99.BREPM12609	T-T-A-TC-A-A-C-T-T-G-T-A	2144
29 BF.BR.02.BREPM119	T-T-A-TC-A-A-C-T-T-G-T-A	2302
31 BC.BR.02.110PA	T-T-A-TC-A-A-C-T-T-G-T-A	2110
33 01B.WV.05.05MYKL007_1	T-T-A-TC-A-A-C-T-T-G-T-A	2370
A1C.TZ.02.C03710	T-T-A-TC-A-A-C-T-T-G-T-A	2315
A1CDGKU.ZA.99.CM4	T-T-A-TC-A-A-C-T-T-G-T-A	2123
A1DHK.NO.97.97NOGLI3	T-T-A-TC-A-A-C-T-T-G-T-A	2938
A1GHU.GA.x.VI354	T-T-A-TC-A-A-C-T-T-G-T-A	2946
A2D.KE.99.KER2003	T-T-A-TC-A-A-C-T-T-G-T-A	2296
AF2.CM.02.02CM.3163MN	T-T-A-TC-A-A-C-T-T-G-T-A	2141
AGU.CM.01.01CM_0989MO	T-T-A-TC-A-A-C-T-T-G-T-A	2129
AHJU.CM.01.01CM_1296NG	T-T-A-TC-A-A-C-T-T-G-T-A	2138
BC.CN.96.YNRL9607	T-T-A-TC-A-A-C-T-T-G-T-A	2120
BC.MM.99.MIDU103	T-T-A-TC-A-A-C-T-T-G-T-A	2120
BF1.BR.02.02BR006	T-T-A-TC-A-A-C-T-T-G-T-A	2838
0708.CN.00.HH069	T-T-A-TC-A-A-C-T-T-G-T-A	2120
U.CD.83.83CD003	T-T-A-TC-A-A-C-T-T-G-T-A	2431
U.CD.90.90CD121E12	T-T-A-TC-A-A-C-T-T-G-T-A	2135
U.GR.99.GR303	T-T-A-TC-A-A-C-T-T-G-T-A	2210
U.NL.x.U.NL.95.H10986_D1	T-T-A-TC-A-A-C-T-T-G-T-A	2821
N.CM.02.DJ00131	T-T-A-TC-A-A-C-T-T-G-T-A	2442
N.CM.04.04CM_1131_03	T-T-A-TC-A-A-C-T-T-G-T-A	2442
N.CM.95.YBF30	T-T-A-TC-A-A-C-T-T-G-T-A	2530
N.CM.97.YBF106	T-T-A-TC-A-A-C-T-T-G-T-A	2528
O.BE.87.MVPE180	T-T-A-TC-A-A-C-T-T-G-T-A	2991
O.CM.91.MVPE180	T-T-A-TC-A-A-C-T-T-G-T-A	2966
O.CM.96.96CMWAB637	T-T-A-TC-A-A-C-T-T-G-T-A	2420
O.SN.99.SEMP1300	T-T-A-TC-A-A-C-T-T-G-T-A	2990
CPZ.CD.90.ANT	T-T-A-TC-A-A-C-T-T-G-T-A	2375
CPZ.CM.01.SIVcpzCAM13	T-T-A-TC-A-A-C-T-T-G-T-A	2516
CPZ.CM.05.SIVcpzEK505	T-T-A-TC-A-A-C-T-T-G-T-A	2508
CPZ.CM.05.SIVcpzL87	T-T-A-TC-A-A-C-T-T-G-T-A	2491
CPZ.CM.05.SIVcpzMB66	T-T-A-TC-A-A-C-T-T-G-T-A	2482
CPZ.GA.88.GAB1	T-T-A-TC-A-A-C-T-T-G-T-A	2478
CPZ.TZ.01.TAN1	T-T-A-TC-A-A-C-T-T-G-T-A	2997
CPZ.US.85.CPZUS	T-T-A-TC-A-A-C-T-T-G-T-A	2580
Pol_p51_RT	F_W_E_V_Q_L_G_I_P_H_P_A_G_L_K_K_K_K_S_V_T_V_L_D_V_G_D_A_Y_F_S_V_P_L_D_E_D_F_R_K_Y_T_A	2996

HIV-1/SIVcpz complete genomes

B. FR. 83. HXB2
TTTACCATACCTAGTATAAACAATGAGACACAGGATTAGATATCAGTACAATGCTTCCACAGGATGGAAAGGATCACAGCAATATTCACCAAGTAGCATGACAAAATCTTAGACCCCTTTAGAA
3066
1 AE. CF. 90. 90CF402
1 AE. CN. 05. FU051
1 AE. HK. x. HK001
1 AE. JP. 93. 93JP_NH1
1 AE. TH. 01. OUR4141
1 AE. TH. 02. OUR7691
1 AE. TH. 90. CM240
1 AE. TH. 90. CM240
2 AG. CM. 02. 02CM_16691E
2 AG. EC. x. EC041
2 AG. FR. 91. DU264
2 AG. GH. 03. GHNUJ196
2 AG. NG. x. IBNG
2 AG. SN. 98. MP1211
2 AG. UZ. 02. 02UZ693
03 AB. RU. 97. KAL153_2
04 CPX. CV. 94. CV032
05 DF. BE. x. VIL1310
06 CPX. AU. 96. BFP90
07 BC. CN. 97. CNE4
08 BC. CN. 97. 97CNGX_6F
09 CPX. GH. 96. 96GHZ911
10 CD. TZ. 96. 96TZ_BF061
11 CPX. GR. x. GR17
12 BF. AR. 99. ARMA159
13 CPX. CM. 96. 1849
14 BG. ES. 99. X397
15 01B. TH. 99. 99TH_MU2079
16 A2D. KR. 97. 97KR004
18 CPX. CU. 99. CU76
19 CPX. CU. 99. CU7
20 BG. CU. 03. CB134
21 A2D. KE. 91. KNH1254
23 BG. CU. 03. CB118
24 BG. CU. 03. CB378
25 CPX. CM. x. 101BA
28 BF. BR. 99. BREPM12609
29 BF. BR. 02. BREPM119
31 BC. BR. 02. 110PA
33 01B. WY. 05. 05MYKL007_1
A1C. TZ. 02. C03710
A1CDGKU.ZA.99.CM4
A1DHK.NO.97.97NOGLI3
A1GHU.GA.x.VI354
A2D.KE.99.KER2003
AF2.CM.02.02CM_3163MN
AGU.CM.01.01CM_0989MO
AHJU.CM.01.01CM_1296NG
BC.CN.96.MYNL9607
BC.MM.99.MINDU103
BF1.BR.02.02BR006
0708.CN.00.HH069
U.CD.83.83CD003
U.CD.90.90CD121E12
U.GR.99.GR303
U.NL.x.U.NL.95.H10986_D1
N.CM.02.DJ00131
N.CM.04.04CM_1131_03
N.CM.95.YBF30
N.CM.97.YBF106
O.BE.87.ANT70
O.CM.91.MVPE180
O.CM.96.96CMABB637
O.SN.99.SEMPI300
CPZ.CO.90.ANT
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzL87
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.GA.88.GAB1
CPZ.TH.01.TAN1
CPZ.UY.85.CPZUS
Pol p51 RT

HIV-1/SIVcpz
complete genomes

B.FR.83.HXB2	AACAAAATCCAGACATAGTATTCTCAATACATGATGATTTGGTATGTAGGATCTCACTTGAATAGGGCAGCATAGAACAAAAATAGAGGAGCTGAGACAACATCTGTTGAGTGGGGACTTACCAC	3196
A1.KE.94.Q23_17	C-A-A-A-G-G-G-A-AT-A-GCT-A-A-C-TT	2654
A1.RW.03.03RU20_06_13	T-A-A-A-T-T-A-GCT-A-A-C-TT	2673
A1.RW.93.93RW037A_13	A-A-A-A-T-T-A-GCT-A-A-C-TT	2673
A1.SE.94.SE7253	T-A-G-A-A-T-T-A-GCT-A-A-C-GT	3189
A1.TZ.01.A173	C-A-G-A-A-T-T-A-GCT-A-A-C-TT	2400
A1.UA.00.98UA0116	C-A-A-A-T-T-A-GCT-A-A-AA-TT	2395
A1.UG.92.92UG037	C-A-A-A-T-T-A-GCT-A-A-AA-TT	3195
A1.UG.98.98UG57136	C-A-TT-GAG-T-T-A-GCT-A-A-AA-TT	2563
A2.CD.97.97CDKFE4	C-A-TT-G-G-A-AT-A-GCT-T-A-A-TT	2401
A2.CD.97.97CDKS10	C-A-TT-G-G-A-AT-A-GCT-T-A-A-TT	2001
A2.CD.97.97CDKTB48	C-AG-G-G-C-C-AT-T-T-A-GGCT-T-A-A-TT	2534
A2.CY.94.94CY017_41	C-A-G-A-AT-A-C-GT-T-A-A-TT	2553
A.SN.01.DDI579	C-A-A-A-G-T-T-A-GCT-A-AA-TT	2394
A.SN.01.DDJ369	C-A-A-A-G-T-T-A-GCT-A-AA-TT	2397
A.SN.96.DDJ360	T-T-A-A-A-T-T-A-GCT-A-AA-TT	2394
A.ZA.04.04ZASK162B1	C-C-A-C-C-A-T-T-A-G-G-A-T-T-A-TT	2637
B.AR.00.ARMS008	---C-G-G-G-G-C-TT	2401
B.AU.96.MBCD36	---C-G-G-G-G-C-TT	2551
B.CO.01.PCM074	A-A-A-R-G-G-TT	2413
B.GA.88.OY1	A-A-A-R-G-G-TT	2739
B.NL.99.671	M-Y-R-R-A-A-TT	2760
B.RU.04.04RU129005	---C-G-G-G-G-C-TT	2700
B.TH.90.BK132	---C-G-G-G-G-C-TT	2547
B.US.90.WEAU160	---C-G-G-G-G-C-TT	3195
B.US.98.1058_11	---C-G-G-G-G-C-TT	2386
C.AR.01.ARG4006	C-A-A-T-T-A-G-G-TT	2380
C.BR.04.04BR013	C-A-A-T-T-A-G-G-TT	2660
C.BR.92.BR025_d	C-A-A-T-T-A-G-G-TT	2534
C.BW.00.00BW07621	C-A-A-T-T-A-G-G-TT	2548
C.ET.86.ETH2220	CC-CC-C-A-T-T-C-C-TT	2589
C.IN.95.95IN21068	C-A-A-T-T-A-G-G-TT	2547
C.IN.99.01INS65_10	C-A-A-T-T-A-G-G-TT	2577
C.KE.00.KER2010	C-A-G-A-T-T-A-G-G-TT	2377
C.TZ.01.BD9_11	C-A-G-A-T-T-A-G-G-TT	2404
C.UY.01.TRA3011	C-A-G-A-T-T-A-G-G-TT	2368
C.ZA.04.SK164B1	C-A-A-C-C-TT	2606
C.ZA.05.05ZASK245B1	C-A-A-C-C-TT	2625
C.ZM.02.02ZM115	C-A-C-A-G-TT	3190
C.ZM.96.96ZM651	C-A-C-C-TT	2525
D.CD.83.ELI	A-G-A-T-T-A-G-G-TT	2742
D.CD.83.NDK	A-G-A-T-T-A-G-G-TT	2731
D.CM.01.01CM_4412HAL	AC-A-TT-C-TT	2410
D.KE.01.NKU3006	AG-G-A-T-T-A-G-G-TT	2401
D.TD.99.MN012	AC-T-T-A-G-TT	2420
D.TZ.01.A280	T-Z.01.A280	2397
D.UG.94.94UG114	A-GA-T-T-A-GGG-C-TT	2551
D.UG.99.99UGD23550	A-A-T-T-A-GGG-C-TT	2401
D.UG.99.99UGK0958	A-A-T-T-A-GGG-C-TT	2395
D.ZA.86.R482	T-T-A-G-G-TT	2460
F1.BE.93.VI850	TGA-C-C-G-G-TT	2533
F1.BR.89.B2126	C-A-T-T-T-A-G-G-TT	2546
F1.BR.93.93BR020_1	C-A-G-C-C-TT	2524
F1.FI.93.FIN9363	C-AG-T-T-A-G-G-TT	2525
F1.FR.96.MPA411	C-A-G-C-C-TT	2398
F2.CM.02.02CM_0016BBY	C-AG-G-G-C-TT	2386
F2.CM.95.MP255	C-A-G-G-G-TT	2392
F2.CM.95.MP257	--G-G-G-G-G-TT	2404
F2.CM.97.CM53657	T-A-T-T-A-G-G-TT	2386
G.BE.96.DRCL	C-A-G-C-C-TT	3153
G.CM.01.01CM_4049HAN	C-A-A-G-C-C-TT	2398
G.ES.99.X138	T-A-A-G-C-TT	2637
G.KE.93.HH8793_12_1	T-A-A-G-C-TT	2597
G.NG.92.92NG083	C-A-T-T-A-G-G-TT	2593
G.SE.93.SE6165	C-A-T-T-A-G-G-TT	2585
H.BE.93.VI991	T-AG-GA-T-T-C-TT	2520
H.BE.93.VI997	T-A-A-T-T-C-TT	2543
H.ICF.90.056	T-T-A-G-TT	2510
J.SE.93.SET7887	--AG-C-A-C-G-G-TT	2511
J.SE.94.SET7022	--AG-C-A-C-G-G-TT	2511
K.CD.97.EQTB11C	GGA-T-T-G-TT	2392
K.CM.96.MP535	T-A-A-G-A-C-TT	2392

B. FR. 83. HXB2
01 AE. CF. 90. 90CF402
01 AE. CN. 05. FJ051
01 AE. HK. x. HK001
01 AE. JP. 93. 93JP. NH1
01 AE. TH. 01. OUR4141
01 AE. TH. 02. OUR7691
01 AE. TH. 90. CM240
02 AG. CM. 02. 02CM_16691E
02 AG. EC. x. EC041
02 AG. FR. 91. DJ264
02 AG. GH. 03. GHNJ196
02 AG. NG. x. IENG
02 AG. SN. 98. MP1211
02 AG. UZ. 02. 02UZ693
03 AB. RU. 97. KAL153_2
04 CPX. CV. 94. CV032
05 DF. BE. x. VIL1310
06 CPX. AU. 96. BFP90
07 BC. CN. 97. CNE54
08 BC. CN. 97. 97CNGX_6F
09 CPX. GH. 96. 96GH2911
10 CD. TZ. 96. 96TZ_BF061
11 CPX. GR. x. GR17
12 BF. AR. 99. ARMA159
13 CPX. CM. 96. 1849
14 BG. ES. 99. X397
15 01B. TH. 99. 99TH_MU2079
16 A2D. KR. 97. 97KR004
18 CPX. CU. 99. CU76
19 CPX. CU. 99. CU7
20 BG. CU. 03. CB134
21 A2D. KE. 91. KMH1254
23 BG. CU. 03. CB118
24 BG. CU. 03. CB378
25 CPX. CM. x. 101BA
28 BF. BR. 99. BREPM12609
29 BF. BR. 02. BREPM119
31 BC. BR. 02. 110PA
33 01B. MY. 05. 05MYKL007_1
A1C. TZ. 02. C03710
A1CDGKU.ZA. 99. CM4
A1LDHK.NO. 97. 97NOGLI3
A1LGHU.GA. x. VI354
A2D. KE. 99. KER2003
AF2. CM. 02. 02CM_3163MN
AGU. CM. 01. 01CM_0989MO
AHJU. CM. 01. 01CM_1296NG
BC. MN. 96. YNPL9607
BC. MM. 99. mIU103
BF1. BR. 02. 02BR006
0708. CN. 00. HH069
U. CD. 83. 83CD003
U. CD. 90. 90CD121E12
U. GR. 99. GR303
U. NL. x. U. NL. 95. H10986_D1
N. CM. 02. DJ00131
N. CM. 04. 04CM_1131_03
N. CM. 95. YBF30
N. CM. 97. YBF106
O. BE. 87. ANI770
O. CM. 91. WVP5180
O. CM. 96. 96CMWAB637
O. SN. 99. 99SEMP1300
CPZ. CD. 90. ANI
CPZ. CM. 01. SIVcpzCAM13
CPZ. CM. 05. SIVcpzEK505
CPZ. CM. 05. SIVcpzLB7
CPZ. CM. 05. SIVcpzMB66
CPZ. CM. 05. SIVcpzMT145
CPZ. GA. 88. GHAN1
CPZ. TZ. 01. TAN1
CPZ. US. 85. CPZUS
Pol. p51 RT

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	ACACGACAAAAACATCAGAAAGAACCTCCATTCCCTTTGGATGGGTTATGAACCTCCATCTGTGATTAATGGACAGTACACGCTTAGCTGCCAGAAAAACACAGCTGGACTGTCATGACATACAGAAG	3326
01 AE.CF.90.90CF402	-----G-----G-----C-----C-----G-----C-----G-----C-----G-----T-----T-----	3362
01 AE.CN.05.FJ051	-----G-----G-----C-----C-----A-----AA-----T-----T-----	3336
01 AE.HK.x.HK001	-----G-----G-----C-----C-----A-----AA-----T-----T-----	2688
01 AE.JP.93.93JP.NH1	-----G-----G-----C-----C-----A-----AA-----T-----T-----	3328
01 AE.TH.01.OUR414T	-----G-----G-----C-----C-----A-----AA-----T-----T-----	2522
01 AE.TH.02.OUR769T	-----G-----G-----C-----C-----A-----AA-----T-----T-----	2525
01 AE.TH.90.CM240	-----G-----G-----C-----C-----A-----AA-----T-----T-----	2900
02 AG.CM.02.02CM_16691E	-----T-----T-----C-----C-----A-----CA-----A-----C-----T-----T-----	2516
02 AG.EC.x.EC041	-----T-----T-----C-----C-----C-----CA-----T-----T-----	2422
02 AG.FR.91.DJ264	-----T-----T-----C-----C-----C-----CA-----T-----T-----	2675
02 AG.GH.03.GHNJ196	-----T-----T-----C-----C-----C-----CA-----T-----T-----	3355
02 AG.NG.x.IBNG	-----G-----G-----C-----C-----C-----CA-----T-----T-----	2851
02 AG.SN.98.MP1211	-----G-----G-----C-----C-----C-----CA-----T-----T-----	2523
02 AG.UZ.02.02UZ693	-----G-----G-----C-----C-----C-----CA-----T-----T-----	2513
03 AB.RU.97.KAL153.2	-----C-----T-----G-----G-----C-----G-----T-----G-----T-----C-----T-----C-----	2692
04 CPX.CV.94.CY032	-----G-----G-----G-----G-----G-----G-----C-----G-----T-----C-----T-----C-----	2552
05 DF.BE.x.VI1310	-----T-----T-----C-----C-----T-----T-----C-----CAAT-----C-----G-----T-----T-----	2708
06 CPX.AU.96.BFP90	-----T-----T-----C-----C-----T-----T-----C-----CAAT-----C-----G-----T-----T-----	3354
07 BC.CN.97.CNE4	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2688
08 BC.CN.97.97CNGX.6F	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2506
09 CPX.GH.96.96GHZ911	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2528
10 CD.TZ.96.96TZ_BF061	-----T-----T-----G-----G-----T-----T-----C-----CA-----A-----GA-----T-----T-----	2705
11 CPX.GR.x.GR17	-----T-----T-----C-----C-----A-----G-----A-----G-----A-----C-----G-----T-----T-----	2628
12 BF.AR.99.ARMAL159	-----T-----T-----G-----G-----C-----C-----G-----G-----T-----T-----	3331
13 CPX.CM.96.1849	-----T-----T-----G-----G-----C-----C-----G-----G-----T-----T-----	2767
14 BG.ES.99.X397	-----T-----T-----G-----G-----C-----C-----G-----G-----T-----T-----	2725
15 01B.TH.99.99TH.MU2079	-----G-----G-----T-----T-----C-----C-----A-----AA-----T-----T-----	2689
16 A2D.KR.97.97KR004	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2631
18 CPX.CU.99.CU76	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2552
19 CPX.CU.99.CU7	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2764
20 BG.CU.03.CB134	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2531
21 A2D.KE.91.KNH1254	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2782
23 BG.CU.03.CB118	-----T-----T-----C-----C-----T-----T-----C-----CA-----T-----T-----	2759
24 BG.CU.03.CB378	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2534
25 CPX.CM.x.101BA	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2692
28 BF.BR.99.BREPM12609	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2500
29 BF.BR.02.BREPM119	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2631
31 BC.BR.02.110PA	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2760
33 01B.WY.05.05MYKL007_1	-----G-----G-----C-----C-----T-----T-----C-----CA-----T-----T-----	2705
A1C.TZ.02.C03710	-----T-----T-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2513
A1CDGKU.ZA.99.CM4	-----T-----T-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	3328
A1DHK.NO.97.97NOGLI3	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2821
A1GHU.GA.x.VI354	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	3336
A2D.KE.99.KER2003	-----T-----T-----A-----A-----T-----T-----G-----G-----T-----T-----	2686
A2D.KE.99.KER2003	-----T-----T-----A-----A-----T-----T-----G-----G-----T-----T-----	2531
AF2.CM.02.02CM.3163MN	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2519
AGU.CM.01.01CM_0989MO	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2528
AHJU.CM.01.01CM.1296NG	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2510
BC.CN.96.YNPL9607	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2704
BC.MM.99.mINDU103	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2510
BE1.BR.02.02BR006	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	3228
0708.CN.00.HH069	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	2510
U.CD.83.83CD003	-----T-----T-----C-----C-----T-----T-----G-----G-----T-----T-----	2525
U.CD.90.90CD121E12	-----T-----T-----C-----C-----T-----T-----G-----G-----T-----T-----	2600
U.GR.99.GR303	-----G-----G-----C-----C-----T-----T-----G-----G-----T-----T-----	3211
U.NL.x.U.NL.95.H10986_D1	-----T-----T-----C-----C-----T-----T-----G-----G-----T-----T-----	2832
N.CM.02.DJ00131	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2830
N.CM.04.04CM_1131_03	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2920
N.CM.95.YBF30	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2918
N.CM.97.YBF106	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	3381
O.BE.87.ANT70	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	3356
O.CM.91.WPDE180	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2810
O.CM.96.96CMAB637	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	3380
O.SN.99.SEMPL3000	-----T-----T-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2765
CPZ.CD.90.ANT	-----T-----T-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2906
CPZ.CM.01.SIVcpzCAM13	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2898
CPZ.CM.05.SIVcpzE505	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2881
CPZ.CM.05.SIVcpzL87	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2872
CPZ.CM.05.SIVcpzMB66	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2868
CPZ.CM.05.SIVcpzMT145	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	3387
CPZ.GA.88.GAB1	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	2970
CPZ.TZ.01.TAN1	-----C-----T-----A-----G-----G-----A-----A-----G-----G-----C-----C-----A-----A-----T-----T-----	3386
CPZ.US.85.CPZUS	-----P-----D-----K-----K-----H-----O-----K-----H-----O-----K-----H-----O-----K-----H-----O-----K-----H-----O-----K-----	

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2
 01 AE.CF.90.90CF402
 01 AE.CN.05.FJ051
 01 AE.HK.x.HK001
 01 AE.JP.93.93JP.NH1
 01 AE.TH.01.OUR414T
 01 AE.TH.02.OUR769T
 01 AE.TH.90.CM240
 02 AG.CM.02.02CM16691E
 02 AG.EC.x.EC041
 02 AG.FR.91.DJ264
 02 AG.GH.03.GHNJ196
 02 AG.NG.x.IBNG
 02 AG.SN.98.MP1211
 02 AG.UZ.02.02UZ693
 03 AB.RU.97.KAL153_2
 04 CPX.CV.94.CV032
 05 DF.BE.x.VI1310
 06 CPX.AU.96.BFP90
 07 BC.CN.97.CNE4
 08 BC.CN.97.97CNGX_6F
 09 CPX.GH.96.96GHZ911
 10 CD.TZ.96.96TFZ_BF061
 11 CPX.GR.x.GR17
 12 BF.AR.99.ARMAL159
 13 CPX.CM.96.1849
 14 BG.ES.99.X397
 15 01B.TH.99.99TH.MU2079
 16 AZD.KR.97.97KR004
 18 CPX.CU.99.CU76
 19 CPX.CU.99.CU7
 20 BG.CU.03.CB134
 21 AZD.KE.91.KNHI254
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 CPX.CM.x.101BA
 28 BF.BR.99.BREPM12609
 29 BF.BR.02.BREPM119
 31 BC.BR.02.110PA
 33 01B.MV.05.05MYKL007_1
 A1C.TZ.02.CO3710
 A1CDGKU.ZA.99.CM4
 A1DHK.NO.97.97NOGLI3
 A1GHU.GA.x.VI354
 A2D.KE.99.KER2003
 AF2.CM.02.02CM.3163MN
 AGU.CM.01.01CM.0989MO
 AHJU.CM.01.01CM.1296NG
 BC.CN.96.YNPL9607
 BC.MM.99.mINDU103
 BF1.BR.02.02BR006
 0708.CN.00.HH069
 U.CD.83.83CD003
 U.CD.90.90CD121E12
 U.GR.99.GR303
 U.NL.x.U.NL.95.H10986_D1
 N.CM.02.DJ00131
 N.CM.04.04CM.1131_03
 N.CM.95.YBF30
 N.CM.97.YBF106
 O.BE.87.MVPE180
 O.CM.91.MVPE180
 O.CM.96.96CMWAB637
 O.SN.99.SEMP1300
 CPZ.CD.90.ANT
 CPZ.CM.01.SIVCPZCAM13
 CPZ.CM.05.SIVCPZEK505
 CPZ.CM.05.SIVCPZLB7
 CPZ.CM.05.SIVCPZMB66
 CPZ.CM.05.SIVCPZMT145
 CPZ.GA.88.GAB1
 CPZ.TZ.01.TAN1
 CPZ.US.85.CPZUS
 Pol p51 RT

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

B. FR. 83. HXB2	TAAAAATCTGAAAACAGGAAATATGCCAAGAAATGAGGGTGTCCACACACTAATGATGTAAAAACAATTTAACAGAGGCGAGTCCAAAAAATAACACACAGAAAGCATAGTAAATATGGGAAAG...ACTCCTAAA	3713
A1. KE.94.Q23.17	...AA--TC--T--	3711
A1. RU.03.03RU20_06_13	...A--A--G--TC--T--	3190
A1. RW.93.93RW037A_1	...G--A--G--TC--T--	3196
A1. SE.94.SE7253	...G--A--G--TC--T--	2917
A1. TZ.01.A173	...G--A--G--TC--T--	2912
A1. UA.00.98UA0116	...G--A--G--TC--T--	3712
A1. UG.92.92UG037	...G--A--G--TC--T--	3080
A1. UG.98.98UGS7136	...G--A--G--TC--T--	2918
A2. CD.97.97CDKPE4	...G--A--G--TC--T--	2518
A2. CD.97.97CDKS10	...G--A--G--TC--T--	0
A2. CD.97.97CDKITB48	...G--A--G--TC--T--	3051
A2. CY.94.94CY017_41	...G--A--G--TC--T--	3070
A. SN.01.DDI579	...G--A--G--TC--T--	2911
A. SN.01.DDJ369	...G--A--G--TC--T--	2914
A. SN.96.DDJ360	...G--A--G--TC--T--	2911
A. ZA.04.04ZASK162B1	...G--A--G--TC--T--	3154
B. AR.00.ARMS008	...G--A--G--TC--T--	2918
B. AU.96.MBCD36	...G--A--G--TC--T--	3068
B. CO.01.PCM074	...G--A--G--TC--T--	2930
B. GA.88.OYI	...G--A--G--TC--T--	3256
B. NL.99.671	...G--A--G--TC--T--	3277
B. RU.04.04RU129005	...G--A--G--TC--T--	3217
B. TH.90.BK132	...G--A--G--TC--T--	3064
B. US.90.WEAU160	...G--A--G--TC--T--	3712
B. US.98.1058_11	...G--A--G--TC--T--	2903
C. AR.01.ARG4006	...G--A--G--TC--T--	2897
C. BR.04.04BR013	...G--A--G--TC--T--	3177
C. BR.92.BR025_d	...G--A--G--TC--T--	3051
C. BW.00.00BW07621	...G--A--G--TC--T--	3066
C. ET.86.ETH2220	...G--A--G--TC--T--	3105
C. IN.95.95IN21068	...G--A--G--TC--T--	3064
C. IN.99.01INS65_10	...G--A--G--TC--T--	3094
C. KE.00.KER2010	...G--A--G--TC--T--	2894
C. TZ.01.BD9_11	...G--A--G--TC--T--	2921
C. UY.01.TRA3011	...G--A--G--TC--T--	2885
C. ZA.04.SK164B1	...G--A--G--TC--T--	3123
C. ZA.05.05ZASK245B1	...G--A--G--TC--T--	3142
C. ZM.02.02ZM115	...G--A--G--TC--T--	3707
C. ZM.96.96ZM651	...G--A--G--TC--T--	3042
D. CD.83.ELI	...G--A--G--TC--T--	3259
D. CD.83.NDK	...G--A--G--TC--T--	3248
D. CM.01.01CM_4412HAL	...G--A--G--TC--T--	2927
D. KE.01.NK03006	...G--A--G--TC--T--	2918
D. TD.99.MN012	...G--A--G--TC--T--	2937
D. TZ.01.A280	...G--A--G--TC--T--	2914
D. UG.94.94UG114	...G--A--G--TC--T--	3068
D. UG.99.99UGD23550	...G--A--G--TC--T--	2918
D. UG.99.99UGK09958	...G--A--G--TC--T--	2912
D. ZA.86.R482	...G--A--G--TC--T--	2977
F1. BE.93.VI850	...G--A--G--TC--T--	3053
F1. BR.89.BZ126	...G--A--G--TC--T--	3063
F1. BR.93.93BR020_1	...G--A--G--TC--T--	3041
F1. FI.93.FIN9363_1	...G--A--G--TC--T--	3042
F1. FR.96.MP411	...G--A--G--TC--T--	2915
F2. CM.02.02CM_0016BBY	...G--A--G--TC--T--	2903
F2. CM.95.MP255	...G--A--G--TC--T--	2909
F2. CM.95.MP257	...G--A--G--TC--T--	2921
F2. CM.97.CM53657	...G--A--G--TC--T--	2903
G. BE.96.DRCBL	...G--A--G--TC--T--	3670
G. CM.01.01CM_4049HAN	...G--A--G--TC--T--	2915
G. ES.99.X138	...G--A--G--TC--T--	3154
G. KE.93.HH8793_12_1	...G--A--G--TC--T--	3113
G. NG.92.92NG083	...G--A--G--TC--T--	3082
G. SE.93.SE6165	...G--A--G--TC--T--	3110
H. BE.93.VI991	...G--A--G--TC--T--	3102
H. BE.93.VI997	...G--A--G--TC--T--	3037
H. CF.90.056	...G--A--G--TC--T--	3060
J. SE.93.SE7887	...G--A--G--TC--T--	3027
J. SE.94.SE7022	...G--A--G--TC--T--	3028
K. CD.97.EQTB11C	...G--A--G--TC--T--	2909
K. CM.96.MP535	...G--A--G--TC--T--	2909

