Characterization of HIV-1 genetic diversity and antiretroviral resistance in the state of Maranhão, Northeast Brazil

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SUPPLEMENTARY MATERIAL

HIV-1 Sequences used in the phylogenetic analysis shown in Figure 1:

A1.KE.1994.Q23_17.AF004885; A1.KE.2000.KER2009.AF457053; A2.CD.1997.97CDKFE4.AF286240; A2.CD.1997.97CDKTB48.AF286238; A3.SN.1996.DDJ360.AY521630; A3.SN.2001.DDJ369.AY521631; A4.CD.1997.97CD_KC22.AM000053; A4.CD.1997.97CD_KTB13.AM000054; A6.RU.2003.03RU20_06_13.AY500393; A6.UZ.2002.02UZ652.AY829203; B.AR.1999.ARM055.AY037282; B.AR.2000.ARM056.AY037269; B.AR.2002.02AR114146.DQ383746; B.AU.1986.MBC200.AF042100; B.BR.1989.BZ167.AY173956; B.BR.1990.BZ167.AB485641; B.BR.2002.02BR002.DQ358805; B.BR.2002.02BR008.DQ358808; B.BR.2003.BREPM1038.EF637048; B.BR.2003.BREPM2012.EF637046; B.BR.2004.BREPM1066.FJ195090; B.BR.2004.BREPM1070.FJ195086; B.BR.2005.BREPM1081.FJ195091; B.BR.2005.BREPM1084.FJ195088; B.BR.2005.BREPM1093.FJ195089; B.FR.1983.HXB2-LAI-IIIB-BRU.K03455; B.FR.1985.NL43xWC001.AF003887; B.US.1985.Ba_L.AB221005; B.US.1986.AD87_ADA.AF004394; B.US.1991.DH12_3.AF069140; B.US.1991.U.S.AB485640; B.US.1997.ARES2.AB078005; C.BR.2002.02BR2022.JN692434; C.BR.2004.04BR013.AY727522; C.BR.2004.04BR021.AY727523; C.BR.2007.BP00040_LH01.JN687655; C.BW.1996.96BW01B03.AF110959; C.IN.1993.IN101.AB023804; C.IN.1995.95IN21068.AF067155; C.ZA.2003.03ZASK212B.DQ978981; D.KE.2001.NKU3006.AF457090; D.UG.1991.UG270.AB485650; D.UG.1998.98UG57146.AF484513; D.UG.1999.99UGA07412.AF484477; F1.AR.2002.ARE933.DQ189088; F1.BR.1989.BZ126.AY173957; F1.BR.1990.BZ163.AB485656; F1.BR.1993.93BR020_1.AF005494; F1.BR.2002.02BR082.FJ771006; F1.BR.2007.07BR844.FJ771010; F1.BR.2010.10BR_PE107.KJ849782; F1.BR.2010.10BR_RJ015.KJ849791; F1.BR.2010.10BR_RJ055.KT427774; F1.BR.2010.10BR_SP029.KT427814; F1.BR.2010.10BR_SP070_1.KT427663; F1.BR.2010.DEMF110BR015.KU749395; F1.BR.2011.DEMF111BR037.KU749396; F1.FI.1993.FIN9363.AF075703; F1.FR.1996.96FR-MP411.AJ249238; F1.RO.1996.BCI_R07.AB485658; F2.CM.1995.95CM-MP255.AJ249236; F2.CM.1997.CM53657.AF377956; F2.CM.2010.DEMF210CM001.JX140672; F2.CM.2011.DEMF211CM025.KU749420; G.GH.2003.GHNJ175.AB231893; G.KE.1993.HH8793.AB485662; G.SE.1993.SE6165_G6165.AF061642; H.BE.1993.VI991.AF190127; H.CD.2001.CG-0536-02_NGSD14.KY392777; J.AO.1993.93AOHDC253.KU310620; J.CD.1997.J_97DC_KTB147.EF614151; J.SE.1993.SE9280_7887.AF082394; K.CD.1997.97ZEEQTBI1.AJ249235; K.CM.1996.96CM-MP535.AJ249239.
HIV-1 Sequences used in the phylogenetic analysis shown in Figure 2:

40_BF.BR.2004.04BRRJ115.EU735538; 40_BF.BR.2005.05BRRJ200.EU735539;
40_BF.BR.2004.04BRSQ46.EU735540; 40_BF.BR.2005.05BRRJ055.EU735537;
90_BF1.BR.2009.BRTO10_66.KY628225; 90_BF1.BR.2010.BRG04141.KY628219;
90_BF1.BR.2007.BRGO3027.KY628215; 90_BF1.BR.2010.BRGOAP801.KY628223;
39_BF.BR.2003.03BRRJ103.EU735534; 39_BF.BR.2003.03BRRJ327.EU735536;
F2.CM.2011.DEFMF211CM025.KU749420; F2.CM.2010.DEFMF210CM001.JX140672;
F2.CM.1995.95CM-MP255.AJ249236; F2.CM.1997.CM53657.AF377956;
F2.CM.2004.04BRRJ179.EU735535; F1.BR.2010.10BR_SP029.KT427814;
F1.BR.2010.DEFM110BR015.KU749395; F1.BR.1993.93BR020_1.AF005494;
F1.BR.2010.10BR_SP070_1.KT427663; F1.BR.2011.DEFM111BR037.KU749396;
28_BF.BR.2005.0679SV.JF804812; D.UG.1999.99UJA7412.AF484477; D.KE.2001.NKU3006.AF457090;
D.UG.1998.98UG57146.AF484513; 47_BF.BR.2010.10BR_J026.KJ849798;
47_BF.BR.2010.10BR_RJ026.KJ849798; 47_BF.BR.2010.10BR_SP029.KT427814;
F1.BR.2010.DEFM110BR015.KU749395; F1.BR.1993.93BR020_1.AF005494;
F1.BR.2010.10BR_SP070_1.KT427663; F1.BR.2011.DEFM111BR037.KU749396;
28_BF.BR.2005.0679SV.JF804812; D.UG.1999.99UJA7412.AF484477; D.KE.2001.NKU3006.AF457090;
D.UG.1998.98UG57146.AF484513; 47_BF.BR.2010.10BR_J026.KJ849798;
47_BF.BR.2010.10BR_RJ026.KJ849798; 47_BF.BR.2010.10BR_SP029.KT427814;
F1.BR.2010.DEFM110BR015.KU749395; F1.BR.1993.93BR020_1.AF005494;
F1.BR.2010.10BR_SP070_1.KT427663; F1.BR.2011.DEFM111BR037.KU749396;
Figure S1 - Patterns of intersubtype genetic recombination of BC recombinants. Recombination analysis performed by bootscanning methodology using SIMPLOT software. Reference strains: B.FR.1983.HXB2-LAI-IIIB-BRU.K03455 (subtype B, red),
F1.BR.1993.93BR020-1. AF005494 (subtype F, green), C.BR.2004.04BR013.AY727522 (subtype C, blue).

SUPPLEMENTARY MATERIAL S2

Recombination pattern Cluster 2 (coloured by red in figure 2)

Figure S2 - Patterns of intersubtype genetic recombination of URFs BF presented in two major clusters. Cluster 1 with 14 query sequences and Cluster 2 with 9 one. Recombination analysis performed by bootscanning methodology using SIMPLOT software. Reference strains: B.FR.1983.HXB2-LAI-IIIB-BRU.K03455 (subtype B, red), F1.BR.1993.93BR020-1. AF005494 (subtype F, green), C.BR.2004.04BR013.AY727522 (subtype C, blue).

Recombination pattern Cluster 1 (Coloured by green in figure 2)

SUPPLEMENTARY MATERIAL Figure S3
Figure S3 - Patterns of intersubtype genetic recombination of URFs BF recombinants related with CRFs 28 e 29_BF. Recombination analysis performed by bootscanning methodology using SIMPLOT software. Reference strains: B.FR.1983.HXB2-LAI-III-BRU.K03455 (subtype B, red), F1.BR.1993.93BR020-1. AF005494 (subtype F, green), C.BR.2004.04BR013.AY727522 (subtype C, blue).

Cluster C (figure 2):