HIV-1/SIVcpz
complete genomes

B.FR.83.HXB2	TTTAAACGCCCATCAAAAGAAACATGGGAACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTTCCTCAGTGGAGTTTGTAAATACCCCTCCCTTAGTGAATAATTATGGTACACATTAGAGAAG	3843
A1.KE.94.Q23_17	---G--A--A--A--C--TG-C--G-T--T-A--A--C--TC-A--G--	3301
A1.RU.03.03RU20_06_13	---G--A--A--G--TG--C--G-T--T-A--A--C--TC-A--C--G--	3320
A1.RW.93.93RW037A_1	---G--A--A--G--TG--C--G-T--T-A--A--C--TC-A--C--G--	3326
A1.SE.94.SE7253	---A--A--A--TG-C-C--G-T--A--A--C--TC-A--C--G--	3047
A1.TZ.01.A173	---A--A--A--TG-C-C--G-T--A--A--C--TC-A--C--G--	3042
A1.UA.00.98UA0116	---GG--A--A--G--TG-C--G-T--A--A--C--TC-A--C--G--	3842
A1.UG.92.92UG037	---G--A--A--TG-C--G-T--A--A--C--TC-A--C--G--	3210
A1.UG.98.98UG57136	---G--A--A--TG-C--G-T--A--A--C--TC-A--C--G--	3048
A2.CD.97.97CDKFE4	---G-T-A--A--G--G--TG-C--G-T--A--A--C--TC-A--C--G--	2648
A2.CD.97.97CDKS10	0
A2.CD.97.97CDKTB48	---G--A--A--G--G--TG--C--G--G--T--A--A--C--TC-A--C--G--	3181
A2.CY.94.94CY017_41	---T--A--A--G--G--TG--C--G--G--T--A--A--C--TC-A--C--G--	3200
A.SN.01.DDI579	---G--A--A--TG--C--G-T--AT-C--A--A--C--TC-A--C--G--	3041
A.SN.01.DDJ369	---A--A--A--C--G--T--T--A--A--C--TC-A--C--G--	3044
A.SN.96.DDJ360	---A--A--A--C--G--T--T--A--A--C--TC-A--C--G--	3041
A.ZA.04.04ZASK162B1	---T-A--A--A--TG--G--G--C-T--T--A--A--C--TC-G-A--C--	3284
B.AR.00.ARMS008	---T-A--G--G--TG--A--A--A--C--C--	3048
B.AU.96.MBCD36	---A--A--A--G--A--A--C--C--	3198
B.CO.01.PCM074	---A--A--T--A--C--A--A--C--A--	3059
B.GA.88.OYI	---A--A--G--G--A--A--A--	3386
B.NL.99.671	---T--A--A--C--C--C--C--C--A--A--	3407
B.RU.04.04RU129005	---T--A--A--A--A--A--C--R--R--	3347
B.TH.90.BK132	---C--A--A--A--C--C--A--A--	3194
B.US.90.WEAU160	---A--A--A--C--C--C--T--	3842
B.US.98.1058_11	---G--A--T--T--A--C--	3033
C.AR.01.ARG4006	---G-T-A--C--G-A--GT--C--C-A--G--C-G--	3027
C.BR.04.04BR013	---G-A--C--G-A--G--C--C-A--G--C-G-A--	3307
C.BR.92.BR025_d	---G-T-A--C--G-A--G--C--G--A--C-G--	3181
C.BW.00.00BW07621	---C--G--A--C--A--G--C--C--C--A--C-G-A--	3196
C.ET.86.ETH2220	---G-T-A--C--G-A--G--C--C--C--A--C--	3235
C.IN.95.95IN21068	---G-T-A--C--A--G--C--A--A--C--G-A--G--	3194
C.IN.99.01IN565_10	---G-T-A--C--A--G--C--A--A--C--C-G--	3224
C.KE.00.KER2010	---G-T--A--C--A--G--C--C--A--C--C-G--	3024
C.TZ.01.BD9_11	---G--A--C--A--A--TG--C--C--A--C--C-G--	3051
C.UY.01.TRA3011	---G-T-A--C--G-A--G--C--C--A--C--C-G--	3015
C.ZA.04.SK164B1	---G--A--C--A--G--C--C--A--C--T--C--	3253
C.ZA.05.05ZASK245B1	---G--A--C--A--G--T--T--A--A--C--C-G--	3272
C.ZM.02.02ZM115	---G--A--C--A--G--C--C--A--C--G-A--	3837
C.ZM.96.96ZM651	---G--A--C--A--G--C--C--T--A--C-G--	3172
D.CD.83.ELI	---G--A--G--G--T--T--A--A--C--T--A--A--G--	3389
D.CD.83.NDK	---G--A--T--T--A--A--C--T--A--A--G--	3378
D.CM.01.01CM_4412HAL	---G--A--A--CG--TG--C--T--A--A--G--	3057
D.KE.01.NK03006	---G--A--A--C--G--C--T--C--G--A--G--	3048
D.TD.99.MN012	---G--A--A--TG--C--T--A--A--G--	3067
D.TZ.01.A280	---G--A--A--TG--C--T--A--A--G--	3044
D.UG.94.94UG114	---G--A--A--G--C--T--T--A--C--C--T--	3198
D.UG.99.99UGD23550	---G--A--A--G--C--T--T--A--C--C--T--	3048
D.UG.99.99UGK0958	---G--A--A--G--C--T--T--A--C--C--T--	3042
D.ZA.86.R482	---G--A--A--T--T--A--A--A--C--T--A--A--GG--	3107
F1.BE.93.VI850	---A--TG--A--G--T--T--A--A--C--C--TC--C--A-C--	3183
F1.BR.89.B2126	---A--TG--A--G--T--T--A--A--C--C--TC--C--A-C--	3193
F1.BR.93.93BR020_1	---G--A--T--T--A--G--T--C--C--TC--A--C--T--C--A-C--	3171
F1.FI.93.FIN9363_1	---A--A--T--T--A--G--T--C--C--TC--A--C--T--A--C--	3172
F1.FR.96.MP411	---GG--A--A--G--G--T--A--A--C--C--TC--A--C--T--A--C--	3045
F2.CM.02.02CM_0016BBY	---G--A--A--A--A--A--TC--A--A--A--A--C--	3033
F2.CM.95.MP255	---G--A--A--T--T--A--A--TC--A--A--A--A--C--	3039
F2.CM.95.MP257	---G--A--A--T--T--A--A--TC--A--A--A--A--C--	3051
F2.CM.97.CM53657	---GG--A--A--A--G--G--T--A--A--TC--A--A--A--C--	3033
G.BE.96.DRCBL	---T--A--T--A--A--GTG--C--C--C--T--T--C--A--C--	3800
G.CM.01.01CM_4049HAN	---A--T--G--A--A--GT--C--C--C--T--T--C--A--C--	3045
G.ES.99.X138	---A--T--G--A--A--GT--C--C--C--T--T--C--A--C--	3284
G.KE.93.HH8793_12_1	---A--T--G--A--A--GT--C--C--C--T--T--G--A--C--	3243
G.NG.92.92NG083	---A--T--G--A--A--GT--C--C--C--T--T--A--A--C--	3212
G.SE.93.SE6165	---A--A--G--A--T--C--C--C--T--T--G--A--C--	3240
H.BE.93.VI991	---G-T-A--T--A--G--C--C--ATC--C--T--C--	3232
H.BE.93.VI997	---T--A--T--A--A--C--C--ATC--C--T--C--AGC--	3167
H.CF.90.056	---G--A--T--A--A--A--ATC--C--T--T--A--C--	3190
J.SE.93.SE7887	---G--A--GA--G--C--C--C--TC--A--A--A--G--	3158
J.SE.94.SE7022	---G--A--G--G--C--C--C--TC--A--A--A--G--	3158
K.CD.97.EQTB11C	---G-T-A--A--A--GG--A--A--C--T--C--A--C--	3039
K.CM.96.MP535	---G--A--A--A--GG--A--A--C--T--C--A--C--	3039

HIV-1/SIVcpz complete genomes

(RT is heterodimer of p51 and p66)
 p51 end, p66 RT continue // p51 p15 RNase H start
 AACCCNTAGTAGACAGAAACCTTCTAATGATAGTAGGGACCTTAAAGGAAACGAGATATGTTACTAATAGGAAACAAAGATTTGTCACCCCTACTACACAAATCA

B. FR. 83. HXB2
 A1. KE.94.023_17
 A1. RU.03.03RU20_06_13
 A1. RW.93.93RW037A
 A1. SE.94. SE7253
 A1. TZ.01. A173
 A1. UA.00.98UA0116
 A1. UG.92.92UG037
 A1. UG.98.98UG57136
 A2. CD.97.97CDKFEA
 A2. CD.97.97CDKSL0
 A2. CD.97.97CDKTB48
 A2. CY.94.94CY0117_41
 A. SN.01. DDH579
 A. SN.01. DDJ369
 A. SN.96. DDJ360
 A. ZA.04.04ZASK162B1

B. AR.00. ARMS008
 B. AU.96. MBCD36
 B. CO.01. PCMO74
 B. GA.88. OY1
 B. NL.99. 671
 B. RU.04.04RU129005
 B. TH.90. RK132
 B. US.90. WEAU160
 B. US.98.1058_11

C. AR.01. ARG4006
 C. BR.04.04BR013
 C. BR.92. BR025_1
 C. BW.00.00BW07621
 C. ET.86. ETH2220
 C. IN.95.95IN21068
 C. IN.99.01IN565_10
 C. KE.00. KER2010
 C. TZ.01. BD9_11
 C. UY.01. TRA3011
 C. ZA.04. SK164B1
 C. ZA.05.05ZASK245B1
 C. ZM.02.02ZM115
 C. ZM.96.96ZM651

D. CD.83. ELI
 D. CD.83. NDK
 D. CM.01.01CM_4412HAL
 D. KE.01. NKU3006
 D. TD.99. MN012
 D. TZ.01. A280
 D. UG.94.94UG114
 D. UG.99.99UGD2550
 D. UG.99.99UGK03958
 D. ZA.86. K482

F1. BE.93. VI850
 F1. BR.89. B2126
 F1. BR.93.93BR020_1
 F1. FI.93. FIN9363_1
 F1. FR.96. MP411
 F2. CM.02.02CM_0016BBY
 F2. CM.95. MP255
 F2. CM.95. MP257
 F2. CM.97. CM53657

G. BE.96. DRCEL
 G. CM.01.01CM_4049HAN
 G. ES.99. X138
 G. KE.93. HH8793_12_1
 G. NG.92.92NG083
 G. SE.93. SE61165

H. BE.93. VI991
 H. BE.93. VI997
 H. CF.90.056

J. SE.93. SE7887
 J. SE.94. SE7022

K. CD.97. EOTB11C
 K. CM.96. MP535

3973
3431
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3169
3181
3163
3930
3175
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3287
3288
3169
3169

(RT is heterodimer of p51 and p66)
 p51 end_p66 RT continue // p1 p15 RNase H start
 AACCCNATAGACGAGAACCCTTCTATGATAGTGCCGACCTAAACGGAGACATAATAGGAAGACAAAAGATTGTCCACCTACTACACACAATAATCA 3973
 C-T-A-G G-T GCA G-C-G-C G-A-TT G- 4009
 C-T G-T GC A-G-G G-G-G-T G- 3983
 C-G G-GT A-GC G-C-G-C G-A-TT G- 3985
 C-G G-T A-GC G-C-G-C G-G-A-TT G- 3975
 C-AE.TH.01.OUR4141 G-T A-GC G-C-G-C G-A-TT G- 3169
 C-AE.TH.02.OUR7691 G-T A-GC G-C-G-C G-A-TT G- 3172
 C-AE.TH.90.CM240 G-T A-GC G-C-G-C G-A-TT G- 3547
 C-AG.CM.02.02CM_16691E G-T A-GC G-C-G-C G-A-TT G- 3544
 C-AG.EC.x.EC041 G-T A-GC G-C-G-C G-A-TT G- 3163
 C-AG.FR.91.DJ264 G-T A-GC G-C-G-C G-A-TT G- 3069
 C-AG.GH.03.GHNJ196 G-T A-GC G-C-G-C G-A-TT G- 3322
 C-AG.NG.x.IBNG G-T A-GC G-C-G-C G-A-TT G- 4002
 C-AG.SN.98.MP1211 G-T A-GC G-C-G-C G-A-TT G- 3498
 C-AB.RU.97.KAL153_2 G-T A-GC G-C-G-C G-A-TT G- 3170
 C-CPX.CV.94.CV032 G-T A-GC G-C-G-C G-A-TT G- 3160
 C-DP.BE.x.VI1310 G-T A-GC G-C-G-C G-A-TT G- 3199
 C-CPX.AU.96.BEP90 G-T A-GC G-C-G-C G-A-TT G- 3339
 C-BC.CN.97.CNS4 G-T A-GC G-C-G-C G-A-TT G- 3355
 C-CPX.CN.97.CNS4 G-T A-GC G-C-G-C G-A-TT G- 4001
 C-CPX.CN.97.97CNGX_6F G-T A-GC G-C-G-C G-A-TT G- 3335
 C-CPX.GH.96.96GHD2911 G-T A-GC G-C-G-C G-A-TT G- 3153
 C-CD.TZ.96.96TZ_BF061 G-T A-GC G-C-G-C G-A-TT G- 3175
 C-GR.x.GR17 G-T A-GC G-C-G-C G-A-TT G- 3352
 C-AR.ARMAL159 G-T A-GC G-C-G-C G-A-TT G- 3275
 C-CPX.CM.96.1849 G-T A-GC G-C-G-C G-A-TT G- 3978
 C-BG.ES.99.X397 G-T A-GC G-C-G-C G-A-TT G- 3378
 C-AD.KR.97.97KR04 G-T A-GC G-C-G-C G-A-TT G- 3414
 C-CPX.CU.99.CU76 G-T A-GC G-C-G-C G-A-TT G- 3372
 C-CPX.CU.99.CU76 G-T A-GC G-C-G-C G-A-TT G- 3336
 C-BG.CU.03.CB134 G-T A-GC G-C-G-C G-A-TT G- 3278
 C-AD.KR.97.97KR04 G-T A-GC G-C-G-C G-A-TT G- 3199
 C-AD.KR.97.97KR04 G-T A-GC G-C-G-C G-A-TT G- 3411
 C-BG.CU.03.CB118 G-T A-GC G-C-G-C G-A-TT G- 3178
 C-BG.CU.03.CB378 G-T A-GC G-C-G-C G-A-TT G- 3429
 C-CPX.CM.x.101BA G-T A-GC G-C-G-C G-A-TT G- 3406
 C-BF.BR.99.BREPM12609 G-T A-GC G-C-G-C G-A-TT G- 3181
 C-BF.BR.02.BREPM119 G-T A-GC G-C-G-C G-A-TT G- 3339
 C-BC.BR.02.110PA G-T A-GC G-C-G-C G-A-TT G- 3147
 C-01B.WY.05.05MYKL007_1 G-T A-GC G-C-G-C G-A-TT G- 3407
 C-01B.WY.05.05MYKL007_1 G-T A-GC G-C-G-C G-A-TT G- 3352
 A1C.TZ.02.CO3710 T-T A-A A-G A-G A-TT G- 3160
 A1CDGKU.ZA.99.CM4 T-T A-A A-G A-G A-TT G- 3157
 A1DHK.NO.97.97NOGLI3 T-T A-A A-G A-G A-TT G- 3975
 A1GHU.GA.x.VI354 T-T A-A A-G A-G A-TT G- 3983
 A2D.KE.99.KER2003 T-T A-A A-G A-G A-TT G- 3333
 A2E.CM.02.02CM_3163MN T-T A-A A-G A-G A-TT G- 3178
 A3G.CM.01.01CM_0989MO T-T A-A A-G A-G A-TT G- 3166
 ARUTU.CM.01.01CM_1296NG T-T A-A A-G A-G A-TT G- 3175
 BC.CN.96.YNKL9667 T-T A-A A-G A-G A-TT G- 3157
 BC.MM.99.middul03 T-T A-A A-G A-G A-TT G- 3351
 BF1.BR.02.02BR006 T-T A-A A-G A-G A-TT G- 3875
 0708.CN.00.HH069 T-T A-A A-G A-G A-TT G- 3157
 U.CD.83.83CD003 T-T A-A A-G A-G A-TT G- 3468
 U.CD.90.90CD121E12 T-T A-A A-G A-G A-TT G- 3172
 U.GR.99.GR303 T-T A-A A-G A-G A-TT G- 3244
 U.NL.x.U.NL_95_H10986_D1 T-T A-A A-G A-G A-TT G- 3858
 N.CM.02.DJ00131 T-T A-A A-G A-G A-TT G- 3479
 N.CM.04.04CM_1131_03 T-T A-A A-G A-G A-TT G- 3477
 N.CM.95.YBF30 T-T A-A A-G A-G A-TT G- 3567
 N.CM.97.YBF106 T-T A-A A-G A-G A-TT G- 3565
 O.BE.87.ANI70 T-T A-A A-G A-G A-TT G- 4028
 O.CM.91.MVP5180 T-T A-A A-G A-G A-TT G- 4003
 O.CM.96.96CMAB637 T-T A-A A-G A-G A-TT G- 3457
 O.SN.99.SEMPL300 T-T A-A A-G A-G A-TT G- 4027
 CPZ.CD.90.ANT T-T A-A A-G A-G A-TT G- 3412
 CPZ.CM.01.SIVcpzCAM13 T-T A-A A-G A-G A-TT G- 3553
 CPZ.CM.05.SIVcpzEK505 T-T A-A A-G A-G A-TT G- 3545
 CPZ.CM.05.SIVcpzL187 T-T A-A A-G A-G A-TT G- 3528
 CPZ.CM.05.SIVcpzMB66 T-T A-A A-G A-G A-TT G- 3519
 CPZ.CM.05.SIVcpzWT145 T-T A-A A-G A-G A-TT G- 3515
 CPZ.GA.88.GAB1 T-T A-A A-G A-G A-TT G- 4034
 CPZ.TZ.01.ITANI T-T A-A A-G A-G A-TT G- 3617
 CPZ.US.85.CPZUS T-T A-A A-G A-G A-TT G- 4033
 E_P_I_V_G_A_E_T_F_V_D_G_A_A_N_R_E_T_K_L_G_K_A_G_Y_V_T_N_R_G_R_Q_K_V_V_T_L_T_D_T_N_Q
 Pol1 p51/p66 RT p51 end_p66 RT continue / Pol p15 RNase H start (RT is heterodimer of p51 and p66)



HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	GAAGCTGAGTTACAGCAATTTATCTAGCTTTTCGGAGTTCCGGATTAGGAAGTAAACACATAGTAAACAGACTCACAAATATGCTATTAGGAATCATTTCAAGCACAACAGATCAAAGTGAATCAGAGTTAGTTC	4103
A1.KE.94.Q23_17	A--AC--T--CC--T--C--A--C--A--C--G--CA--G--A--	3561
A1.RU.03.03RU020_06_13	A-R--A--T--CC--C--C--T--T--G--CAGG--A--	3580
A1.RW.93.93RW037A_13	A--A--T--T--CCT--A--C--C--G--T--CAG--A--	4096
A1.SE.94.SE7253	A--AC--T--C--A--G--C--CAGT--A--T	3307
A1.TZ.01.A173	AC--T--CC--G--C--AC--A--CC--CAG--C--A--T	3302
A1.UA.00.98UA0116	A--A--T--CC--C--T--G--T--G--G--CAGG--A--	4102
A1.UG.92.92UG037	A--A--T--CC--C--C--A--G--C--C--G--CAGG--A--	3470
A1.UG.98.98UG57136	A--AC--T--CC--C--C--G--T--C--G--CA--C--AA	3308
A2.CD.97.97CDKF34	A--A--T--C--T--G--A--A--A--G--AGG--A--	2908
A2.CD.97.97CDKFS10	A--A--T--C--T--G--A--A--A--G--AGG--A--	220
A2.CD.97.97CDKTB48	A--A--T--C--T--G--A--A--G--C--G--AGG--A--	3441
A2.CY.94.94CY017_41	A--A--T--C--T--G--A--G--G--T--G--AAG--A--	3460
A.SN.01.DDI579	A--A--T--C--C--C--A--C--G--C--G--C--A--	3301
A.SN.01.DDJ369	A--A--T--C--C--C--A--C--G--C--G--CAGG--A--	3304
A.SN.96.DDJ360	A--A--T--C--C--C--A--C--G--C--G--CA--G--A--	3301
A.ZA.04.04ZASK162B1	A--A--G--T--C--C--C--A--CC--CAGG--G--A--	3544
B.AR.00.ARMS008	A--A--C--C--C--A--C--T--A--G--A--G--A--	3308
B.AU.96.MBCD36	C--C--C--A--A--A--A--A--A--A--AA	3458
B.CO.01.PCM074	C--C--C--A--A--A--A--A--A--A--AA	3319
B.GA.88.OYI	A--A--C--C--C--A--A--A--A--A--A--	3646
B.NL.99.671	C--C--C--A--A--A--A--A--A--A--	3667
B.RU.04.04RU129005	A--A--C--C--R--G--C--K--A--G--A--	3607
B.TH.90.BK132	A--C--C--T--C--C--T--G--A--A--A--	3454
B.US.90.WEAU160	T--C--C--T--G--C--C--C--A--A--	4102
B.US.98.1058_11	C--C--AC--A--A--A--A--A--A--	3293
C.AR.01.ARG4006	C--G--A--A--A--A--A--G--A--G--A--	3287
C.BR.04.04BR013	A--G--A--A--A--C--G--T--A--G--A--	3567
C.BR.92.BR025_d	C--G--A--A--A--A--C--G--T--A--G--A--	3441
C.BW.00.00BW07621	A--A--C--C--G--A--A--CC--T--G--C--	3456
C.ET.86.ETH2220	A--A--G--CC--G--G--A--A--C--TG--A--G--A--	3495
C.IN.95.95IN21068	A--G--C--C--A--A--A--C--T--G--A--G--A--	3454
C.IN.99.01IN565_10	A--G--C--C--A--A--A--C--T--G--A--G--A--	3454
C.KE.00.KER2010	A--G--C--G--A--A--A--C--T--G--A--G--A--	3284
C.TZ.01.BD9_11	A--A--G--C--G--A--A--A--C--T--G--A--G--A--	3311
C.UY.01.TRA3011	C--G--G--A--A--C--A--G--T--T--A--G--A--	3275
C.ZA.04.SK164B1	A--A--G--C--G--A--A--C--CT--C--A--G--A--	3513
C.ZA.05.05ZASK245B1	A--A--G--C--G--A--A--C--C--G--A--G--A--	3532
C.ZM.02.02ZM115	CC--G--C--A--A--A--G--C--G--C--A--	4097
C.ZM.96.96ZM651	A--A--C--C--A--A--A--A--C--T--T--A--G--A--	3432
D.CD.83.ELI	A--A--C--C--C--A--A--T--T--T--A--G--A--	3649
D.CD.83.NDK	A--A--A--A--A--T--T--T--T--A--G--A--	3638
D.CM.01.01CM_4412HAL	A--A--A--A--G--T--T--C--T--A--G--A--AA	3317
D.KE.01.NK03006	A--A--C--A--C--A--GC--A--G--C--A--A--	3308
D.TD.99.MN012	A--A--C--G--A--A--T--C--C--G--T--G--A--A--	3327
D.TZ.01.A280	C--AA--C--C--A--A--G--C--G--A--G--A--	3304
D.UG.94.94UG114	A--A--C--A--A--C--A--A--G--A--G--G--	3458
D.UG.99.99UGD23550	A--A--C--A--A--C--A--A--G--A--G--G--	3308
D.UG.99.99UGK09958	A--A--G--C--A--A--T--T--T--T--C--G--	3302
D.ZA.86.R482	CA--G--AT--A--A--T--T--T--T--GA--G--C--	3367
F1.BE.93.VI850	T--G--T--A--C--G--G--G--A--G--A--AA	3443
F1.BR.89.B2126	C--GT--A--A--A--C--G--G--A--G--A--AA	3453
F1.BR.93.93BR020_1	C--GT--A--A--A--C--G--G--A--G--A--AA	3431
F1.FI.93.FIN9363_1	G--G--T--T--A--A--C--G--G--T--G--A--A--	3432
F1.FR.96.MP411	C--T--T--A--A--C--G--G--T--G--T--A--A--	3305
F2.CM.02.02CM_0016BBY	A--A--C--T--C--A--C--C--C--A--G--A--	3293
F2.CM.95.MP255	A--A--C--CT--C--A--C--C--G--T--A--G--	3299
F2.CM.95.MP257	A--A--C--GT--C--A--C--C--C--A--G--A--	3311
F2.CM.97.CM53657	A--A--C--T--C--A--C--C--C--A--G--A--	3293
G.BE.96.DRCLB	A--G--A--T--C--G--C--ACA--C--G--AGG--AA	4060
G.CM.01.01CM_4049HAN	A--G--A--T--C--C--C--CA--CC--G--AGG--AA--T	3305
G.ES.99.X138	A--AG--A--C--NA--A--A--C--A--C--AGG--A--	3544
G.KE.93.HH8793_12_1	A--A--A--T--C--G--G--A--A--C--A--C--AG--AC	3503
G.NG.92.92NG083	A--G--A--T--C--G--G--A--AA--CC--G--AGG--G--A--	3472
G.SE.93.SE6165	A--G--A--T--C--G--G--A--A--AA--C--C--AGG--G--A--	3500
H.BE.93.VI991	A--A--A--G--A--G--A--GCC--G--T--A--G--AC--T	3492
H.BE.93.VI997	A--A--A--G--A--A--A--G--G--T--A--G--G--T	3427
H.CF.90.056	A--A--A--G--A--A--A--G--T--G--C--A--G--T	3450
J.SE.93.SE7887	AC--C--C--T--A--G--A--GC--T--G--G--T--A--A--	3417
J.SE.94.SE7022	AC--C--C--T--A--A--A--GA--T--G--G--T--A--A--	3418
K.CD.97.EQTB11C	A--A--A--CC--T--A--A--A--C--G--A--A--T	3299
K.CM.96.MP535	AG--A--A--C--G--T--A--A--G--A--A--T	3299

B. FR. 83. HXB2	GAAGCTGAGTTACAGCAATTTATCTAGCTTTTCAGGATTCGGGATTTAGAAAGTAAACATAGTAAACAGACTCACAAATATGCTATTAGGAATCATTCAAGCAACACAGATCAAAGTGAATCAGAGTTAGTTC	4103
01 AE. CF. 90. 90CF402	A---A---T---G---CC---T---C---A---CC---A---CC---T---G---CAGG---G---TA	4139
01 AE. CN. 05. FJ051	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4113
01 AE. HK. x. HK001	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3465
01 AE. JP. 93. 93JP_NH1	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4105
01 AE. TH. 01. OUR4141	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3299
01 AE. TH. 02. OUR7691	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3302
01 AE. TH. 90. CM240	A---A---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3677
02 AG. CM. 02. 02CM_16691E	A---G---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3293
02 AG. EC. x. EC041	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3199
02 AG. FR. 91. DJ264	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3452
02 AG. GH. 03. GHNJ196	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4132
02 AG. NG. x. IEBG	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3628
02 AG. SN. 98. MP1211	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3300
02 AG. UZ. 02. 02UZ693	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3290
03 AB. RU. 97. KAL153_2	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3329
04 CPX. CV. 94. CV032	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3469
05 DF. BE. x. VIL1310	---AG---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3485
06 CPX. AU. 96. BFP90	---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4131
07 BC. CN. 97. CNE4	---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3465
08 BC. CN. 97. 97CNGX_6F	---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3283
09 CPX. GH. 96. 96GH2911	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3305
10 CD. TZ. 96. 96TZ_BF061	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3482
11 CPX. GR. x. GR17	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3405
12 BF. AR. 99. ARMA159	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4108
13 CPX. CM. 96. 1849	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3508
14 BG. ES. 99. X397	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3544
15 01B. TH. 99. 99TH_MU2079	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3502
16 A2D. KR. 97. 97KR004	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3466
18 CPX. CU. 99. CU76	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3408
19 CPX. CU. 99. CU7	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3329
20 BG. CU. 03. CB134	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3541
21 A2D. KE. 91. KMH1254	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3308
23 BG. CU. 03. CB118	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3559
24 BG. CU. 03. CB378	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3536
25 CPX. CM. x. 101BA	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3311
28 BF. BR. 99. BREPM12609	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3469
29 BF. BR. 02. BREPM119	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3277
31 BC. BR. 02. 110PA	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3537
33 01B. WY. 05. 05MYK1007_1	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3482
A1C. TZ. 02. C03710	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3290
A1CDGKU. ZA. 99. CM4	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4105
A1DHK. NO. 97. 97NOGLI3	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4113
A1GHU. GA. x. VI354	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3463
A2D. KE. 99. KER2003	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3308
AF2. CM. 02. 02CM_3163MN	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3296
AGU. CM. 01. 01CM_0989MO	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3305
AHJU. CM. 01. 01CM_1296NG	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3287
BC. CN. 96. YNRL9607	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3481
BC. MM. 99. mIU103	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4005
BE1. BR. 02. 02BR006	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3287
0708. CN. 00. HH069	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3598
U. CD. 83. 83CD003	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3302
U. CD. 90. 90CD121E12	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3374
U. GR. 99. GR303	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3988
U. NL. x. U. NL. 95. H10986_D1	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3609
N. CM. 02. DJ00131	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3607
N. CM. 04. 04CM_1131_03	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3697
N. CM. 95. YBF30	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3695
N. CM. 97. YBF106	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4158
O. BE. 87. MWPE180	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4133
O. CM. 91. WPE180	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3587
O. CM. 96. 96CMWBB637	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	4157
O. SN. 99. SEMPI300	A---A---G---T---G---CC---T---C---A---A---C---T---G---CAGG---G---AG	3542
CPZ. CD. 90. ANT	AC-AG-A-A---G---G---CT-A-G---C-AG---AA-C-GGCC---C-T-C-T---G---TC-G---A---CT---C---A---A---G---G	3542
CPZ. CM. 01. SIVcpzCAM13	AC-G-A---GGG---CT-G---C-A---A---C---T---G---TG---G---G---GTACC---C---CCCTA---T	3683
CPZ. CM. 05. SIVcpzEK505	AC-AG-A---G---TG-CCTCA-G-C-A-A-G-A-C-A-CA-C---T---T---TCC---A---CT---A---A---A	3675
CPZ. CM. 05. SIVcpzLB7	---G---C---C-AT---C-A-A-C-A-C-CTT-G---T---T---TCC---A---CT---A---A---A	3658
CPZ. CM. 05. SIVcpzMB66	---AG-A-A---T---AC-AT-G---A-A-A-A-G---T---T---TCC---A---CT---A---A---A	3649
CPZ. CM. 05. SIVcpzMT145	A-AG-A-A---G---TAA-G---C-A---C---C-AG---C-TG-G-C-T---C---TGC-G---T---A---T---C---C	3645
CPZ. GA. 88. GAB1	AC-AG-A-A---A-G---TT-GCT---G---C---AA-A-C-A-ATCA-C-G-T---G---TTA-G---G-TT-A-G-G-TT	4164
CPZ. TZ. 01. TAN1	A---G-A---C-CAC---GG-A-CT---A-AA-A---A-AGAAATAC---T-TG---C-T-G-C---TC---C-CT-T-G	3747
CPZ. US. 85. CPZUS	A---G-A---C-CAC---GG-A-CT---A-AA-A---A-AGAAATAC---T-TG---C-T-G-C---TC---C-CT-T-G	4163
Pol. p66 RT	K_T_E_L_Q_A_I_Y_L_A_L_Q_D_S_G_L_E_V_N_I_V_T_D_S_Q_Y_A_L_I_G_I_I_Q_A_Q_P_D_Q_S_E_S_E_L_V	Pol

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Accession	Genomic Coordinates	Sequence
B.FR.83.HXB2	Pol p66 RT and p15 RNase H end / p31 Int	AATCAATAATAGACGTTAATAA... 4233
A1.KE.94.Q23_17		A-A-C-G-C-A-T-C-T-T-C-G-G-A-G-G-G-3691
A1.RU.03.03RU20_06_13		A-A-C-G-G-A-GA-C-T-TA-G-G-G-3710
A1.RW.93.93RW037A_13		A-C-G-G-C-A-C-T-T-T-C-G-G-C-4226
A1.SE.94.SE7253		A-C-G-G-C-A-C-T-T-T-C-G-G-C-3437
A1.TZ.01.A173		A-C-G-G-A-C-A-C-T-T-TA-G-G-G-3432
A1.UA.00.98UA0116		A-AC-G-A-GA-C-T-T-TA-G-G-GT-4232
A1.UG.92.92UG037		A-C-G-C-A-T-T-T-G-G-GT-3600
A1.UG.98.98UG57136		A-C-G-A-T-A-C-T-T-T-G-G-GA-3438
A2.CD.97.97CDKFE4		AA-G-G-G-T-T-T-G-G-G-3038
A2.CD.97.97CDKS10		AA-G-A-G-G-C-T-T-T-G-G-G-350
A2.CD.97.97CDKT848		AA-G-G-G-T-T-TG-G-G-GT-3571
A2.CY.94.94CY017_41		AA-A-G-G-C-AT-T-T-T-G-G-3590
A.SN.01.DDI1579		AA-C-G-A-A-T-T-T-T-T-G-3431
A.SN.01.DDU369		AA-C-G-G-A-A-C-T-T-AA-G-G-G-3434
A.SN.96.DDU360		AA-C-G-G-A-A-C-T-T-T-G-G-G-3431
A.ZA.04.04ZASK162B1		AA-C-G-A-G-G-G-T-T-T-G-G-3674
B.AR.00.ARMS008		A-A-C-C-G-G-3438
B.AU.96.MBCD36		A-A-C-C-G-3588
B.CO.01.PCM074		A-A-C-C-G-3449
B.GA.88.OYI		A-A-C-C-G-3776
B.NL.99.671		A-A-C-C-G-3797
B.RU.04.04RU129005		A-A-C-A-C-T-T-A-T-G-G-3737
B.TH.90.BK132		A-A-C-C-G-3584
B.US.90.WEAU160		A-A-C-C-G-T-A-T-G-4232
B.US.98.1058_11		A-A-C-C-A-G-A-T-G-3423
C.AR.01.ARG4006		A-A-C-T-T-T-A-G-G-GT-G-C-3417
C.BR.04.04BR013		A-A-G-G-G-T-T-A-AG-G-G-3697
C.BR.92.BR025_d		A-A-G-G-G-T-T-A-AG-G-G-3571
C.BW.00.00BW07621		A-AC-G-G-T-T-A-AG-G-G-3586
C.ET.86.ETH2220		A-A-GC-G-G-T-T-A-AG-G-G-3625
C.IN.95.95IN219068		A-A-A-A-G-G-T-T-T-A-AG-G-G-3584
C.IN.99.01IN565_10		A-A-A-G-G-T-T-T-A-AG-G-G-3614
C.KE.00.KER2010		A-A-A-G-G-T-T-T-A-AG-G-G-3414
C.TZ.01.BD9_11		A-A-A-G-G-T-T-TA-AG-G-G-3441
C.UY.01.TRA3011		A-A-A-G-T-G-T-T-T-A-AG-G-G-3405
C.ZA.04.SK164B1		A-A-A-G-T-G-T-T-T-A-AG-G-G-3643
C.ZA.05.05ZASK245B1		A-A-A-G-T-G-T-T-T-A-AG-G-G-3662
C.ZM.02.02ZM115		A-A-A-G-T-T-T-T-T-A-AG-G-G-4227
C.ZM.96.96ZM651		A-A-A-G-G-T-T-T-T-T-A-CAAG-G-G-3562
D.CD.83.ELI		A-C-T-T-C-T-T-C-CAA-T-G-G-G-3779
D.CD.83.NDK		A-C-T-T-C-T-T-C-CAG-T-G-G-3768
D.CM.01.01CM_4412HAL		A-C-T-T-C-T-T-C-C-T-AG-G-G-3447
D.KE.01.NK03006		A-C-T-T-C-T-T-C-AA-T-AG-G-G-3438
D.TD.99.MN012		A-T-G-G-T-T-C-AG-T-AG-G-G-3457
D.TZ.01.A280		A-G-G-T-T-C-A-AG-T-AG-G-G-3434
D.UG.94.94UG114		A-G-G-T-T-C-T-T-AA-T-AG-G-G-3588
D.UG.99.99UGD23550		A-G-A-T-T-C-AT-T-AA-T-AG-G-G-3438
D.UG.99.99UGK03958		A-G-A-T-T-C-AT-T-AA-T-AG-G-G-3432
D.ZA.86.86Z82		A-C-T-T-C-T-T-C-CAG-T-A-A-C-G-3497
F1.BE.93.VI850		A-C-G-G-T-T-G-G-T-T-T-T-G-G-3573
F1.BR.89.B2126		A-C-G-G-T-T-G-G-T-T-T-T-G-G-3583
F1.BR.93.93BR020_1		A-C-G-G-T-T-G-G-T-T-T-T-G-G-3561
F1.FI.93.FIN9363_1		A-C-G-G-T-T-G-G-T-T-T-T-G-G-3562
F1.FR.96.MP411		A-A-A-C-G-G-T-T-T-T-G-G-3435
F2.CM.02.02CM_0016BBY		A-A-C-G-G-T-T-T-T-T-T-T-T-G-G-3423
F2.CM.95.MP255		A-A-C-G-G-T-T-T-T-T-T-T-T-G-G-3429
F2.CM.95.MP257		A-A-C-G-G-T-T-T-T-T-T-T-T-G-G-3441
F2.CM.97.CM53657		A-A-C-G-G-T-T-T-T-T-T-T-T-G-G-3423
G.BE.96.DRCBL		A-C-G-G-T-T-T-T-T-T-T-T-G-G-4190
G.CM.01.01CM_4049HAN		A-C-G-G-T-T-T-T-T-T-T-T-G-G-3425
G.ES.99.X138		A-C-G-G-T-T-T-T-T-T-T-T-G-T-3674
G.KE.93.HH8793_12_1		A-C-G-G-T-T-T-T-T-T-T-T-G-T-3633
G.NG.92.92NG083		A-C-G-G-T-T-T-T-T-T-T-T-G-T-3602
G.SE.93.SE6165		A-C-G-G-T-T-T-T-T-T-T-T-G-T-3630
H.BE.93.VI991		A-G-A-G-T-T-T-T-T-T-T-T-A-T-3622
H.BE.93.VI997		A-G-A-G-T-T-T-T-T-T-T-T-A-T-3557
H.CF.90.056		A-G-A-G-T-T-T-T-T-T-T-T-A-T-3580
J.SE.93.SE7887		A-G-G-G-T-T-T-T-T-T-T-T-G-G-3547
J.SE.94.SE7022		A-G-G-G-T-T-T-T-T-T-T-T-G-G-3548
K.CD.97.EQTB11C		A-A-C-G-G-T-T-T-T-T-T-T-T-G-G-3429
K.CM.96.MP535		A-A-C-G-A-C-AT-T-T-T-T-T-T-G-G-3429

B. FR. 83. HXB2
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01 AE.CF.90.90CF402
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 01 AE.HK.x.HK001
 01 AE.JP.93.93JP.NH1
 01 AE.TH.01.OUP414I
 01 AE.TH.02.OUP7691
 02 AE.TH.90.CM240
 02 AG.CM.02.02CM_16691E
 02 AG.EC.x.EC041
 02 AG.FR.91.DJ264
 02 AG.GH.03.GHNJ196
 02 AG.NG.x.IBNG
 02 AG.SN.98.MPI211
 02 AG.UZ.02.02UZ693
 03 AB.RU.97.KAL153_2
 04 CDX.CV.94.CV032
 05 DF.BE.x.VII1310
 06 CDX.AU.96.BEP90
 07 BC.CN.97.CM54
 08 BC.CN.97.97CNGX_6F
 09 CDX.GH.96.96GH2911
 10 CD.TZ.96.96TZ_BF061
 11 CDX.GR.x.GR17
 12 BF.AR.99.ARMAL59
 13 CDX.CM.96.1849
 14 BG.ES.99.X397
 15 01B.TH.99.99TH_MU2079
 16 A2D.KR.97.97KR004
 18 CDX.CU.99.CU76
 19 CDX.CU.99.CU77
 20 BG.CU.03.CB134
 21 A2D.KR.91.KNH1254
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 CDX.CM.x.101BA
 28 BF.BR.99.BREPMI1609
 29 BF.BR.02.BREPMI19
 31 BC.BR.02.110PA
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 U.CD.90.90CD121E12
 U.GR.99.GR303
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 N.CM.04.04CM_1131_03
 N.CM.95.YBF30
 N.CM.97.YBF106
 O.BE.87.ANT70
 O.CM.91.MVPS180
 O.CM.96.96CMWB8637
 O.SN.99.SEMPL1300
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 CPZ.CM.05.SIVcpzE4505
 CPZ.CM.05.SIVcpzL57
 CPZ.CM.05.SIVcpzMB6
 CPZ.CM.05.SIVcpzMT145
 CPZ.GA.88.GAB1
 CPZ.TZ.01.TAN1
 CPZ.US.85.CPZUS
 Pol p66 RT/p31 Integrase N_Q_I_I_E_Q_L_I_I_K_K_E_K_V_Y_L_A_W_V_P_A_H_K_G_I_G_G_N_E_Q_V_D_K_L_V_S_A_G_I_R_K_V_L_F_Pol 4233

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B.FR.83.HXB2
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HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	GCTAAAAGGAGGACCATGCGAAGTAGACTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAAAGGAAAAGTTTCTTGGTAGCAGTTTCATGTAGCCAGTGGATATAGAACGAGAA	4490
A1.KE.94.Q23_17	-----G-----C-----T-----C-----G-----A-----TG-----C-----	3948
A1.RU.03.03RU20_06_13	AT-----G-----T-----G-----A-----A-----A-----C-----C-----A-----	3967
A1.RW.93.93RW037A_13	-----G-----G-----T-----C-----A-----A-----C-----C-----C-----	4483
A1.SE.94.SE7253	-----G-----C-----G-----C-----C-----A-----T-----C-----C-----	3694
A1.TZ.01.A173	-----G-----G-----AG-----T-----G-----G-----T-----C-----C-----	3689
A1.UA.00.98UA0116	-----G-----G-----T-----C-----C-----C-----A-----A-----C-----	4489
A1.UG.92.92UG037	-----G-----G-----T-----C-----C-----C-----A-----T-----C-----	3857
A1.UG.98.98UGS7136	-----G-----G-----G-----G-----T-----C-----G-----A-----T-----	3695
A2.CD.97.97CDKFE4	-----G-----G-----T-----C-----C-----C-----C-----C-----C-----	3295
A2.CD.97.97CDKFS10	-----G-----G-----C-----C-----C-----C-----C-----C-----C-----	607
A2.CD.97.97CDKTB48	-----G-----G-----C-----C-----C-----C-----A-----G-----C-----	3830
A2.CY.94.94CY017_41	-----G-----G-----C-----C-----C-----T-----G-----C-----C-----	3847
A.SN.01.DDI579	-----G-----G-----T-----C-----C-----C-----TA-----A-----C-----	3688
A.SN.01.DDJ369	-----G-----G-----A-----C-----C-----C-----TA-----A-----C-----	3691
A.SN.96.DDJ360	-----G-----G-----C-----C-----C-----C-----TA-----A-----C-----	3688
A.ZA.04.04ZASK162B1	-----G-----G-----G-----G-----C-----C-----CC-----C-----C-----	3931
B.AR.00.ARMS008	-----G-----G-----C-----C-----C-----C-----C-----C-----C-----	3695
B.AU.96.MBCD36	-----G-----G-----C-----C-----C-----A-----A-----A-----G-----	3845
B.CO.01.PCM074	-----G-----G-----C-----C-----AG-----A-----A-----A-----A-----	3706
B.GA.88.OYI	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	4033
B.NL.99.671	-----G-----G-----R-----R-----A-----A-----A-----A-----A-----K-----	4054
B.RU.04.04RU129005	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3994
B.TH.90.BK132	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3841
B.US.90.WEAU160	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	4489
B.US.98.1058_11	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3680
C.AR.01.ARG4006	-----G-----G-----T-----T-----CA-----A-----C-----C-----C-----	3674
C.BR.04.04BR013	-----G-----G-----C-----C-----C-----G-----A-----C-----C-----	3954
C.BR.92.BR025_d	-----G-----G-----CA-----CA-----A-----C-----C-----C-----C-----	3828
C.BW.00.00BW07621	-----G-----G-----A-----A-----A-----G-----ACC-----C-----C-----	3843
C.ET.86.ETH2220	-----G-----G-----A-----A-----T-----C-----C-----G-----A-----C-----	3882
C.IN.95.95IN21068	-T-----G-----C-----C-----C-----G-----A-----C-----C-----C-----	3841
C.IN.99.01INS65_10	-----G-----G-----C-----C-----C-----G-----G-----A-----C-----	3871
C.KE.00.KER2010	-----G-----G-----CA-----CA-----A-----C-----C-----C-----C-----	3671
C.TZ.01.BD9_11	-----G-----G-----T-----T-----C-----C-----C-----A-----A-----	3698
C.UY.01.TRA3011	-----G-----G-----CA-----CA-----G-----GT-----C-----C-----	3662
C.ZA.04.SK164B1	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3900
C.ZA.05.05ZASK245B1	-----G-----G-----A-----A-----C-----C-----C-----A-----A-----	3919
C.ZM.02.02ZM115	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	4484
C.ZM.96.96ZM651	-A-----G-----G-----CA-----CA-----A-----C-----C-----C-----	3819
D.CD.83.ELI	-----G-----G-----C-----C-----C-----C-----C-----C-----C-----	4036
D.CD.83.NDK	-----G-----G-----T-----T-----C-----C-----G-----C-----C-----	4025
D.CM.01.01CM_4412HAL	-----G-----G-----T-----T-----C-----C-----G-----C-----C-----	3704
D.KE.01.NK03006	-----G-----G-----T-----T-----C-----C-----C-----C-----G-----	3695
D.TD.99.MN012	A-----G-----G-----G-----G-----T-----T-----C-----C-----	3714
D.TZ.01.A280	-----G-----G-----T-----T-----G-----G-----C-----C-----C-----	3691
D.UG.94.94UG114	-----G-----G-----T-----T-----G-----G-----C-----C-----G-----	3845
D.UG.99.99UGD23550	-----G-----G-----T-----T-----T-----T-----C-----C-----C-----	3695
D.UG.99.99UGK0958	-----G-----G-----T-----T-----T-----T-----C-----C-----C-----	3689
D.ZA.86.R482	-----G-----G-----T-----T-----T-----T-----C-----C-----C-----	3754
F1.BE.93.VI850	-----G-----G-----C-----C-----C-----C-----C-----C-----C-----	3830
F1.BR.89.B2126	-----G-----G-----T-----T-----G-----G-----B2126-----C-----	3840
F1.BR.93.93BR020_1	-----G-----G-----T-----T-----C-----C-----C-----C-----C-----	3818
F1.FI.93.FIN9363_1	-----G-----G-----T-----T-----C-----C-----C-----C-----C-----	3819
F1.FR.96.MP411	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3692
F2.CM.02.02CM_0016BBY	-T-----G-----G-----A-----A-----C-----C-----C-----C-----	3680
F2.CM.95.MP255	-----G-----G-----G-----G-----T-----T-----C-----C-----C-----	3686
F2.CM.95.MP257	-----G-----G-----G-----G-----T-----T-----C-----C-----C-----	3698
F2.CM.97.CM53657	-----G-----G-----G-----G-----C-----C-----C-----C-----C-----	3680
G.BE.96.DRCBL	-T-----G-----G-----G-----G-----T-----T-----G-----G-----	4447
G.CM.01.01CM_4049HAN	-----G-----G-----G-----G-----C-----C-----C-----C-----C-----	3692
G.ES.99.X138	A-----G-----G-----C-----C-----T-----T-----G-----G-----	3931
G.KE.93.HH8793_12_1	-----G-----G-----G-----G-----T-----T-----C-----C-----	3890
G.NG.92.92NG083	A-----G-----G-----G-----G-----T-----T-----C-----C-----	3887
G.SE.93.SE6165	-----G-----G-----G-----G-----T-----T-----C-----C-----	3879
H.BE.93.VI991	-----G-----G-----T-----T-----G-----G-----C-----C-----S-----	3837
H.BE.93.VI997	-----G-----G-----T-----T-----G-----G-----C-----C-----C-----	3804
H.CF.90.056	-----G-----G-----T-----T-----G-----G-----C-----C-----C-----	3805
J.SE.93.SE7887	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3687
J.SE.94.SE7022	-----G-----G-----G-----G-----G-----G-----G-----G-----G-----	3686
K.CD.97.EQTB11C	-----G-----G-----A-----A-----A-----A-----A-----A-----T-----	3687
K.CM.96.MP535	-----G-----G-----A-----A-----A-----A-----A-----A-----T-----	3686

B. F.R. 83. HXB2
GCTAAAAGAGAACCCATGCAAGTACAGTGGTGCAGGTAATGGCAACTAGATTGTCACACATTTAGAAGGAAAGTTCCTTGGTAGCAGTTTCATGTAGCCAGTTGGATATAGAGCGAGAA
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3923
3698
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3692
3674
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3868
4392
3674
3985
3689
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4375
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3994
4084
4082
4545
4520
3974
4544
3929
4070
4062
4045
4036
4032
4551
4134
4550
Pol p31 Integrase
L_K_G_E_A_M_H_G_Q_V_D_C_S_P_G_I_W_Q_I_D_C_T_H_L_E_G_K_V_I_I_V_A_V_H_V_A_S_G_Y_I_E_A_E

B.FR.83.HXB2	GTATTCCAGCAGAAACAGGAGGAAACAGCATATTTCTTTTAAATTTAGCAGGAGATGCCCAATAAACAATACATACTGACAAATGGCAGCAATTTTCACGGTGTCTACGGTTTAGGGCCGCTGTT	4620
A1.KE.94.Q23.17	---C---A---A---G---C---AC---T---G---C---A---C---G---A---AA---A---	4078
A1.RU.03.03RU20_06_13	---C---A---G---G---GT---G---C---A---T---CC---A---CAG---G---A---A---T---	4097
A1.RW.93.93RW037A_1	---C---G---A---G---C---A---AC---C---A---G---C---A---AA---A---T---	4613
A1.SE.94.SE7253	---C---G---A---G---C---A---AC---C---A---G---C---A---AA---A---T---	3824
A1.TZ.01.A173	---C---A---C---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3819
A1.UA.00.98UA0116	---C---A---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4619
A1.UG.92.92UG037	---C---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3987
A1.UG.98.98UG57136	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3825
A2.CD.97.97CDKFE4	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3425
A2.CD.97.97CDKSI0	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	737
A2.CD.97.97CDKTB48	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3960
A2.CY.94.94CY017_41	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3977
A.SN.01.DDU1579	---C---A---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3818
A.SN.01.DDU369	---C---C---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3821
A.SN.96.DDU360	---C---C---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3818
A.ZA.04.04ZASK162B1	---C---C---G---GGGT---G---C---A---T---CC---A---CAGG---A---A---T---	4061
B.AR.00.ARMS008	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3825
B.AU.96.MBCD36	---C---C---CA---T---C---CA---C---G---T---C---A---AA---G---A---AA---A---	3975
B.CO.01.PCM074	---C---C---C---C---C---G---G---T---C---A---AA---G---A---AA---A---	3836
B.GA.88.OY1	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4163
B.NL.99.671	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4184
B.RU.04.04RU129005	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4124
B.TH.90.BK132	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3971
B.US.90.WEAU160	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4619
B.US.98.1058_11	---G---C---C---A---C---C---G---G---T---C---A---AG---G---C---A---	3810
C.AR.01.ARG4006	---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3804
C.BR.04.04BR013	---C---C---GT---A---A---AA---G---A---AA---A---	4084
C.BR.92.BR025_d	---C---C---GT---A---A---AA---G---A---AA---A---	3958
C.BW.00.00BW07621	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3973
C.ET.86.ETH2220	---C---C---GT---A---A---AA---G---A---AA---A---	4012
C.IN.95.95IN21068	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3971
C.IN.99.01INS65_10	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4001
C.KE.00.KER2010	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3801
C.TZ.01.BD9_11	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3828
C.UY.01.TRA3011	---C---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3792
C.ZA.04.SK164B1	---C---C---GT---A---A---AA---G---A---AA---A---	4030
C.ZA.05.05ZASK245B1	---C---C---GT---A---A---AA---G---A---AA---A---	4049
C.ZM.02.02ZM115	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4614
C.ZM.96.96ZM651	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3949
D.CD.83.ELI	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4166
D.CD.83.NDK	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4155
D.CM.01.01CM_4412HAL	---T---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3834
D.KE.01.NKU3006	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3825
D.TD.99.MN012	---G---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3844
D.TZ.01.A280	---C---C---A---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3821
D.UG.94.94UG114	---C---C---A---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3975
D.UG.99.99UGD23550	---C---C---C---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3825
D.UG.99.99UGK09958	---C---C---C---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3819
D.ZA.86.R482	---T---G---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3884
F1.BE.93.VI850	---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3960
F1.BR.89.B2126	---K---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3970
F1.BR.93.93BR020_1	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3948
F1.FI.93.FIN9363_1	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3949
F1.FR.96.MP411	---C---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3822
F2.CM.02.02CM_0016BBY	---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3810
F2.CM.95.MP255	---C---C---CA---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3816
F2.CM.95.MP257	---C---C---CA---C---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3828
F2.CM.97.CM53657	---C---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3810
G.BE.96.DRCLB	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4577
G.CM.01.01CM_4049HAN	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3822
G.ES.99.X138	---C---A---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4061
G.KE.93.HH8793_12_1	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4020
G.NG.92.92NG083	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3989
G.SE.93.SE6165	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4017
H.BE.93.VI991	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	4009
H.BE.93.VI997	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3944
H.ICF.90.056	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3967
J.SE.93.SE7887	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3934
J.SE.94.SE7022	---C---C---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3935
K.CD.97.EQTB11C	---C---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3817
K.CM.96.MP535	---C---G---A---GT---G---C---A---T---CC---A---CAGG---A---A---T---	3816

B.FR.83.HXB2
01 AE.CF.90.90CF402
01 AE.CN.05.FJ051
01 AE.HK.x.HK001
01 AE.JP.93.93JP.NH1
01 AE.TH.01.01UR4141
01 AE.TH.02.02UR7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM_16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153_2
04 CPX.CV.94.CY032
05 DF.BE.x.VI1310
06 CPX.AU.96.BFP90
07 BC.CN.97.CNE4
08 BC.CN.97.97CNGX_6F
09 CPX.GH.96.96GHZ911
10 CD.TZ.96.96TZ_BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMAL159
13 CPX.CM.96.1849
14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 A2D.KE.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPM12609
29 BF.BR.02.BREPM119
31 BC.BR.02.110PA
33 01B.WV.05.05MYK1007_1
A1C.TZ.02.C03710
A1CDGKU.ZA.99.CM4
A1DHK.NO.97.97NOGLI3
A1GHU.GA.x.VI354
A2D.KE.99.KER2003
AF2.CM.02.02CM.3163MN
AGU.CM.01.01CM_0989MO
AHJU.CM.01.01CM.1296NG
BC.CN.96.YNPL9607
BC.MM.99.mIU103
BF1.BR.02.02BR006
0708.CN.00.HH069
U.CD.83.83CD003
U.CD.90.90CD121E12
U.GR.99.GR303
U.NL.x.U.NL.95.H10986_D1
N.CM.02.DJ00131
N.CM.04.04CM_1131_03
N.CM.95.YBF30
N.CM.97.YBF106
O.BE.87.ANT70
O.CM.91.MVPE180
O.CM.96.96CMWAB637
O.SN.99.SEMPI3000
CPZ.CD.90.ANT
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzL87
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.GA.88.GAB1
CPZ.TZ.01.TAN1
CPZ.US.85.CPZUS
Pol p31 Integrase

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	GGTGGCGGGAATCAAG.CAGGAATTTGGAATCCCTACAAATCCCACAAAGTCAAGGAGTAGTAGAATCTTATGAATAAAGAATTAAAGAAAATATAGGACAGGTTAAGAGATCAGGCTGAACATCTTAA	4749
A1.KE.94.Q23.17	---AAAT-C-A---	4207
A1.RU.03.03RU20.06.13	---AAAT-C-A---	4226
A1.RW.93.93RW037A_1	---AAAT-C-A---	4742
A1.SE.94.SE7253	---AA-T-C-A---	3953
A1.TZ.01.A173	---AA-TG-C-A---	3948
A1.UA.00.98UA0116	---AAAT-C-A---	4748
A1.UG.92.92UG037	---AAATG-T-A---	4116
A1.UG.92.98UG57136	---AAAC-C-A---	3954
A2.CD.97.97CDKFE4	A-TG-C-A-A-	3554
A2.CD.97.97CDKS10	A-G-C-A-A-	866
A2.CD.97.97CDKTB48	A-ATG-A-A-	4089
A2.CY.94.94CY017_41	A-T-C-A-A-	4106
A.SN.01.DDI579	---AAAT-C-A---	3947
A.SN.01.DDJ369	---AAAT-C-A---	3950
A.SN.96.DDJ360	A-AT-A-A-	3947
A.ZA.04.04ZASK162B1	---AAATG-C-A---	4190
B.AR.00.ARMS008	---G---C---A---G---	3954
B.AU.96.MBCD36	---G---C---C---A---	4104
B.CO.01.PCM074	A-G-T-A-T-T-R-A-	3965
B.GA.88.OYI	A-G---	4292
B.NL.99.671	A-G---	4313
B.RU.04.04RU129005	A-G-C-A-A-	4253
B.TH.90.BK132	A-G-C-C-A-	4100
B.US.90.WEAU160	---G---C---A---	4748
B.US.98.1058_11	---GG---	3939
C.AR.01.ARG4006	A-T-C-C-C-G-C-G-	3933
C.BR.04.04BR013	A-C-A-C-G-C-	4213
C.BR.92.BR025_d	A-T-C-A-A-	4087
C.BW.00.00BW07621	A-T-C-C-C-	4102
C.ET.86.ETH2220	A-T-TCA-	4141
C.IN.95.95IN21068	A-T-C-A-C-G-	4100
C.IN.99.01IN565_10	A-T-C-A-C-G-	4130
C.KR.00.KER2010	A-T-C-A-C-G-	3930
C.TZ.01.BD9_11	A-T-C-A-C-G-	3957
C.UY.01.TRA3011	A-T-C-A-A-	3921
C.ZA.04.SK164B1	A-C-C-A-C-G-	4159
C.ZA.05.05ZASK245B1	A-T-C-A-C-G-	4178
C.ZM.02.02ZM115	A-T-C-A-C-G-	4743
C.ZM.96.96ZM651	A-T-A-A-C-G-	4078
D.CD.83.ELI	A-T-A-	4295
D.CD.83.NDK	A-G-A-	4284
D.CM.01.01CM.4412HAL	A-T-T-C-T-C	3963
D.KE.01.NKU3006	A-C-T---	3954
D.TD.99.MN012	A-T-T-C-G-	3973
D.TZ.01.A280	A-C---	3950
D.UG.94.94UG114	A-C---	4104
D.UG.99.99UGD23550	A-C-T---	3954
D.UG.99.99UGK0958	A-C-T---	3948
D.ZA.86.R482	A-T-A-A-T-C-A-	4013
F1.BE.93.VI850	A-T-C-A-C-G-A-G-C-A-	4089
F1.BR.89.B2126	A-T-C-A-C-G-A-G-C-A-	4099
F1.BR.93.93BR020_1	A-T-C-T-C-T-C-GC-C-A-GC-C-A-A-	4077
F1.FI.93.FIN9363_1	A-T-C-T-C-T-C-GC-C-A-GC-C-A-A-	4078
F1.FR.96.MP411	A-T-AC-	3951
F2.CM.02.02CM.0016BBY	A-T-C-A-T-C-A-	3939
F2.CM.95.MP255	A-T-C-T---	3945
F2.CM.95.MP257	A-T-C-T---	3957
F2.CM.97.CM53657	A-T-C-T---	3939
G.BE.96.DRCBL	AA-C-CA-C-G-G-G-A-G-C-A-	4706
G.CM.01.01CM.4049HAN	AAAT-CA-C-C-CA-C-CG-T-G-A-A-C-	3951
G.ES.99.X138	AAAT-CA-A-Y-G-G-C-C-G-C-A-C-	4190
G.KE.93.HH8793_12_1	A-AT-T-CA-A-C-C-G-C-G-C-G-C-	4149
G.NG.92.92NG083	AAAT-CA-C-G-G-G-G-C-G-C-G-	4148
G.SE.93.SE6165	AAAT-CA-C-G-G-G-G-C-G-C-G-	4146
H.BE.93.VI991	A-AT-C-C-C-G-G-C-G-A-A-C-G-	4138
H.BE.93.VI997	A-AT-C-A-C-G-A-G-C-G-A-C-G-	4073
H.ICF.90.056	A-AT-C-A-G-G-G-C-A-A-C-	4096
J.SE.93.SE7887	A-AT---	4063
J.SE.94.SE7022	A-AT-A-	4064
K.CD.97.EQTB11C	A-AT---	3946
K.CM.96.MP535	A-TG---	3945

HIV-1/SIVcpz complete genomes

B.FR.83.HXB2	CAGCAGTACAAATGGCAGTATTTCACCAATTTTAAAGAAAGGGGGGATTTGGGGGTACAGTTCAGGGGAAAGAAATAGTAGACATATAAGCAACAGACATACAACAACCTAAAGAAATTAACAAAACCAAAAT	4879
A1.KE.94.Q23_17	-----T-----T-----A-----A-----C-----	4337
A1.RU.03.03RU20_06_13	-----T-----T-----GAT...A-----GAT...A-----C-----	4353
A1.RW.93.93RW037A_	-----T-----T-----T-----A-----A-----A-----	4872
A1.SE.94.SE7253	-----T-----T-----T-----A-----A-----A-----	4083
A1.TZ.01.A173	-----T-----T-----T-----A-----A-----A-----	4078
A1.UA.00.98UA0116	-----T-----T-----T-----A-----A-----A-----	4878
A1.UG.92.92UG037	-----G-----T-----T-----A-----A-----T-----	4246
A1.UG.98.98UG57136	-----T-----T-----T-----A-----A-----A-----	4084
A2.CD.97.97CDKFE4	-----T-----T-----T-----A-----A-----T-----	3684
A2.CD.97.97CDKFS10	-----G-----G-----T-----A-----A-----T-----	996
A2.CD.97.97CDKTB48	-----T-----T-----T-----A-----A-----T-----	4219
A2.CY.94.94CY017_41	-----T-----T-----T-----A-----A-----T-----	4236
A.SN.01.DDI579	-----T-----T-----T-----A-----A-----T-----	4077
A.SN.01.DDJ369	-----T-----T-----T-----A-----A-----T-----	4080
A.SN.96.DDJ360	-----T-----T-----T-----A-----A-----T-----	4077
A.ZA.04.04ZASK162B1	-----G-----T-----A-----A-----A-----	4320
B.AR.00.ARMS008	-----T-----T-----T-----A-----A-----T-----	4084
B.AU.96.MBCD36	-----T-----T-----T-----A-----A-----T-----	4234
B.CO.01.PCM074	-----T-----T-----T-----A-----A-----T-----	4095
B.GA.88.OYI	-----T-----T-----T-----A-----A-----T-----	4422
B.NL.99.671	-----T-----T-----T-----A-----A-----T-----	4443
B.RU.04.04RU129005	-----T-----T-----T-----A-----A-----T-----	4383
B.TH.90.BK132	-----T-----T-----T-----A-----A-----T-----	4230
B.US.90.WEAU160	-----T-----T-----T-----A-----A-----T-----	4878
B.US.98.1058_11	-----G-----T-----AC-T-----G-----A-----C-----	4069
C.AR.01.ARG4006	-----T-----T-----T-----A-----A-----T-----	4063
C.BR.04.04BR013	-----G-----T-----T-----A-----A-----T-----	4343
C.BR.92.BR025_d	-----T-----T-----T-----A-----A-----T-----	4216
C.BW.00.00BW07621	-----G-----T-----G-----A-----T-----C-----	4232
C.ET.86.ETH2220	-----T-----T-----T-----A-----A-----T-----	4271
C.IN.95.95IN21068	-----T-----T-----T-----A-----A-----T-----	4230
C.IN.99.01INS65_10	-----T-----T-----T-----A-----A-----T-----	4260
C.KE.00.KER2010	-----T-----T-----T-----A-----A-----T-----	4087
C.TZ.01.BD9_11	-----T-----T-----T-----A-----A-----T-----	4050
C.UY.01.TRA3011	-----T-----T-----T-----A-----A-----T-----	4289
C.ZA.04.SK164B1	-----T-----T-----T-----A-----A-----T-----	4308
C.ZA.05.05ZASK245B1	-----T-----T-----T-----A-----A-----T-----	4873
C.ZM.02.02ZM115	-----T-----T-----T-----A-----A-----T-----	4873
C.ZM.96.96ZM651	-----T-----T-----T-----A-----A-----T-----	4208
D.CD.83.ELI	-----T-----T-----T-----A-----A-----T-----	4425
D.CD.83.NDK	-----T-----T-----T-----A-----A-----T-----	4414
D.CM.01.01CM_4412HAL	-----T-----T-----T-----A-----A-----T-----	4093
D.KE.01.NK03006	-----T-----T-----T-----A-----A-----T-----	4084
D.TD.99.MN012	-----T-----T-----T-----A-----A-----T-----	4103
D.TZ.01.A280	-----T-----T-----T-----A-----A-----T-----	4080
D.UG.94.94UG114	-----T-----T-----T-----A-----A-----T-----	4234
D.UG.99.99UGD23550	-----T-----T-----T-----A-----A-----T-----	4084
D.UG.99.99UGK0958	-----T-----T-----T-----A-----A-----T-----	4078
D.ZA.86.R482	-----T-----T-----T-----A-----A-----T-----	4143
F1.BE.93.VI850	-----T-----T-----T-----A-----A-----T-----	4219
F1.BR.89.B2126	-----T-----T-----T-----A-----A-----T-----	4229
F1.BR.93.93BR020_1	-----C-----C-----A-----A-----C-----A-----G-----	4208
F1.FI.93.FIN9363_1	-----T-----T-----T-----A-----A-----T-----	4081
F1.FR.96.MP411	-----T-----T-----T-----A-----A-----T-----	4069
F2.CM.02.02CM_0016BBY	-----G-----G-----T-----T-----T-----A-----A-----	4075
F2.CM.95.MP255	-----T-----T-----T-----A-----A-----T-----	4087
F2.CM.95.MP257	-----T-----T-----T-----A-----A-----T-----	4069
F2.CM.97.CM53657	-----T-----T-----T-----A-----A-----T-----	4069
G.BE.96.DRCBL	-----G-----G-----T-----T-----T-----A-----A-----	4836
G.CM.01.01CM_4049HAN	-----G-----G-----T-----T-----T-----A-----A-----	4081
G.ES.99.X138_	-----G-----G-----T-----T-----T-----A-----A-----	4320
G.KE.93.HH8793_12_1	-----G-----G-----T-----T-----T-----A-----A-----	4279
G.NG.92.92NG083	-----G-----G-----T-----T-----T-----A-----A-----	4248
G.SE.93.SE6165	-----G-----G-----T-----T-----T-----A-----A-----	4276
H.BE.93.VI991	-----T-----T-----T-----A-----A-----T-----	4268
H.BE.93.VI997	-----T-----T-----T-----A-----A-----T-----	4203
H.CF.90.056	-----T-----T-----T-----A-----A-----T-----	4226
J.SE.93.SE7887	-----T-----T-----T-----A-----A-----T-----	4193
J.SE.94.SE7022	-----T-----T-----T-----A-----A-----T-----	4194
K.CD.97.EQTB11C	-----T-----T-----T-----A-----A-----T-----	4076
K.CM.96.MP535	-----T-----T-----T-----A-----A-----T-----	4075

B. FR. 83. HXB2	CAGCAGTACAAATGGCAGTATTTCACCAATTTTAAAGAAAGGGGGGATTTGGGGGGTACAGTTCAGCGGGGAAAGAAATAGTAGACATATAGCAACATACAACTTAAGAAATTCACAAAACCAAAAT	4879
01 AE. CF. 90. 90CF402	-----T-----A-----A-----A-----A-----A-----C-----	4915
01 AE. CN. 05. FJ051	-----T-----A-----A-----A-----A-----A-----C-----	4889
01 AE. HK. x. HK001	-----T-----A-----A-----A-----A-----A-----C-----	4241
01 AE. JP. 93. 93JP_NH1	-----T-----A-----A-----A-----A-----A-----C-----	4881
01 AE. TH. 01. OUR4141	-----T-----A-----A-----A-----A-----A-----C-----	4075
01 AE. TH. 02. OUR7691	-----T-----A-----A-----A-----A-----A-----C-----	4078
01 AE. TH. 90. CM240	-----T-----A-----A-----A-----A-----A-----C-----	4453
02 AG. CM. 02. 02CM_16691E	-----T-----A-----A-----A-----A-----A-----C-----	4069
02 AG. EC. x. EC041	-----T-----A-----A-----A-----A-----A-----C-----	3975
02 AG. FR. 91. DJ264	-----T-----A-----A-----A-----A-----A-----C-----	4228
02 AG. GH. 03. GHNJ196	-----T-----A-----A-----A-----A-----A-----C-----	4908
02 AG. NG. x. IENG	-----T-----A-----A-----A-----A-----A-----C-----	4404
02 AG. SN. 98. MP1211	-----T-----A-----A-----A-----A-----A-----C-----	4076
02 AG. UZ. 02. 02UZ693	-----T-----A-----A-----A-----A-----A-----C-----	4066
03 AB. RU. 97. KAL153_2	-----T-----A-----A-----A-----A-----A-----C-----	4105
04 CPX. CV. 94. CV032	-----T-----A-----A-----A-----A-----A-----C-----	4245
05 DF. BE. x. VIL1310	-----T-----A-----A-----A-----A-----A-----C-----	4261
06 CPX. AU. 96. BFP90	-----T-----A-----A-----A-----A-----A-----C-----	4907
07 BC. CN. 97. CNE4	-----T-----A-----A-----A-----A-----A-----C-----	4241
08 BC. CN. 97. 97CNGX_6F	-----T-----A-----A-----A-----A-----A-----C-----	4059
09 CPX. GH. 96. 96GH2911	-----T-----A-----A-----A-----A-----A-----C-----	4081
10 CD. TZ. 96. 96TZ_BF061	-----T-----A-----A-----A-----A-----A-----C-----	4258
11 CPX. GR. x. GR17	-----T-----A-----A-----A-----A-----A-----C-----	4181
12 BF. AR. 99. ARMA159	-----T-----A-----A-----A-----A-----A-----C-----	4884
13 CPX. CM. 96. 1849	-----T-----A-----A-----A-----A-----A-----C-----	4284
14 BG. ES. 99. X397	-----T-----A-----A-----A-----A-----A-----C-----	4320
15 01B. TH. 99. 99TH_MU2079	-----T-----A-----A-----A-----A-----A-----C-----	4276
16 A2D. KR. 97. 97KR004	-----T-----A-----A-----A-----A-----A-----C-----	4242
18 CPX. CU. 99. CU76	-----T-----A-----A-----A-----A-----A-----C-----	4184
19 CPX. CU. 99. CU7	-----T-----A-----A-----A-----A-----A-----C-----	4105
20 BG. CU. 03. CB134	-----T-----A-----A-----A-----A-----A-----C-----	4317
21 A2D. KE. 91. KMH1254	-----T-----A-----A-----A-----A-----A-----C-----	4084
23 BG. CU. 03. CB118	-----T-----A-----A-----A-----A-----A-----C-----	4335
24 BG. CU. 03. CB378	-----T-----A-----A-----A-----A-----A-----C-----	4312
25 CPX. CM. x. 101BA	-----T-----A-----A-----A-----A-----A-----C-----	4087
28 BF. BR. 99. BREPM12609	-----T-----A-----A-----A-----A-----A-----C-----	4245
29 BF. BR. 02. BREPM119	-----T-----A-----A-----A-----A-----A-----C-----	4053
31 BC. BR. 02. 110PA	-----T-----A-----A-----A-----A-----A-----C-----	4313
33 01B. MW. 05. 05MYKL007_1	-----T-----A-----A-----A-----A-----A-----C-----	4258
A1C. TZ. 02. C03710	-----T-----A-----A-----A-----A-----A-----C-----	4066
A1CDGKU. ZA. 99. CM4	-----T-----A-----A-----A-----A-----A-----C-----	4881
A1DHK. NO. 97. 97NOG1I3	-----T-----A-----A-----A-----A-----A-----C-----	4889
A1GHU. GA. x. VI354	-----T-----A-----A-----A-----A-----A-----C-----	4239
A2D. KE. 99. KER2003	-----T-----A-----A-----A-----A-----A-----C-----	4084
A2F. CM. 02. 02CM_3163MN	-----T-----A-----A-----A-----A-----A-----C-----	4072
AGU. CM. 01. 01CM_0989MO	-----T-----A-----A-----A-----A-----A-----C-----	4081
AHJU. CM. 01. 01CM_1296NG	-----T-----A-----A-----A-----A-----A-----C-----	4063
BC. CN. 96. YNPL9607	-----T-----A-----A-----A-----A-----A-----C-----	4063
BC. MM. 99. m1DU103	-----T-----A-----A-----A-----A-----A-----C-----	4257
BE1. BR. 02. 02BR006	-----T-----A-----A-----A-----A-----A-----C-----	4781
0708. CN. 00. HH069	-----T-----A-----A-----A-----A-----A-----C-----	4063
U. CD. 83. 83CD003	-----T-----A-----A-----A-----A-----A-----C-----	4374
U. CD. 90. 90CD121E12	-----T-----A-----A-----A-----A-----A-----C-----	4078
U. GR. 99. GR303	-----T-----A-----A-----A-----A-----A-----C-----	4150
U. NL. x. U. NL. 95. H10986_D1	-----T-----A-----A-----A-----A-----A-----C-----	4764
N. CM. 02. DJ00131	-----T-----A-----A-----A-----A-----A-----C-----	4385
N. CM. 04. 04CM_1131_03	-----T-----A-----A-----A-----A-----A-----C-----	4383
N. CM. 95. YBF30	-----T-----A-----A-----A-----A-----A-----C-----	4473
N. CM. 97. YBF106	-----T-----A-----A-----A-----A-----A-----C-----	4471
O. BE. 87. ANT70	-----T-----A-----A-----A-----A-----A-----C-----	4934
O. CM. 91. WPE180	-----T-----A-----A-----A-----A-----A-----C-----	4909
O. CM. 96. 96CMAB637	-----T-----A-----A-----A-----A-----A-----C-----	4363
O. SN. 99. SEMPI300	-----T-----A-----A-----A-----A-----A-----C-----	4933
CPZ. CD. 90. ANT	-----T-----A-----A-----A-----A-----A-----C-----	4318
CPZ. CM. 01. SIVcpzCAM13	-----T-----A-----A-----A-----A-----A-----C-----	4459
CPZ. CM. 05. SIVcpzE4505	-----T-----A-----A-----A-----A-----A-----C-----	4451
CPZ. CM. 05. SIVcpzL87	-----T-----A-----A-----A-----A-----A-----C-----	4434
CPZ. CM. 05. SIVcpzMB66	-----T-----A-----A-----A-----A-----A-----C-----	4425
CPZ. CM. 05. SIVcpzMT145	-----T-----A-----A-----A-----A-----A-----C-----	4421
CPZ. GA. 88. GAB1	-----T-----A-----A-----A-----A-----A-----C-----	4940
CPZ. TZ. 01. TAN1	-----T-----A-----A-----A-----A-----A-----C-----	4523
CPZ. US. 85. CPZUS	-----T-----A-----A-----A-----A-----A-----C-----	4939
Pol p31 Integrase	T_A_V_Q_M_A_V_F_I_H_N_F_K_R_K_K_G_G_I_G_G_Y_S_A_G_E_R_I_V_D_I_I_A_T_D_I_Q_T_K_E_I_Q_K_Q_I	Pol

HIV-1/SIVcpz
 complete genomes

B.FR.83.HXB2	TACAAAAATTCAAAATTTTCGGGTTTATTACAGGACAGCAGAAATCCACTTTGGAAAGGACAGGAGAGGTTGAAAGGAGTGAAGGGCAGTAGTAAATCAAGATAATAGTACATAAAAGTAGTC	5009
A1.KE.94.Q23_17	G---G---A-AT---G-C---G-C---G---A	4467
A1.RU.03.03RU20_06_13	-T---A---A---A---G---G---C---AC---T---A	4483
A1.RW.93.93RW037A_13	-C-A---G---G---G---G---C---C---G---A	5002
A1.SE.94.SE7253	-A---G-CA---A---A---G---C-A---T---G---A	4213
A1.TZ.01.A173	-G---G---A---A---A---G---C---G---A	4208
A1.UA.00.98UA0116	-T---G---A---A---A---G---C---AC---T---A	5008
A1.UG.92.92UG037	-A---A---A---A---G---G---C---T---A	4376
A1.UG.98.98UG57136	-G---G---A---A---A---G---C---T---G---A	4214
A2.CD.97.97CDKFE4	-GG---A---A---A---A---G---C---C---G---A	3814
A2.CD.97.97CDKS10	-TG---A---T-G-CA---A---A---G---C---G---A	1126
A2.CD.97.97CDKT48	-G---G---A---A---T---C---G---T---A	4349
A2.CY.94.94CY017_41	-G---G---A---A---T---C---G---T---A	4366
A.SN.01.DDI579	-G-C-A---A---A---G---C---G---A	4207
A.SN.01.DDJ369	-G-C-A---A---A---G---C---G---A	4210
A.SN.96.DDJ360	-G-C-A---A---A---G---C---G---A	4207
A.ZA.04.04ZASK162B1	-C---G-CT---G---GA---A---G---C---G---A	4450
B.AR.00.ARMS008	-G---G---A---A---A---G---G---C---T---A	4214
B.AU.96.MBCD36	-G-C---G---A---A---A---G---G---C---T---A	4364
B.CO.01.PCM074	-G-G---G---A---T---A---T---C---A	4225
B.GA.88.OYI	-G-A---G---A---T---T---T---C---A	4552
B.NL.99.671	-G---G---A---A---A---G---G---C---A	4573
B.RU.04.04RU129005	-G-G---G---A---T---T---G---G---A	4513
B.TH.90.BK132	-G---G---G---A---T---T---G---G---A	4360
B.US.90.WEAU160	-C---G---G---G---A---T---T---G---G---A	5008
B.US.98.1058_11	-C---G---G---G---A---T---T---G---G---A	4199
C.AR.01.ARG4006	-T---A---G-TA---C-A-A---C---T---G---A	4193
C.BR.04.04BR013	-T---A---G-TA---C-A-A---C---T---G---A	4473
C.BR.92.BR025_d	-TG---A---G-TA---C-A-A---C---G---A	4346
C.BW.00.00BW07621	-T---C---A---G-TA---C-A-A---C---G---A	4362
C.ET.86.ETH2220	-TT---A---G-C-TA---C-A-A---G---G---A	4401
C.IN.95.95IN21068	-G---G---C-CA---C-A-A---G---G---A	4360
C.IN.99.01INS65_10	-A---A---G-C-TA---C-A-A---A---G---A	4390
C.KE.00.KER2010	-T-C---A---G-C-TA---C-A-A---C---G---A	4190
C.TZ.01.BD9_11	-T-C---A---G-C-TA---C-A-A---C---G---A	4217
C.UY.01.TRA3011	-A---A---G-TA---C-A-A---G-C---C---G---A	4180
C.ZA.04.SK164B1	-T---A---G-C-TA---C-A-A---C---G---A	4419
C.ZA.05.05ZASK245B1	-A---A---G-C-CA---C-A-A---G---G---A	4438
C.ZM.02.02ZM115	-T---A---G-C-TA---C-A-A---G---G---A	5003
C.ZM.96.96ZM651	-T---C---A---G-C-CA---C-A-A---G---G---A	4338
D.CD.83.ELI	-T---A---G---A---A---G---C---G---A	4555
D.CD.83.NDK	-G-T---A---G---A---A---G---C---G---A	4544
D.CM.01.01CM_4412HAL	-T---G---A---T---A---T---G---A	4223
D.KE.01.NKU3006	-G---G---A---A---T---T---G---A	4214
D.TD.99.MN012	-T---G---A---T---A---T---A---A	4233
D.TZ.01.A280	-C---C---G-C-A---T---CC---G---A	4210
D.UG.94.94UG114	-G---G---G---G---T---C---A---G---A	4364
D.UG.99.99UGD23550	-G---G---G---G---T---C---A---G---A	4214
D.UG.99.99UGK0958	-G---G---A---A---G---G---A---G---A	4208
D.ZA.86.R482	-G---G---A---A---A---T---A---T---T-C---G---A	4273
F1.BE.93.VI850	-G---G---C---G---A---A---G---C---G---A	4349
F1.BR.89.B2126	-T---G---C---G---C---G---A---G---A	4359
F1.BR.93.93BR020_1	-G---G---G---C---G---A---G---A	4337
F1.FI.93.FIN9363	-C---C---G---C---G---A---G---A	4338
F1.FR.96.MP411	-T---C---C---G---C---G---A---G---A	4211
F2.CM.02.02CM_0016BBY	CT---C---T---A---G-C-A---A---G---A	4199
F2.CM.95.MP255	-T---G---G---G---A---A---G---A	4205
F2.CM.95.MP257	-T---G---G---G---A---A---G---A	4217
F2.CM.97.CM53657	-C---G-C-A---A---A---A---G---A	4199
G.BE.96.DRCEL	-G---G---A---A---A---A---G---C---AC---A	4966
G.CM.01.01CM_4049HAN	-G---G---A---A---A---A---G---C---AC---A	4211
G.ES.99.X138	-T---G---C---A---A---A---G---C---AC---A	4450
G.KE.93.HH8793_12_1	-G---G---G---A---A---G---C---AC---A	4409
G.NG.92.92NG083	-T---G---G---A---A---G---C---AC---A	4378
G.SE.93.SE6165	-G---G-C-G---C-A---A---G---C---AC---A	4406
H.BE.93.VI991	-T---C---A---A---A---A---T---C---A---A	4398
H.BE.93.VI997	-T---T---A---A---A---A---T---C---A---A	4333
H.CF.90.056	-T---C---A---A---A---A---T---C---A---A	4356
J.SE.93.SE7887	-G-C-A---A---A---A---G-C---A---G---A	4323
J.SE.94.SE7022	-G-C-A---A---A---A---G-C---A---G---A	4324
K.CD.97.EQTB11C	-TT---C---G-A---A---A---G---G---A	4201
K.CM.96.MP535	-TT---C---G-A---A---A---G---G---A	4205

B.FR.83.HXB2
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5069

B.FR.83.HXB2
01 AE.CF.90.90CF402
01 AE.CN.05.FJ051
01 AE.HK.x.HK001
01 AE.JP.93.93JP.NH1
01 AE.TH.01.OUR4141
01 AE.TH.02.OUR7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM.16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153.2
04 CPX.CV.94.CV032
05 DF.BE.x.VII1310
06 CPX.AU.96.BFP90
07 BC.CN.97.CNE4
08 BC.CN.97.97CNGX.6F
09 CPX.GH.96.96GH2911
10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMA159
13 CPX.CM.96.1849
14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 A2D.KR.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPM12609
29 BF.BR.02.BREPM119
31 BC.BR.02.110PA
33 01B.WV.05.05MYKL007.1
A1C.TZ.02.C03710
A1CDGKU.ZA.99.CM4
A1DHK.NO.97.97NOGLI3
A1GHU.GA.x.VI354
A2D.KE.99.KBR2003
AF2.CM.02.02CM.3163MN
AGU.CM.01.01CM.0989MO
AHJU.CM.01.01CM.1296NG
BC.MM.99.mIU103
BC.MM.99.mIU103
BF1.BR.02.02BR006
0708.CN.00.HH069
U.CD.83.83CD003
U.CD.90.90CD121E12
U.GR.99.GR303
U.NL.x.U.NL.95.H10986_D1
N.CM.02.DJ00131
N.CM.04.04CM.1131_03
N.CM.95.YBF30
N.CM.97.YBF106
O.BE.87.MNT70
O.CM.91.MVPE180
O.CM.96.96CMAB8637
O.SN.99.SEMP1300
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CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzE4505
CPZ.CM.05.SIVcpzE4505
CPZ.CM.05.SIVcpzE4505
CPZ.CM.05.SIVcpzE4505
CPZ.CM.05.SIVcpzE4505
CPZ.GA.88.GAB1
CPZ.TZ.01.TAN1
CPZ.US.85.CPZUS

Pol p31 Integrase

	/ Vif start	Pol Integrase end \	
B.FR.83.HXB2	CCNAGNAGAAAAGCAAGATCATTAGGGATTATGGAAAACACAGATGGCGCGGATGATTGTGTGGCRAAGTAGACAGAGTACAGAGATGGAGATTAAGACATGGGAAGATTAGTA...	AAACACCATATGATGTTTC	5136
A1.KE.94.Q23_17GT	4594
A1.RU.03.03RU20_06_13CC	4610
A1.RW.93.93RW037A_1AT	5129
A1.SE.94.SE7253CC	4340
A1.TZ.01.AL173GT	4335
A1.UA.00.98UA0116GT	5135
A1.UG.92.92UG037AC	4503
A1.UG.98.98UG57136CG	4341
A2.CD.97.97CDKPE4TT	3941
A2.CD.97.97CDKS10GT	1253
A2.CD.97.97CDKTB48CT	4476
A2.CY.94.94CY0117_41TT	4493
A.SN.01.DDI1579GT	4334
A.SN.01.DDU369CA	4337
A.SN.96.DDU360GC	4334
A.ZA.04.04ZASK162B1AC	4577
B.AR.00.ARMS008CT	4341
B.AU.96.MBCD36CA	4491
B.CO.01.PCM074GA	4352
B.GA.88.OY1CA	4679
B.NL.99.671AC	4700
B.RU.04.04RU1129005TA	4640
B.TH.90.BK132AC	4487
B.US.90.WEAU160AA	5135
B.US.98.1058_11TG	4326
C.AR.01.ARG4006GT	4320
C.BR.04.04BR013CG	4600
C.BR.92.BR025_dAC	4473
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G.ES.99.X138CT	4577
G.KE.93.HH8793_12_1CT	4536
G.NG.92.92NG083GT	4505
G.SE.93.SE6165GC	4533
H.BE.93.VI991GT	4625
H.BE.93.VI997GGT	4460
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 Pol p31 Integrase
 Vif
 W E N R W Q V M T V W Q V D R M R I R T W K S L V K H H M Y V S
 Vif start Pol Integrase end /

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Accession	Sequence	Position
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A1.SE.94.SE7253	AA--A-AG	4464
A1.TZ.01.A173	AA--A-AG	4459
A1.UA.00.98UA0116	AA--A-AG	5259
A1.UG.92.92UG037	AA--A-AG	4627
A1.UG.98.98UG57136	AA--A-AG	4465
A2.CD.97.97CDKFE4	AA--A-AG	4065
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A2.CD.97.97CDKTB48	AA--A-AG	4600
A2.CY.94.94CY017_41	AA--A-AG	4617
A.SN.01.DDI1579	AA--A-AG	4458
A.SN.01.DDU369	AA--A-AG	4461
A.SN.96.DDU360	AA--A-AG	4458
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B.AR.00.ARMS008	AA--A-AG	4465
B.AU.96.MBCD36	AA--A-AG	4615
B.CO.01.PCM074	AA--A-AG	4476
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B.NL.99.671	AA--A-AG	4824
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B.TH.90.BK132	AA--A-AG	4611
B.US.90.WEAU160	AA--A-AG	5259
B.US.98.1058_11	AA--A-AG	4450
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C.BR.04.04BR013	AA--A-AG	4724
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D.TZ.01.A280	AA--A-AG	4461
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J.SE.94.SE7022	AA--A-AG	4575
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K.CM.96.MP535	AA--A-AG	4456

Table with 3 columns: Accession ID, Nucleotide Sequence, and Position. The table lists HIV-1/SIVcpz complete genomes with their corresponding sequences and positions from 5260 to 5320.

HIV-1/SIVcpz complete genomes

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02 AG.EC.x.EC041
02 AG.FR.91.DJ264
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CPZ.GA.88.GAB1
CPZ.TZ.01.TAN1
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Vif

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

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D.UG.99.99UGK09958 A-C-G-A-A-G-G-AG-T-AA-T-A-GAA-G-G-... 4716

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08 BC.CN.97.97CNGX.6F
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10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
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13 CPX.CM.96.1849
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Vif

HIV-1/SIVcpz complete genomes

Table with columns for sample ID (e.g., B.FR.83.HXB2), sequence alignment (Vpr start to Vif end), and accession number (e.g., 5629, 5665, 5639, etc.). The alignment shows nucleotide differences between samples.

HIV-1/SIVcpz complete genomes

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01 AE.TH.90.CM240
02 AG.CM.02.02CM.16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.HG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153_2
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05 DF.BE.x.VI1310
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07 BC.CN.97.CNE4
08 BC.CN.97.97CNGX_6F
09 CPX.GH.96.96GH2911
10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMAL159
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14 BG.ES.99.X397
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16 AZD.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 AZD.KE.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPM12609
29 BF.BR.02.BREPM119
31 BC.BR.02.110PA
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CPZ.TZ.01.TAN1
CPZ.US.85.CPZUS
Vpr

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Table with columns for sample ID, sequence alignment (indicated by dashes for gaps), and a reference sequence at the bottom. The reference sequence is: CTGTTTATCCATTTCAGATTTGGTTCGACATAGCAGATAGCCGTT...ACTCGACAG...AGGAGAGCAAGA.../That exon 1 start \Vpr end ATGGAGCCAGTAGACTAGACTAGAGCCCTGGGAGCATCC

B.FR.83.HXB2 | HXB2 frameshift \HXB2 premature end of Vpr | Tat exon 1 start \Vpr end
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5872
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5936
5303
5453
5439
5425
5422
5412
5934
5509
5942
Vpr
Vpr
Tat

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

AGGAAGTCAGCCTAAACCTGTTACCAAATGCTATTTGAAGAAAGTTTGTCCTTCATTTGCCAAAGTTTGTTCATAACAAAGAAGCCTTAGGCATCTCCTATGCGAGGAGGAGCAGCAGCAGGAGAGA
 / Rev exon 1 start
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Accession	Sequence
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01 AE.CF.90.90CF402	G-----C-----G-----T-----T-----GG-----GG-----C-----A-----C-----TC-----G-----A-----G-----G-----
01 AE.CN.05.FJ051	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
01 AE.HK.x.HK001	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
01 AE.JP.93.93JP.NH1	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
01 AE.TH.01.OUR4141	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
01 AE.TH.02.OUR7691	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
01 AE.TH.90.CM240	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.CM.02.CM.1669LE	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.EC.x.EC041	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.FR.91.DJ264	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.GH.03.GHNJ196	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.NG.x.IENG	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.SN.98.MPI211	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
02 AG.UZ.02.02DZ693	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
03 AB.RU.97.KALI53.2	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
04 CPX.CY.94.CY032	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
05 DF.BE.x.VII310	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
06 CPX.AU.96.BFP90	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
07 BC.CN.97.CN54	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
08 BC.CN.97.97CNX3.6F	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
09 CPX.GH.96.96GH2911	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
10 CD.TZ.96.96TZ.BF061	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
11 CPX.GR.x.GR17	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
12 BF.AR.99.ABMA159	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
13 CPX.CM.96.1849	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
14 BG.ES.99.X397	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
15 01B.TH.99.99TH.MU2079	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
16 A2D.KR.97.97KR004	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
18 CPX.CU.99.CU76	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
19 CPX.CU.99.CU7	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
20 BG.CU.03.CB134	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
21 A2D.KE.91.KNH1254	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
23 BG.CU.03.CB118	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
24 BG.CU.03.CB378	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
25 CPX.CM.x.101BA	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
28 BF.BR.99.BREPML2609	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
29 BF.BR.02.BREPML19	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
31 BC.BR.02.110PA	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
33 01B.WY.05.05WYKL007_1	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
A1C.TZ.02.CO3710	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
A1CDGKU.ZA.99.CM4	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
A1DJK.NO.97.97NOGIL3	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
ALGHU.GA.x.VI354	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
A2D.KE.99.KER2003	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
AGU.CM.02.02CM.3163MN	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
AGU.CM.01.01CM.0989WO	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
AHJU.CM.01.01CM.1296NG	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
BC.CN.96.YNRL9607	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
BC.MM.99.mIDU103	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
BF1.BR.02.02BR006	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
0708.CN.00.HH069	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
U.CD.83.83CD003	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
U.CD.90.90CD121E12	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
U.GR.99.GR303	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
U.NL.x.U.NL.95.H10986_D1	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
N.CM.02.DJ00131	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
N.CM.04.04CM.1131_03	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
N.CM.95.YBF30	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
N.CM.97.YBF106	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
O.BE.87.ANT170	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
O.CM.91.MVP5180	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
O.CM.96.96CMWAB637	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
O.SN.99.SEMP1300	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CD.90.ANT	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CM.01.SIVcpzCAM13	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CM.05.SIVcpzEK505	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CM.05.SIVcpzLB7	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CM.05.SIVcpzMB66	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.CM.05.SIVcpzMT145	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.GA.88.GAB1	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.TZ.01.TANI	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
CPZ.US.85.CPZUS	G-----A-----C-----C-----G-----G-----T-----A-----C-----TC-----G-----A-----G-----C-----G-----
Tat exon 1	G S Q P K T A C T N C Y C K K C C F H C Q V C F I T K A L G I S Y M A G R K R R Q R R E R Tat

HIV-1/SIVcpz complete genomes

Table with columns for sequence identifiers (e.g., B.FR.83.HXB2), sequence coordinates (e.g., 01 AE.CF.90.90CF402), and sequence alignments. The alignments show conserved regions across various HIV-1/SIVcpz strains, with gaps indicated by dashes. Key features include Tat, Rev, and Vpu start sites, and intron start sites.

Tat, Rev exon 1 end / intron start / Vpu start (ACG in HXB2)

Tat, Rev exon 1 end / intron start / Vpu start (ACG in HXB2)

Tat exon 1 / Vpu Rev exon 1

HIV-1/SIVcpz complete genomes


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B.FR.83.HXB2
TAGTAGCAATAGTA...GCATTA...GTAGTAGCA...ATAATAATAGCAATAGTAGTTCTGTGGTCCCATAGTAATAGAAAAATTAAGACAA...AGAAAATAA
CTGT...GCG...AA...A...A...T...GGCT...A...T...AG...G...
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B.FR.83.HXB2
TAGTAGCAATAGTA...GCATTA...GTAGTAGCA...ATAATAATAGCAATAGTAGTTCTGTGGTCCCATAGTAATAGAAAAATTAAGACAA...AGAAAATAA
CTGT...GCG...AA...A...A...T...GGCT...A...T...AG...G...
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B.FR.83.HXB2
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Vpu

B.FR.83.HXB2
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CTGT...GCG...AA...A...A...T...GGCT...A...T...AG...G...
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Vpu
    
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HIV-1/SIVcpz
complete genomes

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.....GACAGGTTAATTGATAGACTAATAAGAGACAGACAGTGGCAATGAGTGAAGG.....AATATACGACTTGG.....GGGTGGAGATGGGG    6277
.....T.....G.....G.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....T.....C.....
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A1.RU.03.03RU20_06_13.....G.....A.....G.....G.....G.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....T.....C.....    5751
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A2.CD.97.97CDKTB48.....C.....G.....A.....GT.....T.....G.....ACACAGAG.....T.....G.....AA.....A.....G.....GA.....    5623
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A.SN.01.DDU369.....G.....A.....G.....G.....G.....G.....T.....G.....ATACAGAG.....T.....TA.....C.....G.....    5487
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B.US.90.WEAU160.....A.....G.....A.....G.....G.....G.....G.....T.....G.....ATCAGAG.....T.....T.....T.....G.....ATCAGAG.....T.....    6272
B.US.98.1058_11.....A.....A.....G.....G.....G.....G.....T.....G.....ATCAGAG.....T.....T.....T.....G.....ATCAGAG.....T.....    5463
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C.BR.04.04BR013.....C.....BR.....04.....04BR013.....G.....G.....ATACAGAG.....T.....G.....GA.....A.....A.....G.....T.....    5632
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C.WO.00.00W07621.....C.....C.....R.....02.....5_d.....G.....G.....ATACAGAG.....T.....G.....GA.....A.....A.....G.....T.....    5686
C.ET.86.ETH220.....T.....A.....A.....ACT.....GG.....T.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5624
C.IN.95.95IN21068.....T.....A.....A.....A.....T.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5624
C.IN.99.01INS65_10.....T.....A.....A.....A.....T.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5466
C.KE.00.KER2010.....T.....A.....A.....A.....T.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5466
C.TZ.01.BD9_11.....T.....G.....A.....A.....T.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5493
C.UY.01.TRA3011.....T.....G.....G.....A.....T.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5466
C.ZA.04.SK164B1.....A.....A.....G.....G.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5695
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C.ZM.02.02ZM115.....T.....T.....G.....A.....A.....T.....GG.....T.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    6289
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D.CD.83.NDK.....T.....T.....C.....A.....A.....T.....GG.....T.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5487
D.CM.01.01CM_4412HAL.....C.....C.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5478
D.KE.01.NKU3006.....T.....G.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5497
D.TD.99.MN012.....TATC.....A.....G.....A.....G.....G.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5474
D.TZ.01.A280.....T.....TZ.....01.....A280.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5628
D.UG.94.94UG114.....T.....T.....G.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5502
D.UG.99.99UGD23550.....TT.....G.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5472
D.UG.99.99UGK09958.....T.....T.....G.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5537
D.ZA.86.R482.....T.....T.....T.....A.....A.....G.....G.....T.....G.....ATACAGAG.....T.....G.....A.....A.....G.....T.....    5623
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B.FR.83.HXB2ATGCTCCTGGGATGTTGATG.....ATCTGT.....AGTGTACA...GAA.....AAATTG...TGGGTCAAGTCTATTATGGGTACTCTGTGTGG	6359	
A1.KE.94.Q23_17	G-TT.....A-T-G---CAA-A-A-A-T.....GTC.....C-T-T-T.....	5823	
A1.RU.03.03RU20_06_13	A-Y.....T-T-R-A-A-A-A-G.....AG-CG.....G-A-C-C.....	5833	
A1.RW.93.93RW037A	A-T.....A-T-G---AA-A-A-A-T.....G-FT.....T-T-T-C.....	6358	
A1.SE.94.SE7253	A-T.....AA-T-G---A-A-A.....C.....C-T-T-C.....	5572	
A1.TZ.01.A173	A-T.....A-T-G-AT-A-A-A.....G.....C-A-T-T-C.....	5579	
A1.UA.00.98UA0116	A-T.....T-T-T-A-A-A-A-G.....AG-G.....C-A-G-A-C.....	6358	
A1.UG.98.98UG0537	G-TT.....A-T-G---A-A-A-A-T.....A-A-G.....T-T-T-C.....	5735	
A1.UG.98.98UG57136	A-T.....A-T-T-G---G-A-AT-A.....T.....C-T-T-C.....	5750	
A2.CD.97.97CDKPE4	A-T.....T-T-TT.....AA.....G-T-G.....	5100	
A2.CD.97.97CDKSL0	A-T.....T-G-TT-A-A-A.....G.....A-C-A.....	2475	
A2.CD.97.97CDKT48	A-T.....T-A-TT-G---A-A-A.....G.....A-C-A.....	5702	
A2.CY.94.94CY017_41	A2.CY.94.94CY017_41AA.....G-T.....	5719	
A.SN.01.DDJ579	G-TA.....ATC---CT-T-A-A-A-A-T.....AA.....G-C-A.....	5566	
A.SN.01.DDJ369	G-TA.....ATC---AT-A-A-A-T.....AG.....G-C-C.....	5569	
A.SN.96.DDJ360	G-TG.....AT---A-A-A-A-T.....AG.....G-C-C.....	5566	
A.ZA.04.04ZASK162B1	A-TT.....A-T-G---A-A-A-A-TG.....G-T.....CC-G-C.....	5797	
B.AR.00.ARMS008	B.AR.00.ARMS008A.....AAATAAATAACT-T.....	5596	
B.AU.96.MBCD36	B.AU.96.MBCD36A-A-A-A.....GA-GAA-C.....	5713	
B.CO.01.PCM074	B.CO.01.PCM074A-A.....A.....	5571	
B.GA.88.OYI	B.GA.88.OYIA.....G.....	5898	
B.NL.99.671	B.NL.99.671A.....R-G.....	5919	
B.RU.04.04RU129005	B.RU.04.04RU129005A-A.....TA.....	5859	
B.TH.90.RK122	B.TH.90.RK122A.....G.....	5706	
B.US.90.WEAU160	B.US.90.WEAU160A.....G.....	6354	
B.US.98.1058_11	B.US.98.1058_11A-A.....G.....	5554	
C.AR.01.ARG4006	C.AR.01.ARG4006T-C-M.....A-TG-GG.....	5547	
C.BR.04.04BR013	C.BR.04.04BR013T.....A-TGGT.....	5841	
C.BR.92.BR025_d	C.BR.92.BR025_dT-A.....A-TA-GG.....	5714	
C.BW.00.00BW07621	C.BW.00.00BW07621G-T.....A-TA-TL.....	5730	
C.ET.86.ETH2220	C.ET.86.ETH2220T.....A-GA-TG.....	5768	
C.IN.95.95IN21068	C.IN.95.95IN21068T.....A-TGGT.....	5706	
C.KE.00.KER2010_10	C.KE.00.KER2010_10T.....A-TGGT.....	5739	
C.KE.00.KER2010	C.KE.00.KER2010CT.....TGGG.....	5548	
C.TZ.01.BD9_11	C.TZ.01.BD9_11T.....A-TGGT.....	5575	
C.UY.01.TRA3011	C.UY.01.TRA3011G-T.....A-TA-GG.....	5548	
C.ZA.04.SK164B1	C.ZA.04.SK164B1T.....G-GGGAG.....	5777	
C.ZA.05.05ZASK245B1	C.ZA.05.05ZASK245B1T.....A-TGGGG.....	5796	
C.ZM.02.02ZM115	C.ZM.02.02ZM115T-A.....A-TGGG.....	6371	
C.ZM.96.96ZM651	C.ZM.96.96ZM651T.....A-TGTGG.....	5696	
D.CD.83.ELI	D.CD.83.ELIA.....G.....	5901	
D.CD.83.NDK	D.CD.83.NDKC.....TC.....	5890	
D.CM.01.01CM_4412HAL	D.CM.01.01CM_4412HALC-ATG-CA-A.....G-T.....	5572	
D.KE.01.NKU3006	D.KE.01.NKU3006C.....AG.....	5560	
D.TD.99.MN012	D.TD.99.MN012C.....A-T.....	5582	
D.TZ.01.A280	D.TZ.01.A280A-G.....AG.....	5556	
D.UG.94.94UG114	D.UG.94.94UG114CA-A.....T.....	5710	
D.UG.99.99UGD23550	D.UG.99.99UGD23550CC-C.....G-C.....	5593	
D.UG.99.99UGK03958	D.UG.99.99UGK03958CA-A.....G-T.....	5554	
D.ZA.86.R482	D.ZA.86.R482G.....T.....	5619	
F1.BE.93.VI850	F1.BE.93.VI850T-AT-G---A-A-A-A.....A-G.....	5705	
F1.BR.89.B2126	F1.BR.89.B2126T-AT-G---A-A-A-A.....A.....	5702	
F1.BR.93.93BR020_1	F1.BR.93.93BR020_1T-AT-G---CA-A-A-A.....A-G.....	5690	
F1.FI.93.FIN9363_1	F1.FI.93.FIN9363_1T-AT-G---A-A-A.....AA-G-G.....	5694	
F1.FR.96.MP411	F1.FR.96.MP411T-AT-T-G---A-A-A-A.....T.....	5562	
F2.CM.02.02CM_0016BBY	F2.CM.02.02CM_0016BBYT-AT-G---A-A-A-A.....G.....	5548	
F2.CM.95.MP255	F2.CM.95.MP255T-AT-G---A-A-A-A.....G.....	5560	
F2.CM.95.MP257	F2.CM.95.MP257T-AT-G---A-A-A-A.....G.....	5566	
F2.CM.97.CM53657	F2.CM.97.CM53657T-AT-G---A-A-A-A.....T.....	5548	
G.BE.96.DRCL	G.BE.96.DRCLT-A.....T-G.....	6319	
G.CM.01.01CM_4049HAN	G.CM.01.01CM_4049HANT-A.....CT.....	5566	
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01 AE.TH.02.OUR7691	T-A-T-G-A-T-T-C-CT-T-T		T-T-T-T-T-T-T-T-T-T-T-T	C-T-T-T-T-T-T-T-T-T-T-T	5558
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HIV-1/SIVcpz complete genomes

Table with columns for accession number (e.g., B.FR.83.HXB2), full genome sequence (e.g., AAGRAAGCAACCACCACTTATTTTGTGCATCAGATGCTAAAGCATATGATACAGAGGTTACATAAATGTTTTGGGCCACACATGCTGTGTACCCACAGACCCCAAGAGTATGTGTAATGC), and NCBI accession ID (e.g., 6489, 5953, 5963, 6488, etc.). The table lists various HIV-1/SIVcpz strains and their corresponding genomic data.

HIV-1/SIVcpz complete genomes

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A1.RU.03.03RU20_06_13	AAACATGGGT-AC-...AAC-C-CGCAT-GT-T-ATT-A-A-G	6178
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A1.TZ.01.A173	CA-G-C-GT-A-...GACACGTGACAATGCCC-CC-A-TC-ACC-TC-CC-GGAAT-TT-A-G	5913
A1.UA.00.98UA0116	---GACC-GCTC-A-C-AC-G-A-...GT-AC-AA-C-ACGAT-CTG-TCT-A-A-G	6694
A1.UG.92.92UG037	CT-AAC-TC-CCA-A-TC-...-C-TC-C-AAT-CTCAG-T-ACAT-G-A-A-	6074
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A2.CD.97.97CDKPE4	CA-GCC-C-CCA-...-C-CIT-CCGCCCT-GC-...GCCCT-A-A	5100
A2.CD.97.97CDKSI0	CA-GCC-C-CCAC-AC-CC-AT-...-C-FA-CGCCCT-GC-...GCCCT-A-A	2808
A2.CD.97.97CDKTB48	CA-GCC-T-CCAG-C-...-A-...-TA-C-CCCA-GCCCAT-T-A-A	6014
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A.SN.01.DDU369	CA-CA-C-C-GCAC-GGT-GA-...-CC-A-...-C-G-A-G-G	5905
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D.TZ.01.A280	CGC-C-CGAC-AC-G-GGG-...AATGGG-C-AC-CG-CT-ATCTCTGGC-T-T-A-...CCAC-GA-GGC	5901
D.UG.94.94UG114	A-C-G-GTC-C-...C-CO-AT-...AAC-ATGCC-CT-AT-TGC-CAC-GA-G-G-	6019
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F1.FR.96.MP411	A-G-C-T-TCCAC-G-G-...ACT-CC-C-A-GA-ACC-C-CCCAGGAA--TC--G-CA-C	5904
F2.CM.02.02CM_0016BBY	G-T-T-T-ACGG-...-AT-...ACC-...-CAGCC-ATAAC-TC-CCC-GGAA-C-G-A	5890
F2.CM.95.MP255	---G-T-T-TCACC-TG-G-...TCTAAT-...-T-A-G-ACC-CC-...-AGGAA-TG-C-A	5896
F2.CM.95.MP257	A-GGCT-TC-T-A-GTC-CTT-T-...TTAAT-...-C-CTTGTC-CTCT-ATG-T-CCAFTCG-AG-A-G	5911
F2.CM.97.CM53657	G-T-CTGT-A-C-TC-C-AT-...GGAAAC-GC-CCCTGGATAAC-TC-CC-GGAA-ACC-...-T-	5893
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K.CM.96.MP535	---AC-AGGAAC-A-GC-...-A-A-GCAACT--C-CTG-GG-ARAGCCC-C-A-...-T-	5894

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01 AE.CF.90.90CF402
02 AE.CF.90.90CF402
03 AE.CF.90.90CF402
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B.FR.83.HXB2	TTCAATATCAGCACAAGCAATAGAGTTAAGTGCGAGAAAGATATGATTTTTTATAAACCCTTGTATATAATACCAATAGATAAT	6782
A1.KE.94.Q23_17	---G-C-GAAC-G-A-AGA-T-T-C-G-G-TA-G-A	6223
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A.SN.01.DDJ369	---A-C-GAAC-A-AGA-GT-T-T-C-C-C-G-G-G-TA	6005
A.SN.96.DDJ360	---G-G-CT-GAA-A-AG-A-C-C-C-G-G-G-A-T	5981
A.ZA.04.04ZASK162B1	---C-GA-G----AA-GAAG-A---C-C-A-C-G-G-G	6238
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C.KC.00.KER2010	---T-G-A-C-GAAT-A-AAA-G-G-G-GA-C-TA-GGC	5990
C.TZ.01.BD9_11	---G-C-GTAC-A-AAA-G-G-C-C-C-G-G	6017
C.UY.01.TRA3011	---GCA-C-GAAT-A-ACA-TGA-C-T-G-G	5963
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C.ZA.05.05ZASK245B1	---A-C-GAG-A-AAAA-T-TG-C-C-T-G-C-TA	6246
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D.CM.01.01CM_4412HAL	---T-GGG-A-C-GAAT-A-A-C-TGC-C-T-G-G	5986
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D.UG.99.99UGK09958	---G-A-CT-GTAG-A-AAA-C-T-T-GC	5960
D.ZA.86.R482	---G-C-GTAC-A-A-AAA-C-T-T-T-T-C-GC	6037
F1.BE.93.VI850	---GTC-GAAG-RRR-CA-T-T-C-C	6102
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G.ES.99.X138	---G-A-C-GAA-GGG-C-AA-A-G-C-GC	6236
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J.SE.94.SE7022	---G-A-CT-GAA-AA-AG-A-C-G-C-GC	6102
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HIV-1/SIVcpz complete genomes

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14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 AZD.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU77
20 BG.CU.03.CB134
21 AZD.KE.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
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Env gp120

HIV-1/SIVcpz complete genomes

7037

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B.F.R. 83_HXB2

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01 AE.JP.93.93JP.NH1 -G---A---AT---G---G---G---G---G---A---G---G---G---G---G---G---G---G---G---G---G---
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01 AE.TH.02.0UR7691 -G---A---A---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
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05 DF.BE.X.VI1310 -G---G---A---A---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
06 CPX.AU.96.BFP90 -G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
07 BC.CN.97.CN54 -G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
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23 BG.CU.03.CB118 GG-G---GA---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
24 BG.CU.03.CB378 GG-G---GA---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
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33 01B.MV.05.05MYK1007_1 -G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---G---
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HIV-1/SIVcpz complete genomes

Table with columns for accession numbers (e.g., B.FR.83.HXB2, O1.AE.CF.90.90CF402), sequence alignment (V3 loop start, V3 loop start), and genomic coordinates (7152, 7214, 7154, 6524, 7159, 6356, 6350, 6328, 6308, 6225, 6500, 7204, 6672, 6341, 6323, 6346, 6536, 6551, 7220, 6524, 6336, 6347, 6521, 6421, 7161, 6570, 6604, 6520, 6456, 6292, 6590, 6367, 6631, 6614, 6410, 6522, 6312, 6638, 6548, 6347, 7156, 7145, 6349, 6343, 6365, 6359, 6343, 6555, 7049, 6340, 6636, 6316, 6441, 7045, 6615, 6655, 6727, 6697, 7179, 7181, 6665, 7205, 6599, 6757, 6683, 6678, 6788, 6667, 7207, 6787, 7181, Env). The table contains multiple rows of sequence data and accession numbers.

HIV-1/SIVcpz complete genomes

Env gp120

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01 AE.TH.02.OUP7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM.16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SG.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153.2
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07 BC.CN.97.CM54
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12 BF.AR.99.ARMAL159
13 CPX.CM.96.1849
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15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
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20 BG.CU.03.CB134
21 A2D.KR.91.KNH1254
23 BG.CU.03.CB118
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CFZ.TZ.01.TAN1
CFZ.US.85.CFPZUS
Env gp120
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- V3 tip - | - V3 tip - |
V3 loop end - |
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Env

HIV-1/SIVcpz
complete genomes

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A1.UG.00.98UA0116	-C-A-T-GAAC.....A-T-T-GAAT.....C.....-A-C.....TTT	7324
A1.UG.92.92UG037	-C-C-G-T-GAAC.....A-T-T-GAAT.....C.....-A-C.....TTT	6710
A1.UG.98.98UG57136	GC-A-G-T-GAAC.....T-C-AG.....C.....GCTA-C.....T-T	6527
A2.CD.97.97CDKFE4	-C-A-G-GAAC.....A-C-CCCT.....-A-T.....-CCA-C.....T-T	5100
A2.CD.97.97CDKS10	-C-A-G-T-GAAC.....C-CCCT.....A.....-TAGC.....T	3453
A2.CD.97.97CDKTIB48	-C-A-G-GAAC.....GA-CCCT.....C.....CTA-C.....T	6653
A2.CY.94.94CY017_41	-C-G-G-AAC.....A-G-C-AAC.....C.....CTGG.....A-TTT	6538
A.SN.01.DDI579	-T-TA-G-G-T-GAAC.....A-G-C-AAC.....C.....CTGC-C.....TTT	6550
A.SN.01.DDU369	-C-G-G-GA-C.....A-C.....C.....CTAGGC.....A-TTT	6523
A.SN.96.DDU360	TCTG-ACAG-TAGTT-G-AA-TT-AGA.....A-GG.....A.....G-TA-TC.....TTT	6780
A.ZA.04.04ZASK162B1	-GCA-G-G-AA.....G.....G-GAAT.....C-A.....G-T-TC-A.....T	6586
B.AR.00.ARMS008	-G-G-TA-C-G.....C.....AAG.....A-C.....G.....G	6724
B.AU.96.MBCD36	-G-G-AA-CA.....C.....AG.....T.....T	6567
B.CO.01.PCM074	-G-G-CA.....A.....AAG.....G-T-G.....T	6882
B.GA.88.OY1	-C-TA.....TT-A-AAG.....G.....T-C.....T	6894
B.NL.99.671	-G-A-T-GAA.....A.....AAC.....T.....A	6846
B.RU.04.04RU129005	-G-T-AA.....A.....AAC.....T.....G-T.....A	6669
B.TH.90.BK132	-T-GAA.....GAAATTA.....AAG.....G-T.....A	7341
B.US.90.WEAU160	-G-AG-G-T-A.....A.....A.....T.....A	6517
B.US.98.1058_11	-C-TG-AT-AG-AA.....A.....A-G-TC-CCCT.....C-CAA-CCA.....T	6522
C.AR.01.ARG4006	-C-G-AG-AG-CA.....GC.....C-CCCT.....A.....CAA-GAG.....AT	6828
C.BR.04.04BR013	-C-G-G-G-AA.....GC.....C-CCCT.....G-A.....GCAA-GCA.....A-T	6677
C.BR.92.BR025_d	G-GCAG-T-GGAA.....AG.....C-CCCT.....C.....CTC-T.....G	6678
C.BW.00.00BW07621	-C-A-TG-AG-AA-G.....GC.....C-CCCT.....A.....GAA.....C	6728
C.ET.86.ETH2220	-T-TA-TG-AG-AA.....GC.....C-CCCT.....C.....CAIC-A.....T	6693
C.IN.95.95IN21068	-C-G-AGG-AA.....GA.....C-CCCT.....C.....GAA.....C	6717
C.IN.99.01IN565_10	-C-G-G-AG-AA.....GA.....T-C-CCCT.....A.....TAC.....T	6562
C.KE.00.KER2010	-C-G-G-AG-AT.....GC.....C-CCCT.....G.....CAA-GCA.....T	6508
C.TZ.01.BD9_11	-C-G-AG-AG-AA.....G.....A-T-C-CCCT.....C.....GAA.....G	6710
C.UY.01.TRA3011	-C-G-G-AAG-AG.....G-A.....A-T-C-CCCT.....C.....CTC.....T	6791
C.ZA.04.SK164B1	-C-G-G-AGC-AA.....CA.....A-G-C-CTTT.....C.....GCA-C.....A	7334
C.ZA.05.05ZASK245B1	-CG-G-G-AGG-A.....C.....C-CCCT.....A.....A-C.....A-C	6701
C.ZM.02.02ZM115	-C-AG-G-A.....G.....ACC-TTC-AAC.....A.....A-C.....A-C	6870
C.ZM.96.96ZM651	-C-G-G-CA-C-G.....C.....TTC-AAC.....A.....A-C.....A-C	6853
D.CD.83.ELI	-C-G-G-ACAA.....G.....A-G-TTC-AAC.....A.....TTC.....C	6526
D.CD.83.NDK	-C-G-G-AA.....G.....A-G-TTC-AAC.....A.....TTC.....C	6574
D.CM.01.01CM_4412HAL	-C-G-G-AGGCA-G.....AG.....TCT-T-CCCT.....G.....A-C-T.....G	6536
D.KE.01.NK03006	-C-G-G-AA.....G.....A-G-TTC-AAC.....A.....A-GTA-AAC.....A	6528
D.TD.99.MN012	-C-AT-G-AA.....AG.....A-GTA-AAC.....A.....A-GTA-AAC.....A	6652
D.TZ.01.A280	-C-G-G-GAA.....G.....A-C-TTC-AAC.....C.....G.....G	6556
D.UG.94.94UG114	-C-G-AG-AA.....AA.....C-TTC-AAC.....C.....GAT.....A-C-CA	6499
D.UG.99.99UGD23550	-C-G-G-AA.....G.....A-C-TTC-AAC.....A.....A-C-CA.....C	6499
D.UG.99.99UGK0958	-C-G-G-AA.....G.....A-C-TTC-AAC.....A.....A-C-CA.....C	6582
D.ZA.86.R482	GG-GT-TG-AAGCGAG.....AG.....TCG-T-CCCT.....C-G-AA.....C	6650
F1.BE.93.VI850	-G-G-G-AGGCA-G.....AG.....TCT-T-CCCT.....G.....A-C-TTC-AAC.....T	6677
F1.BR.89.B2126	-G-A-G-AAGCA-G.....G.....TCT-T-CCCT.....G.....A-C-TTC-AAC.....T	6665
F1.BR.93.93BR020_1	-C-G-GAG-AAGCGAG-G.....AG.....CTT-T.....CAA.....CTC.....T	6663
F1.FI.93.FIN9363_1	-C-G-G-CAAGAA-G.....C-G.....CTT-T.....CAA.....CTC.....T	6531
F1.FR.96.MP411	-TAG-G-GCAG-GG-C-A.....A-C-TCAC-AAT.....TTT-AA.....G--C-A	6514
F2.CM.02.02CM_0016BBY	-T-A-TG-AG-G-AG-G-C-A.....A-C-C-C.....TTCT-G-GC.....TTC.....TGT	6520
F2.CM.95.MP255	-T-A-TG-AG-G-AG-G-C-A.....A-C-C-C.....TTCT-G-GC.....TTC.....TGT	6515
F2.CM.95.MP257	-G-GGAG---AAG-GG-CCA.....AGC-CC---T-G-GG.....C-A-C-A.....G	6537
F2.CM.97.CM53657	-GGG-TG-CCAGCA-C-CAG.....T-C-A-ATT.....G-GC-GAA.....CTC-T	7291
G.BE.96.DRCLB	-G-C-AG-CA-A-CACTTC-CAT.....A-GA-A-AAT.....G-GC-C.....G	6535
G.CM.01.01CM_4049HAN	-TA-TG-GT-AA-C-A.....ATC-AAC.....C.....G-C-C.....T	6781
G.ES.99.X138	-G-GA--G-AAAGCAC-C.....A-ATC-A.....C.....G-CTC-T.....T	6734
G.KE.93.HH8793_12_1	-G-TG-CA-AGCAC-GC-G.....A-ATC-A-AAT.....G-AC.....CTC-T.....G	6687
G.NG.92.92NG083	-C-GA-TG-C-GCAG-C-G-G.....A-ATC-A-AAT.....AAG-GC.....CTC-T.....T	6761
H.BE.93.VI991	-C-CA-G-ATC-G.....G.....AGCT-C-AC.....T-A.....C-A-C-C.....G	6727
H.BE.93.VI997	-C-C---G-T-CAC---G.....AT-T-C-GAAC.....G---T---G.....A-C-CA	6657
H.CF.90.056	-C-C---G-T-CAC---G.....AT-T-C-GAAC.....G---T---G.....A-C-CA	6656
J.SE.93.SE7887	-CGTAGAG---AA-C-C.....C.....CAATC-C.....CAATC-C.....TAT	6635
J.SE.94.SE7022	-C-AG-AAG-AAG---G---A.....A.....C-A-C-CA.....A-C-CA	6642
K.CD.97.EQTB11C	-G-CAGAG-AAGGAA---GC-A.....A.....T---AAG.....GG---CA.....A-C-C-AA.....ACC	6544
K.CM.96.MP535	-G-CAGAG-AAGGAA---GC-A.....A.....T---AAG.....GG---CA.....A-C-C-AA.....ACC	6536

B.FR.83.HXB2	GAATTTTCTACTGTAATCAACACACTGTTTAAAT	AGTACTTTGG	TTTAACTACTTGGACTACTG	7431
A1.KE.94.Q23.17	--G-CAC-A-T	T	A-T-GGCT	6868
A1.RW.03.03RU20_06_13	--G-AC-A-T	C	A-GT-A-GCACTT-G-A-	6899
A1.RW.93.93RW037A_13	AC-A-T	C	GAGC-Y-GGCA	6899
A1.SE.94.SE7253	AC-A-T	A	CAATGAA-GCA	7412
A1.TZ.01.A173	AC-A-T	C	CCAAAATGAC	6626
A1.UA.00.98UA0116	AC-A-T	T	GGCTGTTTAAATG-C-C-	6640
A1.UG.92.92UG037	AC-A-T	C	AGCAACA-GGCC	7415
A1.UG.98.98UG57136	AC-A-T	T	AGCAACA-GGCC	6792
A2.CD.97.97CDKFE4	AC-A-T	T	AGCAACA-GGCC	6624
A2.CD.97.97CDKSI0	AC-A-T	T	AGCAACA-GGCC	5100
A2.CD.97.97CDKTB48	AC-A-T	T	AGCAACA-GGCC	3547
A2.CY.94.94CY017_41	AC-A-TT	C	GAAAATG-C--A	6744
A.SN.01.DDI579	AC-A-T	C	GG--C-A-GG-AC-T-G-AC	6806
A.SN.01.DDU369	AC-A-T	C	GAC-GGCC-TC-A	6635
A.SN.96.DDU360	AC-A-T	C	TATAA-G-C-TGGAAT-AC--	6653
A.ZA.04.04ZASK162B1	AC-T-T	C	A-GCACT-CC-TCA	6617
B.AR.00.ARMS008	AA-T	C	AA-G-C-CGC--A-GAAA	6880
B.AU.96.MBCD36	AA-T	C	GTA-A-G-C-TTAA	6680
B.CO.01.PCM074	A	C	G--G--A-A	6824
B.GA.88.OYI	A	C	G-GCT-A-GAAA	6658
B.NL.99.671	A	C	A	6964
B.TH.90.BK132	A	C	GA-GT-A-G-A	6985
B.US.90.WEAU160	A	C	G-CATG-GGA-A	6943
B.US.98.1058_11	A	C	A-GCA	6754
C.AR.01.ARG4006	AC-A-T	C	CA-GCT-A-GG-A	7432
C.BR.04.04BR013	AC-A-T	C	G--A-A-ARAAGA-GCA	6614
C.BR.92.BR025_d	AC-A-T	C	TRC--AATG--A-	6616
C.BW.00.00BW07621	AC-A-T	C	A-G-T-CAGAAA	6919
C.ET.86.ETH2220	AC-A-T	C	ACCT-A-G-A	6768
C.IN.95.95IN21068	AC-A-T	C	A-AAT	6807
C.IN.99.01IN565_10	AC-A-T	C	G-A-AC	6787
C.TZ.01.BD9_11	AC-A-T	C	AA-AC-CG-A-	6808
C.UY.01.TRA3011	AC-CAA-T	C	GAA-CFA	6620
C.ZA.04.SK164B1	AC-A-T	C	A-AC	6644
C.ZA.05.05ZASK245B1	AC-A-T	C	AAATACA-CAG-G-AGAA--C-G-A	6611
C.ZM.02.02ZM115	AC-A-T	C	A	6786
C.ZM.96.96ZM651	AC-A-T	C	G--A-AC	6876
D.CD.83.ELI	AC-A	C	TA-A-AT	7412
D.CD.83.NDK	AC-T-A	TGC	AA-T--G-A--A-A	6970
D.CM.01.01CM_4412HAL	AC-T	T	A	6935
D.KE.01.NK03006	AC-A	C	A	6620
D.TD.99.MN012	AC-A	C	G-A-A	6674
D.TZ.01.A280	AC-A-T	C	GA--A-G-CATGGA	6630
D.UG.94.94UG114	AC-A-T	C	A-GT-CA-TAA	6630
D.UG.99.99UGD23550	AC-A	C	A-AT-CA-TAA	6616
D.UG.99.99UGK0958	AC-A	C	ATT-AGGG-A	6746
D.ZA.86.R482	AC-A	C	AA-GGAAT-A-G-	6647
F1.BE.93.VI850	AC-A	C	TGGACATCA-A-A	6587
F1.BR.89.B2126	AC-T	T	ACAG-GGG-	6679
F1.BR.93.93BR020_1	AC-T	T	G--A-G-AAT-G-AT	6728
F1.FI.93.FIN9363_1	AC-G-T	A	GAC-AG-C	6755
F1.FR.96.MP411	AC-T	A	GAC-AG-A	6743
F2.CM.02.02CM_0016BBY	AC-T	A	GAC-AAA	6609
F2.CM.95.MP255	AC-T	A	AGTA	6590
F2.CM.95.MP257	AC-T	A	GAA-G-GAA	6598
F2.CM.97.CM53657	AC-T	A	GAA-AGA	6626
G.BE.96.DRCLB	AC-A	T	CAC-AA-A	6626
G.CM.01.01CM_4049HAN	AC-A	T	GCA-AAC	6596
G.ES.99.X138	AC-A	T	A-G-ATA	7370
G.KE.93.HH8793_12_1	AC-A	T	A-T-G--A	6617
G.NG.92.92NG083	AC-A	T	A-T-G--A	6866
G.93.SE61165	AC-A	T	A-T-G--A	6812
H.BE.93.VI991	AC-A	T	A-T-G--A	6839
H.93.VI997	AC-A	T	A-T-G--A	6836
H.ICF.90.056	AC-A	T	A-T-G--A	6750
J.SE.93.SE7887	AC-A	T	ACCAANTAGAGCT--CC-A-GAC-CCTA-A	6836
J.SE.94.SE7022	AC-A	T	ACTG-GGAC	6745
K.CD.97.EQTB11C	AC-A	T	GAA-TGCAT-C-A-T	6750
K.CM.96.MP535	AC-A	T	GA-AA-A-GCA	6736
	AC-A	T	GA-GAGAA-AC-T-A	6622
	AC-A	T	GAG-AG-	6614

Table with 3 columns: Accession ID (e.g., B.FR.83.HXB2), Nucleotide sequence (e.g., GAAATTTGTAACGCACAGTTTAAATTTGTTGAGGG), and Position (e.g., 7431). The table lists various HIV-1 and SIVcpz strains and their corresponding genomic coordinates.

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Accession	Genome	Position
B.FR.83.HXB2	AAGGGTCAAAATACACTGAGGAAGTGAC...ACAATCACC...CTCCCATGAGCAATTAATAAACAATAGGAGAAAGCAATGTATGCCCTCCATCAGTGGACAAATAG	7555
A1.KE.94.Q23.17	-CACTGAC-GC-CTCAG-GTC-A...T-A-T...G-G-C...C-CA-GT--A-A	6992
A1.RU.03.03RU20_06_13	CYTRTAA-Y-T-AR-G-CC-A-GA...T-A-T...G-G-C...T-AA-AGT-A-A	7033
A1.RW.93.93RW037A_1	TGCAAGT-G-A-TC-A...T-A-T...G-G-C...T-AA-AGT-A-A	7036
A1.SE.94.SE7253	GG-TA...G-G-GTT-A...T-A-T...T-AA-AGT-A-A	6750
A1.TZ.01.A173	-TCACA-C-G-G-GTT-A-AG...T-A-T...T-AA-AGT-A-A	6764
A1.UA.00.98UA0116	CT-TCA...G-ATG-CC-A-GA...T-A-T...T-AA-AGT-A-A	7539
A1.UG.92.92UG037	CT-AA...A-G-G-GTC-AC...T-T...T-AA-AGT-A-A	6916
A1.UG.98.98UGS7136	T-CA-GAG...G-G-GAC-A-GA...T-T-G-T...T-AA-AGT-A-A	6745
A2.CD.97.97CDKFE4	-CAAACAG-T-G-GTC-A...T-A-G...G-G-C...T-AA-AGT-A-A	5100
A2.CD.97.97CDKRS10	GGCC-AC-CACCT-A-A-CACC-A-GA...GT-A-T...T-AA-AGT-A-A	3671
A2.CY.94.94CY017_41	-CACTATC-CGTGAGA-TTC-C-T...AT-A-T...G-G-C...T-AA-AGT-A-A	6868
A.SN.01.DDI579	-CA-CA-C-G-AT-AA-T-C-CG-G...A-A-T...G-G-C...T-AA-AGT-A-A	6930
A.SN.01.DDU3369	-GCA-AAITTA-CT-ACA-T-AC-CG-GG...GT-A-T...T-AA-AGT-A-A	6759
A.SN.96.DDU360	-CACT-GG...TAA-TTC-A-GA...GT-A-T...T-AA-AGT-A-A	6741
A.ZA.04.04ZASK162B1	-TAACA-TGCAGG-A-CA-TGACACA...GC-TA...T-AA-AGT-A-A	7004
B.AR.00.ARMS008	CTT-GAT...CT-A-CATT-AC-GA...AT-TA...T-AA-AGT-A-A	6804
B.AU.96.MBCD36	-TACTA...GGCA-A-AGCACTGAA-TA...T-A...T-AA-AGT-A-A	6948
B.CO.01.PCM074	CT--AATGG-CT-A-TC-A-AG...T-A-A...T-AA-AGT-A-A	6782
B.GA.88.OYI	GTACTGAG-GGTCA-A-ACCAATGAAAG...C-T-A...T-AA-AGT-A-A	7109
B.NL.99.671	CT-AAGG...G-GA-G-AGGAAGA...AT-TA...T-AA-AGT-A-A	7067
B.TH.90.BK132	CTT-NAG...CTGAA-GG-C-GB-A...AT-TA...T-AA-AGT-A-A	6878
B.US.90.WEAU160	CTAAAA...G-AC-AA-T-ATG-AA-A...AT-TA...T-AA-AGT-A-A	7556
B.US.98.1058_11	--ATTA--GG-TGG-AA-C-ATTCA-M...C-C...A-A-T...T-AA-AGT-A-A	6738
C.AR.01.ARG4006	GCAATTAATG-A-CAGAAA-T-C-AC-CA...TC...A-A...T-AA-AGT-A-A	6740
C.BR.04.04BR013	C-AAAAG-T-CTGGAAC-A-A-TCA...TC...A-A...T-AA-AGT-A-A	7043
C.BR.92.BR025_d	C-AAATG-CA-A-TC-AC-A-TTA...AC...A-A...T-AA-AGT-A-A	6892
C.BW.00.00BW07621	T-AACTGTT--T-GCATAC-A-TTA...AC...A-A...T-AA-AGT-A-A	6887
C.ET.86.ETH2220	-GA-TAATCA-G-G-R-TC-AC-CA...AC...A-A...T-AA-AGT-A-A	6931
C.IN.95.95IN21068	GTACA-AC-G-T-T-G-TGTC--CCCA...AT-TA...T-AA-AGT-A-A	6911
C.IN.99.01IN565_10	TGATGAT-CAT--G-TCTATG-GACA...AC...A-A...T-AA-AGT-A-A	6932
C.KE.00.KER2010	-T--A-G-A-G-A-T-A-CA-GA...CG-T-A...T-AA-AGT-A-A	6744
C.UY.01.BD9_11	C-A-TAATGCA-GTGA-C-AAC-ACA...C...A-A...T-AA-AGT-A-A	6768
C.TZ.01.TRA3011	C-A-T...GT-A-G-ATG-TCA...GTC-T-A...T-AA-AGT-A-A	6735
C.ZA.04.SK164B1	...AT-T...GT-AA-TA-T-C-TCA...AC...A-A...T-AA-AGT-A-A	6910
C.ZA.05.05ZASK245B1	...A-G-A-T-A-AC-ATG-ACA...C-C...A-A...T-AA-AGT-A-A	7000
C.ZM.02.02ZM115	TTACAGAGTCA-T-A-AGCAC-ACACA...AC...A-A...T-AA-AGT-A-A	7534
C.ZM.96.96ZM651	-GACTAAT-G-CAGGTTCAAT-A-G...G...A-A...T-AA-AGT-A-A	6898
D.CD.83.ELI	C-T-...AAT-G-GTG-A-TC-CC-A...T...T-AA-AGT-A-A	7091
D.CD.83.NDK	C-ACAAAT-G-CAGG-G-ATGGAGT...A-TA...T-AA-AGT-A-A	7059
D.CM.01.01CM_4412HAL	-GAATGAT-G-CTGAAA-TA-T-CAAGA...AT-A...T-AA-AGT-A-A	6744
D.KE.01.NKU3006	C-CAAAAAT--CAGAGAC-AT-A-AGT...T-AA-AGT-A-A	6798
D.TD.99.MN012	-T-AGG-G-G-T-A-AC-CC-GA-G...G...A-A...T-AA-AGT-A-A	6754
D.TZ.01.A280	-TACAGGG-TGTCA-A-AGTAC-AG-CA...AT-TA...T-AA-AGT-A-A	6740
D.UG.94.94UGS114	G-AAATATC-CA-T-TCAC-A-T-TCACA...AT-TA...T-AA-AGT-A-A	6870
D.UG.99.99UGD23550	GGTCAAAAT--GGGAG-ATGGTC--A-C-G...G...A-A...T-AA-AGT-A-A	6711
D.UG.99.99UGK0958	...TCCCAAT-A-G...T...TC-G...G...A-A...T-AA-AGT-A-A	6803
D.ZA.86.R482	...TC-G...G...T...TC-C...G...T...T-AA-AGT-A-A	6835
F1.BE.93.VI850	...CCTAAT-A-G...T...TC...G...T...T-AA-AGT-A-A	6859
F1.BR.89.B2126	...A-GTAC-A-G...T...T...T...T-AA-AGT-A-A	6798
F1.FI.93.FIN9363_1	...A-GTAC-A-G...T...T...T...T-AA-AGT-A-A	6848
F1.FR.96.MP411	...A-GTAC-A-G...T...T...T...T-AA-AGT-A-A	6716
F2.CM.02.02CM_0016BBY	T-CITTAAC-CA-CA-TG-TAAT-A-GT...T-TT...T-AA-AGT-A-A	6714
F2.CM.95.MP255	...GTGGCT-A-A-CAG-AC-A...AT-T...T-AA-AGT-A-A	6714
F2.CM.95.MP257	TGACTAAT-TG-CAGAGTCC-A-G...T-T...T-AA-AGT-A-A	6750
F2.CM.97.CM53657	T-AA-AGT--TAT-A--AAT-A--T...T-A...T-AA-AGT-A-A	6720
G.BE.96.DRCLB	-TA-TAGT-CA-T-G-ACT-AG-A-A...T...T-AA-AGT-A-A	7494
G.CM.01.01CM_4049HAN	GT--TAACCTG-CT-A-AGTA-T-A...T...T-AA-AGT-A-A	6741
G.ES.99.X138	...AT-A-C-A-OG...C...T...T-AA-AGT-A-A	6990
G.KE.93.HH8793_12_1	...GT-A-ATTAAT-A-GG...T...T-AA-AGT-A-A	6919
G.NE.92.92NEG083	...T-AG-TCA-T-G-AGT-AG-A-GG...T...T-AA-AGT-A-A	6878
H.BE.93.SE6165	-CA-CAAC-GC-CAGAA-TATC-CA-GA...AT-TA...T-AA-AGT-A-A	6961
H.BE.93.VI991	-TATTAAAT-TGGCA-A--CAG-G-AA-A...AT-TA...T-AA-AGT-A-A	6869
H.CF.90.056	-CACA-----G--AA-G--AC-A...-AC-T-A...T-AA-AGT-A-A	6874
J.SE.93.SE7887	TT-AA-G-T-CA-TGACAC-A-TNAC-CA...T...T-AA-AGT-A-A	6850
J.SE.94.SE7022	-G-ACA--GT-AA-T-AC-ACACA...T...T-AA-AGT-A-A	6860
K.CD.97.EQTB11C	...GAG...AGGA-AC...T...T-AA-AGT-A-A	6712
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02 AG. NG. x. IENG
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02 AG. UZ. 02. 02UZ693
03 AB. RU. 97. KAL153_2
04 CB. CV. 94. CV0332
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07 BC. CN. 97. CNE54
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10 CD. TZ. 96. 96TZ_BF061
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12 BF. AR. 99. ARMA159
13 CPX. CM. 96. 1849
14 BG. ES. 99. X397
15 01B. TH. 99. 99TH_MU2079
16 AZD. KR. 97. 97KR004
18 CPX. CU. 99. CU76
19 CPX. CU. 99. CU17
20 BG. CU. 03. CB134
21 AZD. KE. 91. KMH1254
23 BG. CU. 03. CB118
24 BG. CU. 03. CB378
25 CPX. CM. x. 101B4
28 BF. BR. 99. BREPM12609
29 BF. BR. 02. BREPM119
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AHJU. CM. 01. 01CM_1296NG
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O. CM. 96. 96CMWAB637
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CPZ. CD. 90. ANTI
CPZ. CM. 01. SIVcpzCAM13
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CPZ. CM. 05. SIVcpzL87
CPZ. CM. 05. SIVcpzMB66
CPZ. CM. 05. SIVcpzMT145
CPZ. GA. 88. GHAB1
CPZ. TZ. 01. TAN1
CPZ. US. 85. CPZUS
Env 9p120

HIV-1/SIVcpz complete genomes

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B.AR.00.ARMS008	C-GT-...GGG-C-C-G-G-GA-CAA-A-C-T-G	6918
B.AU.96.MBCD36	C-A-...A-AA-TTTG-T-G-ACAAA-CT	7056
B.CO.01.PCM074	T-CA-...A-CA-C-C-C-C-A-CAAT-C	6892
B.GA.88.OYI	G-G-C-C-C-C-AAG-C-C-G-C-G-AT-A-C	7202
B.NL.99.671	C-C-C-C-C-G-G-G-A-G-GCA-CA-T	7220
B.RU.04.04RUJ129005	C-C-...A-A-GCA-A-T-GCAC-A-G-R-K	7178
B.TH.90.BK132	CA-C-...AACCAA-G-G-C-C-A-T-A	6995
B.US.90.WEAU160	T-...T-A-AGT-G-SAAG-G-CC-A-T	7670
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C.BW.00.00BW07621	G-...A-A-G-G-C-T-A-G-AG-TG-A-ACAA-A-CA	6998
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C.TZ.01.BD9_11	AA-...C-A-AT-GGT-C-T-A-...CAG-T-AA-A-A-CA	6876
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D.TZ.01.A280	C-A-...A-AT-C-...AATGTA-AT-T-G-AGAGAG-A	6854
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D.UG.99.99UGD23550	C-G-...A-AT-G-C-AGT-...GCA-AT-T-G-C-AGT-C-T	6885
D.UG.99.99UGK0958	C-...A-AT-G-...GCA-AT-T-G-C-AGT-C-T	6825
D.ZA.86.R482	C-...A-A-C-...AT-GTTC-A-CAA-C	6914
F1.BE.93.VI850	C-AAC-...TT-A-G-...ATG-G-G-A-CAVTT-C	6943
F1.BR.89.B2126	C-AAC-...T-A-G-...C-G-AT-GT-C-A-T-C	6970
F1.BR.93.93BR020_1	C-AAC-...T-A-G-...CTG-T-G-ACTAAT-C-G	6970
F1.FI.93.FIN9363_1	C-AAC-...T-A-G-...CAG-G-AT-T-G-T-T-C	6962
F1.FR.96.MP411	C-AAC-...C-A-...CAGAGT-GAT-CT-AG-A-T-CT	6833
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G.CM.01.01CM_4049HAN	G-AA-...C-C-A-AA-...AAT-C-GG-T-ACC-A	6855
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G.SE.93.SE6165	AA-...GC-...AATAACAAAT-CA-AT-CA-G-AGT	7084
H.BE.93.VI991	A-...A-AA-G-...TTT-CG-G-...AT-T-CAA-TAAT-TT-C	7065
H.BE.93.VI997	G-...AT-AA-CC-G-TTAT-C-AA-...GG-A-T-...TAAT-TT-C	6980
H.ICF.90.056	G-GT-...A-AA-G-...TT-C-AG-...CGGCTCTGCA-AAAT-T-C	6985
J.SE.93.SE7887	G-CA-...AT-A-G-C-T-A-...AACAGGGGAATGCG-TG-G-GCA-T	6973
J.SE.94.SE7022	CMA-...AT-AT-G-C-T-A-...AACAGGAATGCG-TG-G-GCA-T	6980
K.CD.97.EQTB11C	C-AG-...AA-A-G-...AATGAC-...AT-CT-GGACTGAG-C	6849
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01 AE.TH.01.0UR4141
01 AE.TH.02.0UR7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNJ196
02 AG.NG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL1532
04 CPX.CV.94.CV0332
05 DF.BE.x.VI11310
06 CPX.AU.96.BFP90
07 BC.CN.97.CN54
08 BC.CN.97.97CNGX.6F
09 CPX.GH.96.96GH2911
10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMAL159
13 CPX.CM.96.1849
14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 A2D.KE.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPML12609
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31 BC.BR.02.110PA
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CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzL87
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CPZ.GA.88.GHAB1
CPZ.TZ.01.TAN1
CPZ.US.85.CPZUS
Env 9p120

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Table with columns: Accession ID (e.g., B.FR.83.HXB2), REE Stem I (consensus sequence), Env gp120 end (sequence), Env gp41 start (sequence), and GenBank ID (e.g., 7772, 7209, 7243, etc.).

Table with columns for accession numbers (e.g., B.FR.83.HXB2), sequence identifiers (e.g., REE Stem I), and nucleotide sequences. The table is organized into rows corresponding to different HIV-1/SIVcpz strains. The sequence for each strain is shown in a single line, with gaps indicating missing or unsequenced regions. The table ends with 'Env gp120/gp41 start' and 'Env gp120 end / Env gp41 start' markers.

HIV-1/SIVcpz complete genomes

Accession	RRP Stem I	Stem IIA	Stem IIB	Stem IIB'	Stem IIC	Stem IIC'	Stem IIA'	Stem III-IV	Position
B.FR.83.HXB2	GGTTCCTTCCCTT	GGGAGCACTA	GGCGGAGCG	CAATGACCGTAC	GGCCAGACAA	TTAGTCTGGTA	TAGTGCAGCAGACAA	TTTTCCTGAGGCTT	7898
01 AE.CF.90.90CF402	A A T	G G	A A	A A G	A A	A A G	A A G	A A G	7961
01 AE.CN.05.FU051	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7880
01 AE.HK.X.HK001	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7259
01 AE.JP.93.93JP.NH1	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7885
01 AE.TH.01.01R414I	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7091
01 AE.TH.02.02OUR769I	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7082
01 AE.TH.90.CM240	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7451
02 AG.CM.02.02CM_16691E	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7049
02 AG.EC.X.EC041	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	6960
02 AG.FR.91.DJ264	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7232
02 AG.GH.03.GHNI196	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7945
02 AG.NG.X.IBNG	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7404
02 AG.SN.98.MP1211	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7100
02 AG.UZ.02.02UZ693	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7052
03 AB.RU.97.KAL153_2	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7075
04 CPX.CV.94.CV032	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7268
05 DF.BE.X.VII1310	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7304
06 CPX.AU.96.BFP90	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7946
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08 BC.CN.97.97CNGX_6F	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7077
09 CPX.GH.96.96GH2911	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7070
10 CD.TZ.96.96TZ_BF061	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7250
11 CPX.GR.X.GR17	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7165
12 BF.AR.99.ARMAL159	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7863
13 CPX.CM.96.H849	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7354
14 BG.ES.99.X397	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7270
15 01B.TH.99.99TH_MU2079	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7264
16 A2D.KR.97.97KR004	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7206
18 CPX.CU.99.CU76	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	6964
19 CPX.CU.99.CU76	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7316
20 BG.CU.03.CB134	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7120
21 A2D.KE.91.KNHI254	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7339
23 BG.CU.03.CB118	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7349
24 BG.CU.03.CB378	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7148
25 CPX.CM.X.101BA	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7299
28 BF.BR.99.BREPML2609	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7050
29 BF.BR.02.BREPML19	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7391
31 BC.BR.02.110PA	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7280
33_01B.WY.05.05MYKL007_1	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7088
A1C.TZ.02.CO3710	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7906
A1CDGKU.ZA.99.CM4	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7874
A1DHK.NO.97.97NOGLI3	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7220
A1GHU.GA.X.VI354	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7090
A2D.KE.99.KER2003	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7081
AP2.CM.02.02CM_3163MN	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7112
ARU.CM.01.01CM_0989MO	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7088
ARU.CM.01.01CM_1296NG	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7075
BC.MM.99.MIDDU103	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7296
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0708.CN.00.HH069	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7374
U.CD.83.83CD003	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7069
U.CD.90.90CD121E12	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7182
U.GR.99.GR303	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7804
U.NL.X.U.NL.95.H10986_D1	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7322
N.CM.02.DJ00131	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7365
N.CM.04.04CM_1131_03	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7441
N.CM.95.YBF30	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7406
N.CM.97.YBF106	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7952
O.BE.87.ANI70	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7969
O.CM.91.MVPS180	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7441
O.CM.96.96CMWB637	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7975
O.SN.99.SEMP1300	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7330
O.BE.87.ANI70	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7482
CPZ.CM.01.SIVcpzCAM13	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7381
CPZ.CM.05.SIVcpzEK505	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7409
CPZ.CM.05.SIVcpzLI57	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7522
CPZ.CM.05.SIVcpzMB66	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7407
CPZ.CM.05.SIVcpzWT145	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7935
CPZ.GA.88.GAB1	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7524
CPZ.TZ.01.TAN1	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	7903
CPZ.US.85.CPZUS	A A T	A A	A A	A A G	A A	A A G	A A G	A A G	Env

HIV-1/SIVcpz complete genomes

	Stem III-IV'	Stem V	Stem V'	Stem I'	
B.FR.83.HXB2	AATGAGCCCAACAGCATCTGTTGCAACTCAGCATTCTGGGGCATCAAGCAGCTCCAGCCAGAAATCCTGGCTGTGAAGAAGATACCTAAGGATCAACAGCTCTGGGGATTGGGGTTCTCTGGAAAAC				8028
A1.KE.94.Q23_17	-----A	-----G	-----T	-----G	7465
A1.RU.03.03R020_06_13	-----T	-----A	-----T	-----C	7499
A1.RW.93.93RW037A	-----T	-----G	-----T	-----G	8009
A1.SE.94.SE7253	-----T	-----A	-----G	-----A	7223
A1.TZ.01.A173	-----T	-----A	-----T	-----A	7237
A1.UA.00.98UA0116	-----T	-----C	-----T	-----A	8015
A1.UG.92.92UG037	-----T	-----A	-----T	-----A	7389
A1.UG.98.98UG57136	-----T	-----AG	-----T	-----G	7218
A2.CD.97.97CDKPE4	5100
A2.CD.97.97CDKRS10	-----T	-----A	-----C	-----G	4144
A2.CD.97.97CDKTB48	-----T	-----GA	-----AGG	-----C	7338
A2.CY.94.94CY0117_41	-----A	-----A	-----G	-----C	7400
A.SN.01.DDI579	-----T	-----CA	-----A	-----A	7232
A.SN.01.DDJ369	-----T	-----AA	-----A	-----G	7250
A.SN.96.DDJ360	-----T	-----CT	-----A	-----G	7214
A.ZA.04.04ZASK162B1	-----T	-----A	-----T	-----A	7483
B.AR.00.ARMS008	-----A	-----C	-----A	-----A	7280
B.AU.96.MBCD36	-----A	-----	-----A	-----A	7418
B.CO.01.PCM074	-----C	-----C	-----G	-----C	7254
B.GA.88.OYI	-----C	-----	-----G	-----C	7567
B.NL.99.671	-----T	-----	-----T	-----C	7582
B.RU.04.04RU129005	-----	-----	-----	-----	7537
B.TH.90.RK132	-----	-----	-----	-----	7357
B.US.90.WEAU160	-----	-----	-----	-----	8035
B.US.98.1058_I1	-----	-----CG	-----A	-----G	7219
C.AR.01.ARG4006	-----A	-----A	-----T	-----A	7219
C.BR.04.04BR013	-----A	-----A	-----T	-----G	7519
C.BR.92.BR025_d	-----A	-----A	-----T	-----G	7365
C.BW.00.00BW07621	-----A	-----A	-----G	-----A	7363
C.ET.86.ETH2220	-----A	-----A	-----G	-----C	7404
C.IN.95.95IN21068	-----AA	-----T	-----A	-----C	7399
C.IN.99.01IN565_I0	-----A	-----A	-----A	-----C	7405
C.KE.00.KER2010	-----A	-----A	-----A	-----C	7217
C.TZ.01.BD9_I1	-----A	-----A	-----T	-----C	7238
C.UY.01.TRA3011	-----A	-----A	-----T	-----A	7205
C.ZA.04.SK164B1	-----A	-----CA	-----G	-----G	7398
C.ZA.05.05ZASK245B1	-----A	-----A	-----T	-----C	7470
C.ZM.02.02ZM115	-----A	-----A	-----G	-----A	8019
C.ZM.96.96ZM651	-----A	-----A	-----T	-----C	7383
D.CD.83.ELI	-----A	-----G	-----T	-----A	7564
D.CD.83.NDK	-----A	-----G	-----T	-----A	7532
D.CM.01.01CM_4412HAL	-----A	-----G	-----T	-----A	7217
D.KE.01.NKU3006	-----A	-----A	-----T	-----A	7271
D.TD.99.MN012	-----A	-----G	-----A	-----A	7239
D.TZ.01.A280	-----A	-----T	-----A	-----A	7216
D.UG.94.94UG114	-----A	-----T	-----A	-----C	7346
D.UG.99.99UGD2550	-----A	-----	-----T	-----A	7247
D.UG.99.99UGK03958	-----A	-----	-----T	-----A	7187
D.ZA.86.R482	-----C	-----G	-----T	-----G	7276
F1.BE.93.VI850	-----A	-----G	-----T	-----A	7305
F1.BR.89.B2126	-----A	-----G	-----T	-----A	7332
F1.BR.93.93BR020_1	-----A	-----G	-----T	-----A	7332
F1.FI.93.FIN9363_1	-----A	-----G	-----T	-----A	7324
F1.FR.96.MP411	-----A	-----G	-----T	-----A	7195
F2.CM.02.02CM_0016BBY	-----A	-----A	-----G	-----C	7187
F2.CM.95.MP255	-----A	-----G	-----T	-----A	7187
F2.CM.95.MP257	-----A	-----G	-----T	-----A	7220
F2.CM.97.CM53657	-----A	-----G	-----T	-----A	7199
G.BE.96.DRCHL	-----A	-----G	-----T	-----A	7967
G.CM.01.01CM_4049HAN	-----A	-----G	-----T	-----A	7217
G.ES.99.X138	-----A	-----G	-----T	-----A	7463
G.KE.93.HH8793_12_1	-----A	-----G	-----T	-----A	7398
G.NG.92.92NG083	-----A	-----G	-----T	-----A	7354
G.SE.93.SE61165	-----A	-----G	-----T	-----A	7446
H.BE.93.VI991	-----AC	-----A	-----G	-----A	7427
H.BE.93.VI997	-----AC	-----CA	-----TG	-----A	7342
H.CF.90.056	-----AC	-----G	-----T	-----A	7347
J.SE.93.SE7887	-----A	-----A	-----G	-----A	7335
J.SE.94.SE7022	-----AN	-----A	-----G	-----A	7342
K.CD.97.EQTB11C	-----A	-----A	-----G	-----A	7211
K.CM.96.MP535	-----A	-----A	-----G	-----A	7188

Table with columns: Accession ID, Stem III-IV', Stem V, Stem V', Stem I', and Nucleotide sequence. The table lists various HIV-1 and SIVcpz strains and their corresponding genomic sequences.

HIV-1/SIVcpz complete genomes

Env gp41

	REF end -	TCAATTTGCACCTGCTGTGGCTTGAATGTAGTTGG	AGT...AATAAA	TCTCTGTG	GAACAGATTGG	AATCAC	ACGACCTGGATGGAGTG	
B.FR.83.HXB2		C-C-C	CT	CT	TT	CA	CA	8116
A1.KE.94.Q23.17		C-AA	CT	AA	TG	CA	CA	7553
A1.RU.03.03RU20.06_13		C-AA	CT	AA	AGTG	A	A	7587
A1.RW.93.93RW037A_1		C-AA	CT	AA	AGTA	A	A	8097
A1.SE.94.SE7253		C-AA	CT	AA	A-TG-A-A	G-AG	T	7311
A1.TZ.01.A173		C-AA	CT	AA	TG-C-A	T	C-A	7325
A1.UA.00.98UA0116		C-AA	CT	AA	AGTC	A	T	8103
A1.UG.92.92UG037		C-AA	CT	AA	TG-A-A	G-AA	T	7477
A1.UG.98.98UG57136		C-AA	CT	AA	A-TG-A	GGCA	T	7306
A2.CD.97.97CDKPE4		C-G	A	AGA	GG	CA	T	5100
A2.CD.97.97CDK510		C-G	A	AGA	GG	CA	T	4232
A2.CD.97.97CDKTB48		C-G	A	AGA	GG	CA	T	7426
A3.CY.94.94CY017_41		C-G	A	AGA	GG	CA	T	7488
A.SN.01.DDI579		C-AA	CT	AA	TG-A-A	G-AA	T	7320
A.SN.01.DDU369		C-AA	CT	AA	TAT	AGTG-A-A	G-A-T	7338
A.SN.96.DDU360		C-AA	CT	AA	A-TG-A-A	G-GA-T	T	7302
A.ZA.04.04ZASK162B1		C-AA	CT	AA	CTAT	G-A	T	7571
B.AR.00.ARMS008		C-AA	CT	AA	TT-C-C	GAA	T	7368
B.AU.96.MBCD36		C-AA	CT	AA	GTAAGTAAATAGAT	GGG	T	7518
B.CO.01.PCM074		C-AA	CT	AA	R	GCA	T	7342
B.GA.88.OYI		C-AA	CT	AA	TACA	G-A	T	7655
B.NL.99.671		C-AA	CT	AA	A-T	A	T	7670
B.RU.04.04RU129005		C-AA	CT	AA	M	A-T	T	7625
B.TH.90.BK132		C-AA	CT	AA	TG	A	T	7445
B.US.90.WEAU160		C-AA	CT	AA	TG	A	T	8123
B.US.98.1058_11		C-AA	CT	AA	AGTT-C	A	T	7305
C.AR.01.ARGA4006		C-AA	CT	AA	TA-T	G-A	T	7307
C.BR.04.04BR013		C-AA	CT	AA	AAA	G-A	T	7607
C.BR.92.BR025_d		C-AA	CT	AA	GG-T	A	T	7453
C.BW.00.00BW07621		C-AA	CT	AA	GG-T	A	T	7451
C.ET.86.ETH220		C-AA	CT	AA	AA	G-A	T	7492
C.IN.95.95IN21068		C-AA	CT	AA	C-G	G-A	T	7487
C.IN.99.01IN565_10		C-AA	CT	AA	A	G-A	T	7493
C.KE.00.KER2010		C-AA	CT	AA	AC-G-T-C	G-CA	T	7305
C.TZ.01.BD9_11		C-AA	CT	AA	AC-G-T-C	G-CA	T	7326
C.UY.01.TRA3011		C-AA	CT	AA	TG-T	C-GA	T	7293
C.ZA.04.SK164B1		C-AA	CT	AA	GG-T	A	T	7486
C.ZA.05.05ZASK245B1		C-AA	CT	AA	CT-T	GG-A	T	7558
C.ZM.02.02ZM115		C-AA	CT	AA	GAA	A-TGCT	G-G	8107
C.ZM.96.96ZM651		C-AA	CT	AA	TAC	C-GG-T	G-A	7471
D.CD.83.ELI		C-AA	CT	AA	CAIC	G-A	T	7652
D.CD.83.NDK		C-AA	CT	AA	A	A-TG	C-GA	7620
D.CM.01.01CM_4412HAL		C-AA	CT	AA	A	TG	A	7305
D.KE.01.NK03006		C-AA	CT	AA	A	GG-T	T	7359
D.TD.99.MN012		C-AA	CT	AA	C	GGT-T	G-GA	7327
D.TZ.01.A280		C-AA	CT	AA	A	TG-T	A	7304
D.UG.94.94UG114		C-AA	CT	AA	CT-A	TG-C	A	7434
D.UG.99.99UGD23550		C-AA	CT	AA	G-A	TG-A	A	7335
D.UG.99.99UGK03958		C-AA	CT	AA	A-AA	A-GG	T	7275
D.ZA.86.R482		C-AA	CT	AA	A	AA	A	7364
F1.BE.93.VI850		C-AA	CT	AA	ACTG	C-GA	T	7393
F1.BR.89.B2126		C-AA	CT	AA	A	G	A	7420
F1.BR.93.93BR020_1		C-AA	CT	AA	A	GG	A	7412
F1.FI.93.FIN9363_1		C-AA	CT	AA	T	GG	GGG	7283
F1.FR.96.MP411		C-AA	CT	AA	A	TG	CA	7275
F2.CM.02.02CM_0016BBY		C-AA	CT	AA	AT	TG	GGAA	7275
F2.CM.95.MP255		C-AA	CT	AA	A	GC	T	7275
F2.CM.95.MP257		C-AA	CT	AA	TAT	TG-C	G-CA-T	7308
F2.CM.97.CM53657		C-AA	CT	AA	AA	TG-A	GGAA	7287
G.BE.96.DRCBL		C-AA	CT	AA	A	TG-A	G-GA	8055
G.CM.01.01CM_4049HAN		C-AA	CT	AA	TAT	A	TG-A	7305
G.ES.99.X138		C-AA	CT	AA	T	T	A	7551
G.KE.93.HH8793_12_1		C-AA	CT	AA	TAT	A-TG-A	G-A	7486
G.NG.92.92NG083		C-AA	CT	AA	A	TG-C	A	7442
G.SE.93.SE6165		C-AA	CT	AA	TAT	A-TG-A	G-A	7534
H.BE.93.VI991		C-AA	CT	AA	T	TG-A	G-CA	7515
H.BE.93.VI997		C-AA	CT	AA	CT	C	G-CA	7430
H.CF.90.056		C-AA	CT	AA	A	A	AGTG-A-C	7435
J.SE.93.SE7887		C-AA	CT	AA	TAT	GG-C	G-GA	7423
J.SE.94.SE7022		C-AA	CT	AA	TAT	GG-C	G-GA	7430
K.CD.97.EQTBI1C		C-AA	CT	AA	A	A	AGTG	7299
K.CM.96.MP535		C-AA	CT	AA	TG	G	CA	7276

B.FR.83.HXB2	TCAATTTGCACCACTGCTGTCGTCGTAAGTCTAATGTTGG.....	AGT.....AATAAA.....	TCTCTGTG.....GAACAGATTGG.....	AATCAC.....	ACGACCTGGATGGAGTGTG	8116
01 AE.CF.90.90CF402	---C---T---	---CT-C---G---	---TAT---GCT---	---CA---	---T-A---A---A---	8179
01 AE.CN.05.FU051	---C---C---	---TAT---G---	---TAT---G---	---G-CA---	---T-A---A---A---	8098
01 AE.HK.X.HK001	---C---CAAC-C---	---TAT---G-CA---	---TAT---G-CA---	---CA---CA-CA---	---T-A---A---A---	7477
01 AE.JP.93.93JP.NH1	---C---CT-C-C---	---G---	---T-T---	---CA---CA-CA---	---T-A---A---A---	8103
01 AE.TH.01.OUP414T	---C---CTAC-C---	---G---	---TAT---G---	---CA---	---T-A---A---A---	7309
01 AE.TH.02.OUP7691	---C---CTAC-C---	---G---	---TAT---G---	---CA---	---T-A---A---A---	7300
01 AE.TH.90.CM240	---C---CT-C-C---	---G---	---T-T---	---CA---	---T-A---A---A---	7669
02 AG.CM.02.02CM.16691E	---C---AA---A---A---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7267
02 AG.EC.X.EC041	---C---A---A---A---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7178
02 AG.FR.91.DJ264	---C---A---A---A---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7450
02 AG.GH.03.GHNJ196	---C---AG-CT-C---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	8163
02 AG.NG.X.IBNG	---C---A---A---A---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7622
02 AG.SN.98.MP1211	---C---A---A---A---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7321
02 AG.UZ.02.02UZ693	---C---AA-T---	---TAT---A-TG-C-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7270
03 AB.RU.97.KAL153_2	---C---C---A---A---	---TAT---A-TG-T-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7293
04 CPX.CV.94.CY032	---C---C---A---A---	---TAT---A-TG-T-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7486
05 DF.BE.X.VII1310	---C---T---AG---C---CT---	---TAT---A-TG-T-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	7522
06 CPX.AU.96.BFP90	---C---TC---AA---TC---CA---	---TAT---A-TG-T-A---	---AA-TAT---ACGG-C-A---	---G-CA-T---	---T-A---C---C-A---	8164
07 BC.CN.97.CM54	---C---T---	---CT-C---	---AA---	---G-A---	---T-A---C---C-A---	7468
08 BC.CN.97.97CNGX_6F	---C---T---	---CT-C---	---AA---	---G-A---	---T-A---C---C-A---	7295
09 CPX.GH.96.96GH2911	---C---AA---C---CT-C---	---TAT---A-TG-A---	---AA---	---G-A---	---T-A---C---C-A---	7288
10 CD.TZ.96.96TZ_BF061	---A---C---CT-C---	---TAT---A-TG-A---	---AA---	---G-A-T---	---T-A---C---C-A---	7468
11 CPX.GR.X.GR17	---C---T---	---CT-C---	---AA---	---G-A-T---	---T-A---C---C-A---	7389
12 BF.AR.99.ARMAL159	---C---G---AA---C---CT---	---TAT---A-TG-A---	---AA---	---G-GA-GAAGAA-T---	---T-AA-A---C---	8081
13 CPX.CM.96.1849	---C---G---AA---C---CT---	---TAT---A-TG-A---	---AA---	---G-A---	---T-A---C---C-A---	7541
14 BG.ES.99.X397	---C---G---AA---C---CT---	---TAT---A-TG-A---	---AA---	---G-GG-C---	---T-A---C---C-A---	7572
15 01B.TH.99.99TH_MU2079	---C---CTT---	---G---	---A-C-A---	---G-CA-T---	---T-T---A---A---	7488
16 A2D.KR.97.97KR004	---C---C---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7482
18 CPX.CU.99.CU76	---C---C---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7424
19 CPX.CU.99.CU77	---C---A---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7182
20 BG.CU.03.CB134	---C---TC---AA---CA---A---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7534
21 A2D.KE.91.KNH1254	---C---TC---AA---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7338
23 BG.CU.03.CB118	---C---AA---AA---C---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7557
24 BG.CU.03.CB378	---C---AA---AA---C---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7567
25 CPX.CM.X.101BA	---C---AA---AA---C---CT---	---TAT---A-TG-C---	---A-TAC---	---G-CA-T---	---T-T---C-A---	7366
28 BF.BR.99.BREPML12609	---C---AA---AA---T---	---TAT---A-TG-T---	---A-TAC---	---G-A---	---T-T---C-A---	7517
29 BF.BR.02.BREPML19	---C---AA---AA---T---	---TAT---A-TG-T---	---A-TAC---	---G-A---	---T-T---C-A---	7268
31 BC.BR.02.110PA	---C---C---T---	---TAT---A-TG-T---	---A-TAC---	---G-A---	---T-T---C-A---	7609
33_01B.WY.05.05MYKL007_1	---C---C---T-C-C---	---TAT---	---A-TAC---	---G-CA-T---	---T-A---A---A---	7498
A1C.TZ.02.CO3710	---C---A---C---C---	---TAT---A-TG-C---	---A-TG-C---	---G-CA-T---	---T-T---C-C-A---	7306
A1CDGKU.ZA.99.CM4	---C---A---C---C---	---TAT---A-TG-C---	---A-TG-C---	---G-CA-T---	---T-T---C-C-A---	8124
A1DHK.NO.97.97NOGL13	---C---AA---AA---C---CT---	---TAT---A-TG-C---	---A-TG-C---	---R-CA---	---T-T---	8092
A1GHU.GA.X.VI354	---C---AA---AA---C---CT---	---TAT---A-TG-C---	---A-TG-C---	---GCA---	---T-T---	7438
A2D.KE.99.KER2003	---A---T---A---C---CT---	---TAT---A-TG-C---	---A-TG-C---	---GCA---	---T-T---	7308
A2F.CM.02.02CM.3163MN	---C---C---CAA---C---CT---	---TAT---A-TG-C---	---A-TG-C---	---G-A---	---T-T---C-A---	7299
AGU.CM.01.01CM.0989MO	---C---C---CAA---C---CT---	---TAT---A-TG-C---	---A-TG-C---	---G-A---	---T-T---C-A---	7330
ARJ.U.CM.01.01CM.1296NG	---C---TC---AA---C---T---	---TAT---A-TG-T---	---A-TG-T---	---G-A-T---	---T-A---T---	7305
BC.CN.96.YNRL9607	---C---C---AG---C---T---	---TAT---	---A-TG-T---	---G-A---	---T-T---	7293
BC.MM.99.MDD1003	---C---MM---A---A---C---	---TAT---	---A-TG-T---	---G-A---	---T-T---	7514
BF1.BR.02.02BR006	---C---T---A---	---TAT---	---A-TA-A---	---C-A---	---T-T---	8002
0708.CN.00.HH069	---C---T---A---	---TAT---	---A-TA-A---	---C-A---	---T-T---	7296
U.CD.83.83CD003	---C---A---C---CT---	---TAT---	---TA-C---	---G-CA-T---	---CT---	7592
U.CD.90.90CD121E12	---C---A---C---CT---	---TAT---	---A-TG-C---	---G-CA-T---	---CT---	7287
U.GR.99.GR303	---C---A---C---CT-G---	---TAT---	---AACT-ACATA-G---	---AA---	---T-C-A---	7403
U.NL.X.U.NL.95.H10986_D1	---C---C---AA---C---CT-C---	---TAT---	---A---GG---	---G-CA---	---T-T---	8022
N.CM.02.DJ00131	CT-A---TAT-CA---AG-C---	---TAT---	---TACW-C---	---GG-A-T---	---TTA---CA-C-A---	7543
N.CM.04.04CM.1131_03	CT-A---TAT-CA---AG-C---	---TAT---	---R-W-TACC---	---GGWA-T---	---TTA---CARM-A---	7586
N.CM.95.YBF30	CT-A---TAT-CA---AG-C---	---TAT---	---AGC-AC---	---TACA-C---	---TTA---CAAC-A---	7667
N.CM.97.YBF106	CT-A---TAT-CA---AG-C---	---TAT---	---AGC-AC---	---TACA-C---	---CTC---CAAC-A---	7622
O.BE.87.AN170	---A---C---TA---AT-A---AATA---AGA-CA---	---TAT---	---TACGGA-GA---	---ATAGGA---	---ATA---ATA---ATA---	8164
O.CM.91.MVPS180	---A---C---TTA---AT-A---AATA---CA-ATCA---	---TAT---	---TACGGA-GA---	---ATA---	---ATA---ATA---ATA---	8190
O.CM.96.96CMBAB637	---A---C---TTA---AT-A---AATA---CAGC-CA---	---TAT---	---TACGGA-GA---	---ATA---	---ATA---ATA---ATA---	7656
O.SN.99.99SEMP1300	---A---C---TTA---AT-A---AATA---CAGG-CA---	---TAT---	---TACGGA-GA---	---ATA---	---ATA---ATA---ATA---	8199
CPZ.CD.90.ANT	---G---C---TCA---A-G---AA-TCC---GTAACTTC-CGAA-CATGTGCAAGAACAGAG-GAT---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7575
CPZ.CM.01.SIVcpzCAM13	---C---G---TTAT-CA---CAA-CA---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7700
CPZ.CM.05.SIVcpzE505	---C---G---TTA---CAA---A-C---C---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7602
CPZ.CM.05.SIVcpzLB7	---C---C---T---T---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7627
CPZ.CM.05.SIVcpzMB6	---C---C---T---T---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7740
CPZ.CM.05.SIVcpzMT145	---C---T---TC---TTAT-CA-G---CAAG-CA---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7628
CPZ.GA.88.GAB1	---C---G---TTA---G-AG---A---CAACTC---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	8156
CPZ.TZ.01.TAN1	---C---G---TTA---G-AG---A---CAACTC---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	7772
CPZ.UZ.85.CPZUS	---C---G---TTAT-CA---T---	---TAT---	---TACW-C---	---AGT-G-C---	---ATA---ATA---ATA---	8124
Env gp41	L_I_C_T_T_A_V_P_W_N_A_S_W.....S_L.....E_O_I_W.....N_H.....T_T_W_M_E_W					



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B. FR. 83. HXB2
ATPAACAAATGGCTGGTATATAAAAATTATTCATAATGATAGGAGGCTGGTAGGTTTGAAGATAAGTTTCCTGCTGATTTTACCATTTATTCAGGAGGATATTCACCATTTATCGTTTC
8376
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Env

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01 AE.TH.02.OUR7691
01 AE.TH.90.CM240
02 AG.CM.02.02CM.16691E
02 AG.EC.x.EC041
02 AG.FR.91.DJ264
02 AG.GH.03.GHNU196
02 AG.NG.x.IBNG
02 AG.SN.98.MP1211
02 AG.UZ.02.02UZ693
03 AB.RU.97.KAL153.2
04 CPX.CV.94.CY032
05 DF.BE.x.VI11310
06 CPX.AU.96.BFP90
07 BC.CN.97.CNE4
08 BC.CN.97.97CNGX.6F
09 CPX.GH.96.96GHZ911
10 CD.TZ.96.96TZ.BF061
11 CPX.GR.x.GR17
12 BF.AR.99.ARMAL159
13 CPX.CM.96.1849
14 BG.ES.99.X397
15 01B.TH.99.99TH.MU2079
16 AZD.KR.97.97KR004
18 CPX.CU.99.CU76
19 CPX.CU.99.CU7
20 BG.CU.03.CB134
21 AZD.KR.91.KNH1254
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 CPX.CM.x.101BA
28 BF.BR.99.BREPM12609
29 BF.BR.02.BREPM119
31 BC.BR.02.110PA
33 01B.MV.05.05MYK1007.1
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A1GHU.GA.x.VI354
AZD.KR.99.KER2003
AF2.CM.02.02CM.3163MN
AGU.CM.01.01CM.0989MO
AHJU.CM.01.01CM.1296NG
BC.CN.96.YNPL9607
BC.MM.99.MINDU103
BF1.BR.02.02BR006
0708.CN.00.HH069
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U.CD.90.90CD121E12
U.GR.99.GR303
U.NL.x.U.NL.95.H10986.D1
N.CM.02.DJ00131
N.CM.04.04CM.1131.03
N.CM.95.YBF30
N.CM.97.YBF106
O.BE.87.ANT70
O.CM.91.MVPE180
O.CM.96.96CMABB637
O.SN.99.SEMP1300
CPZ.CD.90.ANT
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzL87
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.GA.88.GAB1
CPZ.TZ.01.TANI
CPZ.US.85.CPZUS
Env gp41

HIV-1/SIVcpz complete genomes

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Tat Rev intron end	Tat Rev exon 2 start	Tat Premature stop in HXB2	8497
B.FR.83.HXB2	AGACCACCTCCACCC	...CCGACAGCCCGGAGGATATAGTAA	CGGATCCCTTGGCACTTATCTGGGA
A1.KE.94.Q23_17	TTAC	A	G
A1.RU.03.03RU20_06_13	TTAC	GA	CA
A1.RW.93.93RW037A_1	TTAC	GA	CA
A1.SE.94.SE7253	TTAC	GA	CA
A1.TZ.01.A173	TTAC	GA	CA
A1.UA.00.98UA0116	TTAC	GA	CA
A1.UG.92.92UG037	TTAC	GA	CA
A1.UG.98.98UG57136	TTAC	GA	CA
A2.CD.97.97CDKPE4	TTAC	GA	CA
A2.CD.97.97CDKS10	TTAC	GA	CA
A2.CD.97.97CDKTB48	TTAC	GA	CA
A2.CY.94.94CY017_41	TTAC	GA	CA
A.SN.01.DD1579	TTAC	GA	CA
A.SN.01.DDQ369	TTAC	GA	CA
A.SN.96.DDQ360	TTAC	GA	CA
A.ZA.04.04ZASK162B1	TTAC	GA	CA
B.AR.00.ARMS008	TTAC	GA	CA
B.AU.96.MBCD36	TTAC	GA	CA
B.CO.01.PCM074	TTAC	GA	CA
B.GA.88.OYI	TTAC	GA	CA
B.NL.99.671	TTAC	GA	CA
B.RU.04.04RU129005	TTAC	GA	CA
B.TH.90.BK132	TTAC	GA	CA
B.US.90.WEAU160	TTAC	GA	CA
B.US.98.1058_11	TTAC	GA	CA
C.AR.01.ARG4006	TTAC	GA	CA
C.BR.04.04BR013	TTAC	GA	CA
C.BR.92.BR025_d	TTAC	GA	CA
C.BW.00.00BW07621	TTAC	GA	CA
C.ET.86.ETH220	TTAC	GA	CA
C.IN.95.95IN21068	TTAC	GA	CA
C.IN.99.01IN565_10	TTAC	GA	CA
C.KE.00.KER2010	TTAC	GA	CA
C.TZ.01.BD9_11	TTAC	GA	CA
C.UY.01.TRA3011	TTAC	GA	CA
C.ZA.04.SK164B1	TTAC	GA	CA
C.ZA.05.05ZASK245B1	TTAC	GA	CA
C.ZM.02.02ZM115	TTAC	GA	CA
C.ZM.96.96ZM651	TTAC	GA	CA
D.CD.83.ELI	TTAC	GA	CA
D.CD.83.NDK	TTAC	GA	CA
D.CM.01.01CM_4412HAL	TTAC	GA	CA
D.KE.01.NKU3006	TTAC	GA	CA
D.TD.99.MN012	TTAC	GA	CA
D.TZ.01.A280	TTAC	GA	CA
D.UG.94.94UG114	TTAC	GA	CA
D.UG.99.99UGD23550	TTAC	GA	CA
D.UG.99.99UGK03958	TTAC	GA	CA
D.ZA.86.R482	TTAC	GA	CA
F1.BE.93.VI850	TTAC	GA	CA
F1.BR.89.B2126	TTAC	GA	CA
F1.BR.93.93BR020_1	TTAC	GA	CA
F1.FI.93.FIN9363_1	TTAC	GA	CA
F1.FR.96.MP411	TTAC	GA	CA
F2.CM.02.02CM_0016BBY	TTAC	GA	CA
F2.CM.95.MP255	TTAC	GA	CA
F2.CM.95.MP257	TTAC	GA	CA
F2.CM.97.CM53657	TTAC	GA	CA
G.BE.96.DRCL	TTAC	GA	CA
G.CM.01.01CM_4049HAN	TTAC	GA	CA
G.ES.99.X138	TTAC	GA	CA
G.KE.93.HH8793_12_1	TTAC	GA	CA
G.NG.92.92NG083	TTAC	GA	CA
G.SE.93.SE6165	TTAC	GA	CA
H.BE.93.VI991	TTAC	GA	CA
H.BE.93.VI997	TTAC	GA	CA
H.CF.90.056	TTAC	GA	CA
J.SE.93.SE7887	TTAC	GA	CA
J.SE.94.SE7022	TTAC	GA	CA
K.CD.97.EQTB11C	TTAC	GA	CA
K.CM.96.MP535	TTAC	GA	CA

Table with columns: Accession ID, Genomic coordinates, and Nucleotide sequence. Includes headers for 'Tat Rev intron end', 'Tat Rev exon 2 start', 'Tat Premature stop in HXB2', and 'Tat ends most strains'. Rows list various HIV-1/SIVcpz strains and their corresponding genomic regions.

Tat Rev intron end / Tat Rev exon 2 start / Tat Premature stop in HXB2 / Tat ends most strains

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

B.FR.83.HXB2	CGATCTGGGAGCCTGTCCTTTCAGCTACACCGCTTGAGAGACTTACTCTTGATTGTAACG.....	AGGATTTGTGGAACCTTCTGGGAGC.....	AGGGGGTGG	8594
A1.KE.94.Q23.17	CA-CTG-C	C	AGCAGTCTCAAGGGCTGAGACT	8052
A1.RU.03.03RU20_06_13	A-Y-C-G	C	AGCAGTCTCAAGGGCTGAGACT	8086
A1.RW.93.93RW037A_1	CA-C-G	C	AGCAGTCTCAAGGGCTGAGACT	8096
A1.SE.94.SE7253	T-A-C	C	AGCAGTCTCAAGGGCTGAGACT	7810
A1.TZ.01.A173	-C-CC	C	AGCAGTCTCAAGGGCTGAGACT	7824
A1.UA.00.98UA0116	CA-C	C	AGCAGTCTCAAGGGCTGAGACT	8602
A1.UG.92.92UG037	G-A-CA-C	C	AGCAGTCTCAAGGGCTGAGACT	7976
A1.UG.98.98UG57136	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	7805
A2.CD.97.97CDKFE4	T-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	5100
A2.CD.97.97CDKSI0	T-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	4731
A2.CD.97.97CDKTB48	T-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	7925
A2.CY.94.94CY017_41	T-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	7987
A.SN.01.DDI579	T-CAC	C	AGCAGTCTCAAGGGCTGAGACT	7789
A.SN.01.DDU369	T-G-CACA	C	AGCAGTCTCAAGGGCTGAGACT	7837
A.SN.96.DDU360	T-CAC	C	AGCAGTCTCAAGGGCTGAGACT	7771
A.ZA.04.04ZASK162B1	-A-CA-G	C	AGCAGTCTCAAGGGCTGAGACT	8049
B.AR.00.ARMS008	-A	C	AGCAGTCTCAAGGGCTGAGACT	7846
B.AU.96.MBCD36	CT-A	C	AGCAGTCTCAAGGGCTGAGACT	7996
B.CO.01.PCM074	-A	C	AGCAGTCTCAAGGGCTGAGACT	7820
B.GA.88.OYI	-A	C	AGCAGTCTCAAGGGCTGAGACT	8133
B.NL.99.671	G-ET	C	AGCAGTCTCAAGGGCTGAGACT	8148
B.RU.04.04RU129005	AC-GA	C	AGCAGTCTCAAGGGCTGAGACT	8103
B.TH.90.BK132	-A	C	AGCAGTCTCAAGGGCTGAGACT	7923
B.US.90.WEAU160	TC-C-A	C	AGCAGTCTCAAGGGCTGAGACT	8601
B.US.98.1058_11	CT-T	C	AGCAGTCTCAAGGGCTGAGACT	7783
C.AR.01.ARG4006	G-AA	C	AGCAGTCTCAAGGGCTGAGACT	7785
C.BR.04.04BR013	-A-A-A	C	AGCAGTCTCAAGGGCTGAGACT	8106
C.BR.92.BR025_d	T-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	7952
C.BW.00.00BW07621	-A-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7950
C.ET.86.ETH2220	T-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	7991
C.IN.95.95IN21068	-A-AG-G-C	C	AGCAGTCTCAAGGGCTGAGACT	7986
C.IN.99.01INS65_10	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	7992
C.KE.00.KER2010	-A-GCA-A	C	AGCAGTCTCAAGGGCTGAGACT	7804
C.TZ.01.BD9_11	T-AA	C	AGCAGTCTCAAGGGCTGAGACT	7825
C.UY.01.TRA3011	T-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7792
C.ZA.04.SK164B1	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	7985
C.ZA.05.05ZASK245B1	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	8057
C.ZM.02.02ZM115	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	8585
C.ZM.96.96ZM651	-A-CA-A	C	AGCAGTCTCAAGGGCTGAGACT	7970
D.CD.83.ELI	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	8130
D.CD.83.NDK	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	8098
D.CM.01.01CM_4412HAL	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7783
D.KE.01.NKU3006	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7837
D.TD.99.MN012	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7805
D.TZ.01.A280	G-A	C	AGCAGTCTCAAGGGCTGAGACT	7782
D.UG.94.94UG114	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7912
D.UG.99.99UGD23550	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7813
D.UG.99.99UGK09958	-A-A	C	AGCAGTCTCAAGGGCTGAGACT	7753
D.ZA.86.R482	G-C	C	AGCAGTCTCAAGGGCTGAGACT	7782
F1.BE.93.VI850	G-A	C	AGGGGCTGAGG	7871
F1.BR.89.B2126	G-A	C	AGGGGCTGAGG	7898
F1.BR.93.93BR020_1	G-A	C	AGGGGCTGAGG	7898
F1.FI.93.FIN9363_1	G-A	C	AGGGGCTGAGG	7890
F1.FR.96.MP411	G-A	C	AGGGGCTGAGG	7761
F2.CM.02.02CM_0016BBY	G-A	C	AGGGGCTGAGG	7753
F2.CM.95.MP255	G-A	C	AGGGGCTGAGG	7753
F2.CM.95.MP257	G-A	C	AGGGGCTGAGG	7786
F2.CM.97.CM53657	G-A	C	AGGGGCTGAGG	7765
G.BE.96.DRCBL	G-A	C	AACAGTCTCAAGGGCTGAGACT	8554
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G.ES.99.X138	G-A	C	AGGAGCTGAGGGCTGAGACT	8050
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G.NG.92.92NG083	G-A	C	AGGAGCTCAAGGGCTGAGACT	7941
G.SE.93.SE6165	G-A	C	AGGAGCTCAAGGGCTGAGACT	8033
H.BE.93.VI991	G-GAGA	C	GGGAGA	7993
H.BE.93.VI997	G-GAGA	C	GGGAGA	7908
H.CF.90.056	G-GAGA	C	GGGAGA	7913
J.SE.93.SE7887	G-A	C	G-AC	7901
J.SE.94.SE7022	G-A	C	G-AC	7908
K.CD.97.EQTB11C	G-AA	C	CTGAAGG-A-T	7777
K.CM.96.MP535	G-AA	C	CTGAGGG-T	7754

Table with columns for accession numbers (e.g., B.FR.83.HXB2, 01.AE.CF.90.90CF402), sequence coordinates (8594-8623), and nucleotide sequences. The sequences are aligned across multiple rows, showing conserved regions and variations between different HIV-1/SIVcpz strains.

HIV-1/SIVcpz complete genomes

B. FR. 83. HXB2 / Rev CAA->TAA (stop) some groups & subtypes Rev end
 GRAAGCCCTCAATATATGGTGGNAT. CTCTACAGATATGGAGTCAGGAACTA...AAGATAGTGTCTTAGCTTGGCTC...AATGCCACACCCATAGCAGTAGCTAGGAGGACAGATAGG 8708
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 ---G---CT-G---T---TCA---C---G---G---A---AT---T---T---G---A---A---T---A---A---CT---A 7934
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 C-GAT---CT-G---G---T---G---G---A---A---T---T---G---A---A---T---A---A---A 8060
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 ---G---G---T---GTTA---G---G---A---T---T---G---AGT---A---T---A---G---A 8185
 ---G---CT-G---T---GTT---G---C---G---G---A---T---T---G---A---T---A---G---T---A 8101
 ---G---CT-G---T---GTT---G---C---G---G---A---T---T---G---A---T---A---G---T---A 8095
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HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

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HIV-1/SIVcpz Complete Genomes

Table with columns for accession numbers (e.g., B.FR.83.HXB2, 01 AE.CF.90.90CF402), sequence identifiers (e.g., Env gp41, gp160 end), and sequence alignments. The table contains multiple rows of sequence data and labels for various HIV-1/SIVcpz strains and proteins like Env gp41, Nef, and Nef start.

HIV-1/SIVcpz complete genomes

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HIV-1/SIVcpz complete genomes

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HIV-1/SIVcpz complete genomes

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HIV-1/SIVcpz complete genomes

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C.ET.86.ETH2220	AA-A-AGA	GG-A	CA-AG	CA-AG
C.IN.95.95IN21068	AA-A-AGA	GG-A	CA-AG	CA-AG
C.IN.99.01IN565_10	AA-A-AGA	GG-A	CA-AG	CA-AG
C.KE.00.KER2010	AA-A-AGA	GG-A	CA-AG	CA-AG
C.TZ.01.BD9_11	AA-A-AGA	GG-A	CA-AG	CA-AG
C.UY.01.TRA3011	AA-A-AGA	GG-A	CA-AG	CA-AG
C.ZA.04.SK164B1	AA-A-AGA	GG-A	CA-AG	CA-AG
C.ZA.05.05ZASK245B1	AA-A-AGA	GG-A	CA-AG	CA-AG
C.ZM.02.02ZM115	AA-A-AGA	GG-A	CA-AG	CA-AG
C.ZM.96.96ZM651	AA-A-AGA	GG-A	CA-AG	CA-AG
D.CD.83.ELI	AA-A-AGA	GG-A	CA-AG	CA-AG
D.CD.83.NDK	AA-A-AGA	GG-A	CA-AG	CA-AG
D.CM.01.01CM_4412HAL	AA-A-AGA	GG-A	CA-AG	CA-AG
D.KE.01.NKU3006	AA-A-AGA	GG-A	CA-AG	CA-AG
D.TD.99.MN012	AA-A-AGA	GG-A	CA-AG	CA-AG
D.TZ.01.A280	AA-A-AGA	GG-A	CA-AG	CA-AG
D.UG.94.94UG114	AA-A-AGA	GG-A	CA-AG	CA-AG
D.UG.99.99UGD2550	AA-A-AGA	GG-A	CA-AG	CA-AG
D.UG.99.99UGK03958	AA-A-AGA	GG-A	CA-AG	CA-AG
D.ZA.86.R482	AA-A-AGA	GG-A	CA-AG	CA-AG
F1.BE.93.VI850	AA-A-AGA	GG-A	CA-AG	CA-AG
F1.BR.89.B2126	AA-A-AGA	GG-A	CA-AG	CA-AG
F1.BR.93.93BR020_1	AA-A-AGA	GG-A	CA-AG	CA-AG
F1.FI.93.FIN9363	AA-A-AGA	GG-A	CA-AG	CA-AG
F1.FR.96.MP411	AA-A-AGA	GG-A	CA-AG	CA-AG
F2.CM.02.02CM_0016BBY	AA-A-AGA	GG-A	CA-AG	CA-AG
F2.CM.95.MP255	AA-A-AGA	GG-A	CA-AG	CA-AG
F2.CM.95.MP257	AA-A-AGA	GG-A	CA-AG	CA-AG
F2.CM.97.CW53657	AA-A-AGA	GG-A	CA-AG	CA-AG
G.BE.96.DRCL	AA-A-AGA	GG-A	CA-AG	CA-AG
G.CM.01.01CM_4049HAN	AA-A-AGA	GG-A	CA-AG	CA-AG
G.ES.99.X138	AA-A-AGA	GG-A	CA-AG	CA-AG
G.KE.93.HH8793_12_1	AA-A-AGA	GG-A	CA-AG	CA-AG
G.NG.92.92NG083	AA-A-AGA	GG-A	CA-AG	CA-AG
G.SE.93.SE6165	AA-A-AGA	GG-A	CA-AG	CA-AG
H.BE.93.VI991	AA-A-AGA	GG-A	CA-AG	CA-AG
H.BE.93.VI997	AA-A-AGA	GG-A	CA-AG	CA-AG
H.CF.90.056	AA-A-AGA	GG-A	CA-AG	CA-AG
J.SE.93.SE7887	AA-A-AGA	GG-A	CA-AG	CA-AG
J.SE.94.SE7022	AA-A-AGA	GG-A	CA-AG	CA-AG
K.CD.97.EQT811C	AA-A-AGA	GG-A	CA-AG	CA-AG
K.CM.96.MP535	AA-A-AGA	GG-A	CA-AG	CA-AG

	TCF-1 alpha binding site	Nef end \	
B_FR_83_HXB2	TCATCAGTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAAGCTGTCGACATCGAGC.TT
01 AE_CF_90_90CF402	AAAG-A-A-TC-A-AAA-AG--CCAA
01 AE_CN_05_FU051	AA-A-A-AAAA-T-C-AC-T-ATAA-AG--
01 AE_HK_x_HK001	AA-A-A-AAA-----T-ATAA-AG--
01 AE_JP_93_93JP_NH1	AA-A-A-AAA-----T-ATAA-AG--
01 AE_TH_01_0UR4141	AA-A-A-AAA-----T-ATAA-AG--
01 AE_TH_02_0UR7691	AA-A-A-AAA-----T-ATAA-AG--
01 AE_TH_90_CM240	AA-A-A-AAA-----T-ATAA-AG--
02 AG_CM_02_02CM_16691E	AA-A-A-AAA-----T-ATAA-AG--
02 AG_EC_x_EC041	AA-A-A-AAA-----T-ATAA-AG--
02 AG_FR_91_DJ264	AA-A-A-AAA-----T-ATAA-AG--
02 AG_GH_03_GHNJ196	AA-A-A-AAA-----T-ATAA-AG--
02 AG_ING_x_IBNG	AA-A-A-AAA-----T-ATAA-AG--
02 AG_SN_98_MP1211	AA-A-A-AAA-----T-ATAA-AG--
02 AG_UZ_02_02UZ693	AA-A-A-AAA-----T-ATAA-AG--
03 AB_RU_97_KAL153_2	AA-A-A-AAA-----T-ATAA-AG--
04 CPX_CV_94_CV032	AA-A-A-AAA-----T-ATAA-AG--
05 DF_BE_x_VII1310	AA-A-A-AAA-----T-ATAA-AG--
06 CPX_AU_96_BFP90	AA-A-A-AAA-----T-ATAA-AG--
07 BC_CN_97_CNS4	AA-A-A-AAA-----T-ATAA-AG--
08 BC_CN_97_97CNX_6F	AA-A-A-AAA-----T-ATAA-AG--
09 CPX_GH_96_96GH2911	AA-A-A-AAA-----T-ATAA-AG--
10 CD_TZ_96_96TZ_BF061	AA-A-A-AAA-----T-ATAA-AG--
11 CPX_GR_x_GR17	AA-A-A-AAA-----T-ATAA-AG--
12 BF_AR_99_ARMAL159	AA-A-A-AAA-----T-ATAA-AG--
13 CPX_CM_96_1849	AA-A-A-AAA-----T-ATAA-AG--
14 BG_ES_99_X397	AA-A-A-AAA-----T-ATAA-AG--
15 01B_TH_99_99TH_MU2079	AA-A-A-AAA-----T-ATAA-AG--
16 AZD_KR_97_97KR004	AA-A-A-AAA-----T-ATAA-AG--
18 CPX_CU_99_CU76	AA-A-A-AAA-----T-ATAA-AG--
19 CPX_CU_99_CU77	AA-A-A-AAA-----T-ATAA-AG--
20 BG_CU_03_CB134	AA-A-A-AAA-----T-ATAA-AG--
21 AZD_KE_91_KNH1254	AA-A-A-AAA-----T-ATAA-AG--
23 BG_CU_03_CB118	AA-A-A-AAA-----T-ATAA-AG--
24 BG_CU_03_CB378	AA-A-A-AAA-----T-ATAA-AG--
25 CPX_CM_x_101BA	AA-A-A-AAA-----T-ATAA-AG--
28 BF_BR_99_BREPM12609	AA-A-A-AAA-----T-ATAA-AG--
29 BF_BR_02_BREPM119	AA-A-A-AAA-----T-ATAA-AG--
31 BC_BR_02_110PA	AA-A-A-AAA-----T-ATAA-AG--
33_01B_WY_05_05MYKL007_1	AA-A-A-AAA-----T-ATAA-AG--
A1C_TZ_02_C03710	AA-A-A-AAA-----T-ATAA-AG--
A1CDGK_ZA_99_CM4	AA-A-A-AAA-----T-ATAA-AG--
A1DGH_NO_97_97NOGLL3	AA-A-A-AAA-----T-ATAA-AG--
A1GHU_GA_x_VI354	AA-A-A-AAA-----T-ATAA-AG--
AP2_KE_99_XER2003	AA-A-A-AAA-----T-ATAA-AG--
AP2_CM_02_02CM_3163MN	AA-A-A-AAA-----T-ATAA-AG--
ARU_CM_01_01CM_0989MO	AA-A-A-AAA-----T-ATAA-AG--
ARU_CM_01_01CM_1296NG	AA-A-A-AAA-----T-ATAA-AG--
BC_CN_96_YNRL9607	AA-A-A-AAA-----T-ATAA-AG--
BC_MM_99_MIDDU103	AA-A-A-AAA-----T-ATAA-AG--
BF1_BR_02_02BR006	AA-A-A-AAA-----T-ATAA-AG--
0708_CN_00_HH069	AA-A-A-AAA-----T-ATAA-AG--
U_CD_83_83CD003	AA-A-A-AAA-----T-ATAA-AG--
U_CD_90_90CD121E12	AA-A-A-AAA-----T-ATAA-AG--
U_GR_99_GR303	AA-A-A-AAA-----T-ATAA-AG--
U_NL_x_U_NL_95_H10986_D1	AA-A-A-AAA-----T-ATAA-AG--
N_CM_02_DJ00131	AA-A-A-AAA-----T-ATAA-AG--
N_CM_04_04CM_1131_03	AA-A-A-AAA-----T-ATAA-AG--
N_CM_95_YBF30	AA-A-A-AAA-----T-ATAA-AG--
N_CM_97_YBF106	AA-A-A-AAA-----T-ATAA-AG--
O_BE_87_ANI70	AA-A-A-AAA-----T-ATAA-AG--
O_CM_91_MVPS180	AA-A-A-AAA-----T-ATAA-AG--
O_CM_96_96CMWAB637	AA-A-A-AAA-----T-ATAA-AG--
O_SN_99_SEMP1300	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CD_90_ANT	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CM_01_SIVcpzCAM13	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CM_05_SIVcpzEK505	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CM_05_SIVcpzL187	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CM_05_SIVcpzMB66	AA-A-A-AAA-----T-ATAA-AG--
CPZ_CM_05_SIVcpzWT145	AA-A-A-AAA-----T-ATAA-AG--
CPZ_GA_88_GAB1	AA-A-A-AAA-----T-ATAA-AG--
CPZ_TZ_01_TAN1	AA-A-A-AAA-----T-ATAA-AG--
CPZ_US_85_CFPZUS	AA-A-A-AAA-----T-ATAA-AG--
NefH_H_V_A_R_E_L_H_P_E_Y_F.....K_N_C*Nef end /TGA-GA----

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz
complete genomes

	NP-kappa-B II	NP-kappa-B I	SPI-III
B.FR.83.HXB2GCTACAA.....GGGACTTTCC.....A.GGGAGCGG
A1.KE.94.Q23_17T-GACT.....G.....G-T
A1.RU.03.03RU20_06_13GAC..TGAAGTT.....G.....G-T
A1.RW.93.93RW037AGAC-A.....G.....G-T
A1.SE.94.SE7253GAC.....A-C.....G-T
A1.TZ.01.A173GAC-TGAAGTT.....G.....G-T
A1.UA.00.98UA0116GACT.....G.....G-T
A1.UG.92.92UG0537GACT.....G.....G-T
A1.UG.98.98UG57136GACT.....G.....G-T
A2.CD.97.97CDKFE4GAC-CAGAAGTT.....A-G.....G-T
A2.CD.97.97CDK510GACG.....G.....G-T
A2.CD.97.97CDKTB48GAC-CAGAAGTT.....G.....G-T
A2.CY.94.94CY017_41GAC-CAGAAGTT.....G.....G-T
A.SN.01.DD1579GAC.....A.....G-T
A.SN.01.DD369GAC-CAGAAGTTG..CTGACAGGACTTTCGCTGA.....G-T
A.SN.96.DD4360GAC-CAGAAGTTG..CTGACAGGACTTTCGCTGA.....G-T
A.ZA.04.04ZASK162B1T.....G.....G-T
B.AR.00.ARMS008TGGGACTTTCATCCGCTGGGACTTTCCAAGGCGGTGGCCGGGTGACT-AG-G.....AA-A
B.AU.96.MBCD36T.....G.....G-T
B.CO.01.PCM074T.....G.....G-T
B.GA.88.OYIT.....G.....G-T
B.NL.99.671T.....G.....G-T
B.RU.04.04RU1129005T.....G.....G-T
B.TH.90.RK132T.....A.....G-T
B.US.90.WEAU160T.....A.....G-T
B.US.98.1058_11T.....A.....G-T
C.AR.01.ARG4006GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-G-A
C.BR.04.04BR013GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.BR.92.BR025_dGACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.BW.00.00BW07621GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.ET.86.ETH2220GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.IN.95.95IN21068GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.IN.99.01IN565_10GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.KE.00.KER2010GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.TZ.01.BD9_11GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.UY.01.TRA3011GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.ZA.04.SK164B1GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.ZA.05.05ZASK245B1GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.ZM.02.02ZM115GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
C.ZM.96.96ZM651GACT--GAC-CAG.....CT.....ACTG.GGGCGTTCCA-A
D.CD.83.ELIT.....G.....G-T
D.CD.83.NDKT.....G.....G-T
D.CM.01.01CM_4412HALT.....G.....G-T
D.KE.01.NKU3006T.....G.....G-T
D.TD.99.MN012T.....G.....G-T
D.TZ.01.A280T.....G.....G-T
D.UG.94.94UG114T.....G.....G-T
D.UG.99.99UGD2550T.....G.....G-T
D.UG.99.99UGK03958T.....G.....G-T
D.ZA.86.R482T.....G.....G-T
F1.BE.93.VI850GAC-CAGAAGAA.....TCTAAAA.....A-G-CG
F1.BR.89.B2126GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F1.BR.93.93BR020_1GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F1.FI.93.FIN9363GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F1.FR.96.MP411GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F2.CM.02.02CM_0016BBYGAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F2.CM.95.MP255GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F2.CM.95.MP257GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
F2.CM.97.CM53657GAC-CAGAAGA.....ATCT.AAA.....A-G-CG
G.BE.96.DRCBLGAC-AGGGACTTTAA.....GTTGCTGACAAA.....G
G.CM.01.01CM_4049HANGAC-AGGGACTTTAA.....GTTGCTGACAAA.....G
G.ES.99.X138GAC-CAGAAGTTG.....CTGACAAA.....G
G.KE.93.HH8793_12_1GAC-A.....G.....G
G.NG.92.92NG083GAC-A.....G.....G
G.SE.93.SE6165GAC-A.....G.....G
H.BE.93.VI991GAC-CAGAAGAT.....TCTATACA.....G-T
H.BE.93.VI997GAC-CAGAAGAT.....TCTATACA.....G-T
H.CF.90.056T--GCG.....G.....G-T
J.SE.93.SE7887T--GCG.....G.....G-T
J.SE.94.SE7022T--GCG.....G.....G-T
K.CD.97.EQTB11CT--GCG.....G.....G-T
K.CM.96.MP535T--GCG.....G.....G-T

	NF-kappa-B_II	NF-kappa-B_I	SPI-III
B.FR.83.HXB2GCTACAA.....GGGACTTTCC.....GGGACTTTCC.....
01 AE.CF.90.90CF402	.GACT--GAC-AAGAGTTGCTG.....A.GGGAGCGG
01 AE.CN.05.FJ051T--ACT.....TCTAACTAG--T
01 AE.HK.x.HK001T--ACT.....A--A--G--T
01 AE.JP.93.93JP.NH1T--ACT.....A--G--T
01 AE.TH.01.OUR4141T--ACT.....A--G--T
01 AE.TH.02.OUR7691T--ACT.....A--G--T
02 AG.CM.02.02CM_16691ET--ACT.....A--G--T
02 AG.EC.x.EC041T--ACT.....A--G--T
02 AG.FR.91.DJ264T--ACT.....A--G--T
02 AG.GH.03.GHNJ196T--ACT.....A--G--T
02 AG.NG.x.IBNGT--ACT.....A--G--T
02 AG.SN.98.MP1211T--ACT.....A--G--T
02 AG.UZ.02.02UZ693T--ACT.....A--G--T
03 AB.RU.97.KAL153_2T--ACT.....A--G--T
04 CPX.CV.94.CV032T--ACT.....A--G--T
05 DF.BE.x.VI1310T--ACT.....A--G--T
06 CPX.AU.96.BEP90T--ACT.....A--G--T
07 BC.CN.97.CNS4T--ACT.....A--G--T
08 BC.CN.97.97CNGX_6FT--ACT.....A--G--T
09 CPX.GH.96.96GH2911T--ACT.....A--G--T
10 CD.TZ.96.96TZ_BF061T--ACT.....A--G--T
11 CPX.GR.x.GR17T--ACT.....A--G--T
12 BF.AR.99.ARMA159T--ACT.....A--G--T
13 CPX.CM.96.1849T--ACT.....A--G--T
14 BG.ES.99.X397T--ACT.....A--G--T
15 01B.TH.99.99TH_MU2079T--ACT.....A--G--T
16 AZD.KR.97.97KR004T--ACT.....A--G--T
18 CPX.CU.99.CU76T--ACT.....A--G--T
19 CPX.CU.99.CU77T--ACT.....A--G--T
20 BG.CU.03.CB134T--ACT.....A--G--T
21 AZD.KE.91.KNH1254T--ACT.....A--G--T
23 BG.CU.03.CB118T--ACT.....A--G--T
24 BG.CU.03.CB378T--ACT.....A--G--T
25 CPX.CM.x.101BAT--ACT.....A--G--T
28 BF.BR.99.BREPM12609T--ACT.....A--G--T
29 BF.BR.02.BREPM119T--ACT.....A--G--T
31 BC.BR.02.110PAT--ACT.....A--G--T
33_01B.WY.05.05MYKL007_1T--ACT.....A--G--T
A1C.TZ.02.CO3710T--ACT.....A--G--T
A1CDGKU.ZA.99.CM4T--ACT.....A--G--T
A1DHK.NO.97.97NOGL13T--ACT.....A--G--T
A1GHU.GA.x.VI354T--ACT.....A--G--T
A2D.KE.99.KER2003T--ACT.....A--G--T
AP2.CM.02.02CM_3163MNT--ACT.....A--G--T
ARU.CM.01.01CM_0989MOT--ACT.....A--G--T
ARU.CM.01.01CM_1296NGT--ACT.....A--G--T
BC.CN.96.YNRL9607T--ACT.....A--G--T
BC.MM.99.MIDDU103T--ACT.....A--G--T
BF1.BR.02.02BR006T--ACT.....A--G--T
0708.CN.00.HH069T--ACT.....A--G--T
U.CD.83.83CD003T--ACT.....A--G--T
U.CD.90.90CD121E12T--ACT.....A--G--T
U.GR.99.GR303T--ACT.....A--G--T
U.NL.x.U.NL_95_H10986_D1T--ACT.....A--G--T
N.CM.02.DJ00131T--ACT.....A--G--T
N.CM.04.04CM_1131_03T--ACT.....A--G--T
N.CM.95.YBF30T--ACT.....A--G--T
N.CM.97.YBF106T--ACT.....A--G--T
O.BE.87.ANI70T--ACT.....A--G--T
O.CM.91.MVPS180T--ACT.....A--G--T
O.CM.96.96CMWAB637T--ACT.....A--G--T
O.SN.99.SEMP1300T--ACT.....A--G--T
CPZ.CD.90.ANTT--ACT.....A--G--T
CPZ.CM.01.SIVcpzCAM13T--ACT.....A--G--T
CPZ.CM.05.SIVcpzEK505T--ACT.....A--G--T
CPZ.CM.05.SIVcpzLI87T--ACT.....A--G--T
CPZ.CM.05.SIVcpzMB66T--ACT.....A--G--T
CPZ.CM.05.SIVcpzMT145T--ACT.....A--G--T
CPZ.GA.88.GAB1T--ACT.....A--G--T
CPZ.TZ.01.TAN1T--ACT.....A--G--T
CPZ.US.85.CPZUST--ACT.....A--G--T

HIV-1/SIVcpz complete genomes

HIV-1/SIVcpz complete genomes

Accession	SPI-III	SPI-II	SPI-I	TATA box	3' LTR	U3 end	3' ITR repeat start	9583
B.FR.83.HXB2	TTGCC	TTGG	TTGGGAGTGGC	GAGCCCTCAGATCCTCATATAGACAGCTGCTTTTGGC	TGTACTGGGCTCTC	TGGTTAG	ACCGATCTCAGCCTGGGAGCTCTCTGGC	9583
A1.KE.94.Q23.17	TT	AGT	C-A	G	C	T	T	9035
A1.RU.03.03RU20.06_13	TT	AGT	T-A	G	C	T	T	9089
A1.RW.93.93RW037A	TT	AGT	T-A	C	C	T	T	9595
A1.SE.94.SET253	TT	AGT	T-A	G	C	T	T	8793
A1.TZ.01.A173	TT	AGT	T-A	G	C	T	T	8766
A1.UA.00.98UA0116	TT	AGT	T-A	G	C	T	T	9605
A1.UG.92.92UG037	TT	AGT	T-A	G	C	T	T	8992
A1.UG.98.98UG57136	TT	AGT	T-A	G	C	T	T	8787
A2.CD.97.97CDKFE4	TT	AGT	T-A	G	C	T	T	5100
A2.CD.97.97CDKS10	TT	AGT	T-A	G	C	T	T	5323
A2.CD.97.97CDKTB48	TT	AGT	T-A	G	C	T	T	8957
A2.CY.94.94CY017_41	TT	AGT	T-A	G	C	T	T	9008
A.SN.01.DDL1579	TT	AGT	T-A	G	C	T	T	8781
A.SN.01.DD4369	TT	AGT	T-A	G	C	T	T	8841
A.SN.96.DD4360	TT	AGT	T-A	G	C	T	T	8757
A.ZA.04.04ZASK162B1	TT	AGT	T-A	G	C	T	T	9076
B.AR.00.ARMS008	C	C	C	G	C	T	A	8850
B.AU.96.MBCD36	C	CG	G	G	C	C	A	8669
B.CO.01.PCM074	C	CC	T-A	G	C	C	A	8839
B.GA.88.OYI	C	CC	G	C	C	C	C	9137
B.NL.99.671	C	A	A	G	C	C	A	9130
B.RU.04.04RUL29005	C	D.Y	A	G	C	C	A	3098
B.TH.90.EK132	C	C	G	G	C	C	A	8918
B.US.90.WEAU160	C	CA	A	G	C	C	A	9583
B.US.98.1058.11	C	C	G	C	C	C	A	8784
C.AR.01.ARG4006	T	T	T	C	C	T	A	8802
C.BR.04.04BR013	T	T	C	C	C	T	A	9050
C.BR.92.BR025.D	T	CC	C	A	C	C	A	8952
C.BW.00.00BW07621	T	C	A	G	C	C	A	8940
C.ET.86.ETH2220	G	T	C	A	C	T	C	8983
C.IN.95.95IN21068	T	C	T	C	A	C	A	8956
C.IN.99.01IN565.10	T	C	T	C	A	C	A	9004
C.KE.00.KER2010	T	C	A	T	C	A	C	8797
C.TZ.01.BD9.11	TT	C	T	C	A	C	C	8819
C.UY.01.TRA3011	GA	T	CCT	C	A	G	T	8808
C.ZA.04.SK164B1	G	T	C	A	C	A	G	8979
C.ZA.05.05ZASK245B1	G	T	C	A	C	A	G	9047
C.ZM.02.02ZM115	G	T	CC	C	C	A	G	9581
C.ZM.96.96ZM651	T	C	T	C	A	C	T	8957
D.CD.83.ELI	A	C	D	T	A	G	T	9122
D.CD.83.NDK	C	T	T	A	C	T	T	9090
D.CM.01.01CM.4412HAL	C	C	C	C	C	C	C	8379
D.KE.01.NKU3006	AC	A	G	G	T	T	T	8828
D.TD.99.MN012	AA	A	G	C	C	C	A	8815
D.TZ.01.A280	AA	A	G	C	C	C	A	8775
D.UG.94.94UG114	AA	A	G	C	C	C	A	8900
D.UG.99.99UGD23550	AA	A	G	C	C	C	A	8805
D.UG.99.99UGK09958	AA	A	G	C	C	C	A	8762
D.ZA.86.R482	C	C	C	C	C	C	C	8640
F1.BE.93.VI850	CCAG	A	C	C	C	C	A	8881
F1.BR.89.BZ126	GCCAG	A	T	C	C	C	A	8934
F1.BR.93.93BR020_1	G	C	A	G	A	C	C	8916
F1.FI.93.FIN9363	CCAG	A	C	C	C	T	A	8903
F1.FR.96.MP411	C	C	C	C	C	C	C	8578
F2.CM.02.02CM.0016BBY	F2	CM	02	02	CM	0016	BBY	8349
F2.CM.95.MP255	F2	CM	95	MP255				8555
F2.CM.95.MP257	F2	CM	95	MP257				8588
F2.CM.97.CM53657	F2	CM	97	CM53657				8762
G.BE.96.DRCBL	C	A	G	C	C	C	C	9570
G.CM.01.01CM.4049HAN	C	C	C	C	C	C	C	8367
G.ES.99.X138	C	A	G	C	C	C	A	8978
G.KE.93.HH8793_12_1	C	A	A	G	C	C	A	8986
G.NG.92.92NG083	C	A	A	G	C	C	A	8935
G.SE.93.SE6165	C	A	A	G	C	C	A	9027
H.BE.93.VI991	T	T	C	A	C	T	A	9001
H.BE.93.VI997	C	T	T	T	A	C	T	8900
H.CF.90.056	AT	T	C	A	C	C	T	8901
J.SE.93.SET887	G	T	T	A	C	T	T	8882
J.SE.94.SET022	G	T	T	A	C	T	T	8892
K.CD.97.EQTB11C	C	C	C	C	C	C	C	8594
K.CM.96.MP535	C	C	C	C	C	C	C	8598



	SPI-III	SPI-II	SPI-I	TATA box	3' LTR U3 end	3' LTR U3 end	3' LTR repeat start	
B.F.R. 83.HXB2	TGGCC.TGG..CGGGAC.TGGGGAGTGGC.GAGCCCTCAGATCCTCATATAGACAGCTGCTTTTGGC.TGTACTGGGCTCTC.TGGTTAG.ACCAGATCTGAGCCCTGGAGCTCTCTGGC.....							9583
01 AE.CF.90.90CF402								9707
01 AE.CN.05.FJ051								9598
01 AE.HK.x.HK001								8363
02 AE.JP.93.93JP.NH1								9584
01 AE.TH.01.OUR4141								8402
01 AE.TH.02.OUR7691								8390
01 AE.TH.90.CM240								9149
02 AG.CM.02.02CM.1669LE								8383
02 AG.EC.x.ECU41								8291
02 AG.FR.91.DJ264								8939
02 AG.GH.03.GHNJ196								9710
02 AG.NG.x.IENG								9110
02 AG.SN.98.MP1211								8809
02 AG.UZ.02.02UZ693								8759
03 AB.RU.97.KAL153_2								8759
04 CPX.CY.94.CY032								8998
05 DF.BE.x.VI1310								9029
06 CPX.AU.96.BFP90								9640
07 BC.CN.97.CN54								8955
08 BC.CN.97.97CNGX 6F								8782
09 CPX.GH.96.96GH2911								8755
10 CD.TZ.96.96TZ.BF061								8937
11 CPX.GR.x.GR17								8884
12 BF.AR.99.ARMA159								9568
13 CPX.CM.96.1849								8916
14 BG.ES.99.X397								8997
15 O1B.TH.99.99TH.MU2079								8957
16 AZD.KR.97.97KR004								9011
18 CPX.CU.99.CU76								8316
19 CPX.CU.99.CU7								8049
20 BG.CU.03.CB134								8954
21 AZD.KE.91.KNH1254								8828
23 BG.CU.03.CB118								8988
24 BG.CU.03.CB378								9033
25 CPX.CM.x.101BA								8862
28 BF.BR.99.BREPM12609								8400
29 BF.BR.02.BREPM119								8680
31 BC.BR.02.110PA								8908
33_O1B.WY.05.05MYKL007_1								8973
A1C.TZ.02.C03710								8616
A1CDGKU.ZA.99.CM4								9629
A1DHK.NO.97.97NOGLT3								9573
A1GHU.GA.x.VI354								8907
AP2.KE.99.KER2003								8797
AP2.CM.02.02CM.3163MN								8382
AGU.CM.01.01CM.0989MO								8428
AHUU.CM.01.01CM.1296NG								8374
BC.CN.96.YNKL9607								8083
BC.MM.99.mIDU103								8972
BF1.BR.02.02BR006								9437
0708.CN.00.HH069								8783
U.CD.83.83CD003								9060
U.CD.90.90CD121E12								8757
U.GR.99.GR303								8893
U.NL.x.U.NL_95.H10986_D1								9510
N.CM.02.DJ00131								8938
N.CM.04.04CM.1131_03								8975
N.CM.95.YBF30								9182
N.CM.97.YBF106								9045
O.BE.87.ANT70								9704
O.CM.91.MVP5180								9700
O.CM.96.96CMBB637								9208
O.SN.99.SEMP1300								9736
CPZ.CD.90.ANT								9046
CPZ.CM.01.SIVcpzCAM13								8623
CPZ.CM.05.SIVcpzEK505								9080
CPZ.CM.05.SIVcpzLB7								9116
CPZ.CM.05.SIVcpzMB66								9227
CPZ.CM.05.SIVcpzMT145								9155
CPZ.GA.88.GAB1								9276
CPZ.TZ.01.TAN1								9276
CPZ.US.85.CPZUS								9648

HIV-1/SIVcpz complete genomes

Poly-A signal | 2° structure region - extensive secondary structure in this region | 3.LTR P repeat end\3.LTR.U5 start see Rizvi J Virol 67:2681-8(1993)

Table with 4 columns: Accession ID (e.g., B.FR.83.HXB2), Sequence (e.g., TAACTAGGGAACCCACTGCTT.AAGCCTCATAAAGCTTGCCTTGGAG.TGCTTCAAGTAGTGTGTCGCCGCTGTTGGTACTAGAGATCCCTCAGACCCCTTTTAGTCAAGTGTGGAAAA), Position (9710), and another Accession ID (e.g., 9834).



3' LTR U5 end \	9719
TCTCTAGCA.....	
B.FR.83.HXB2	9160
A1.KE.94.Q23_17	9159
A1.RU.03.03RU20_06_13	9644
A1.RW.93.93RW037A_1	8813
A1.SE.94.SE7253	8766
A1.TZ.01.A173	9740
A1.UA.00.98UA0116	8999
A1.UG.92.92UG037	8807
A1.UG.98.98UG57136	5100
A2.CD.97.97CDKFE4	5323
A2.CD.97.97CDKS10	8972
A2.CD.97.97CDKTB48	9060
A2.CY.94.94CY017_41	8801
A.SN.01.DDI579	8861
A.SN.01.DDJ369	8777
A.SN.96.DDJ360	9109
A.ZA.04.04ZASK162B1	
B.AR.00.ARMS008	8873
B.AU.96.MBCD36	8669
B.CO.01.PCM074	8859
B.GA.88.OYI	9190
B.NL.99.671	9155
B.RU.04.04RU129005	9160
B.TH.90.BK132	8995
B.US.90.WEAU160	9719
B.US.98.1058_11	8834
C.AR.01.ARG4006	8822
C.AR.04.04BR013	9050
C.BR.92.BR025_d	8959
C.BW.00.00BW07621	9047
C.ET.86.ETH220	9031
C.IN.95.95IN21068	9002
C.IN.99.01IN565_10	9054
C.KE.00.KER2010	8817
C.TZ.01.BD9_11	8819
C.UY.01.TRA3011	8828
C.ZA.04.SK164B1	9011
C.ZA.05.05ZASK245B1	9079
C.ZM.02.02ZM115	9630
C.ZM.96.96ZM651	9009
D.CD.83.ELI	9176
D.CD.83.NDK	9143
D.CM.01.01CM_4412HAL	8379
D.KE.01.NKU3006	8848
D.TD.99.MN012	8850
D.TZ.01.A280	8775
D.TZ.01.A280	8952
D.UG.94.94UG114	8825
D.UG.99.99UGD23550	8782
D.UG.99.99UGK09958	8640
D.ZA.86.R482	8903
F1.BE.93.VI850	9030
F1.BR.89.B2126	8968
F1.BR.93.93BR020_1	8925
F1.FI.93.FIN9363	8578
F1.FR.96.MP411	8349
F2.CM.02.02CM_0016BBY	8555
F2.CM.95.MP255	8588
F2.CM.95.MP257	8782
F2.CM.97.CM53657	9705
G.BE.96.DRCBL	8367
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G.NG.92.92NG083	9074
G.SE.93.SE6165	9056
H.BE.93.VI991	8955
H.BE.93.VI997	8953
H.CF.90.056	8943
J.SE.93.SE7887	8953
J.SE.94.SE7022	8594
K.CD.97.EQTB11C	8598
K.CM.96.MP535	

