

Figure S1

Primer specificity for HIV-1 group M

<http://www.hiv.lanl.gov/content/sequence/HIV/COMPENDIUM/2013compendium.html>

# HIV Sequence Compendium 2013

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## II

### HIV-1/SIVcpz Complete Genomes

#### Contents

II-1	Introduction . . . . .	9
II-2	Annotated features . . . . .	10
II-3	Sequences . . . . .	13
II-4	Alignments . . . . .	18

#### II-1 Introduction

While the "web-alignment" this year has grown to 2229 full-length genomes, the compendium alignment herein has strict page limitations. The selection here was made such that subtypes A-G, CRF's 01 and 02, and CPZ are represented with one sequence from most countries where the subtype has been sequenced. Priority was given to more recently sampled sequences to reflect the current pandemic diversity. For the rare subtypes H-K and groups N-P most available sequences are included, and for CRF's 03 and up, one representative is included. Unique recombinant forms and unclassified sequences are not included. This resulted in 199 sequences of HIV-1/SIVcpz from all over the world.

The HXB2 sequence (accession K03455) is the master sequence in this alignment. This is also the genome coordinate standard used throughout the HIV Database. The alignment was generated by MAFFT v7.043 (E-INS-i with gap open penalty 2.0). The alignment was subsequently codon-aligned using GeneCutter, followed by a few manual edits to fix obvious misalignments. The alignment presented cannot be considered an "optimal alignment" to any single criterion; it is a compromise between optimal alignment, readability, and codon alignment. Most gaps have been introduced in multiples of 3 bases to maintain open reading frames when the alignment is translated.

Also part of this nucleotide alignment is a translation to protein sequence based on the HXB2 sequence; 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 Chapter V.

Forward primer PBS 5'-TAGCAGTGGCGCCCGA-3'

	5' LTR U5 end	Lys tRNA primer binding site	Packaging loops begin	
B.FR.83.HXB2	TTTAGTCAGTGTGG.AAAATCT	TAGCAGTGGCGCCCGA	ACAGGGGACC.TGAAGCGGAAG	.....GGAAACCAGAGG...AGCTCTCTCGAC.GCA...GGACTCGGCTTGCTG.....AAGCGC...GCACGGCAAGAGCGGGGG...G
A1.AU.83.PSI044_Day0	.....	.....	.....	.....
A1.CH.03.HIV_CH_BID_V3538	.....	.....	.....	.....
A1.ES.06.X2110	.....	.....	.....	.....
A1.IT.02.6080B	.....	.....	.....	.....
A1.KE.06.96KECst_001	.....	.....	.....	.....
A1.RU.11.11RU0990B	.....	.....	.....	.....
A1.RM.07.DRC63F	.....	.....	.....	.....
A1.SE.95.5E8538	.....	.....	.....	.....
A1.TZ.01.A341	.....	.....	.....	.....
A1.UG.07.01UADN139	.....	.....	.....	.....
A1.US.07.01US1845	.....	.....	.....	.....
A1.ZA.04.04ZASK162B1	.....	.....	.....	.....
A2.CO.97.97CDK1848	.....	.....	.....	.....
A2.CH.01.01CH_1445HV	.....	.....	.....	.....
A2.CY.94.94CY017_41	.....	.....	.....	.....
B.AR.04.04AR143170	.....	.....	.....	.....
B.AU.04.PS1039_Day174	.....	.....	.....	.....
B.BO.09.DEMB09B0061	.....	.....	.....	.....
B.BR.06.06BR1119	.....	.....	.....	.....
B.CA.07.07_1191_03	.....	.....	.....	.....
B.CH.04.HIV_CH_BTD_V4488	.....	.....	.....	.....
B.CN.10.DEMB10CN002	.....	.....	.....	.....
B.CO.01.FCM001	.....	.....	.....	.....
B.CO.99.C019	.....	.....	.....	.....
B.CY.09.CY206	.....	.....	.....	.....
B.DE.04.HIV_DE_BID_V4131	.....	.....	.....	.....
B.DI.07.PM01_011	.....	.....	.....	.....
B.DO.05.05DD_168884	.....	.....	.....	.....
B.ES.09.P2149_3	.....	.....	.....	.....
B.FR.08.DEMB08FR002	.....	.....	.....	.....
B.GE.03.03GEM7004	.....	.....	.....	.....
B.HI.05.05HT_129389	.....	.....	.....	.....
B.IW.05.05IW_36188	.....	.....	.....	.....
B.JP.05.DR6538	.....	.....	.....	.....
B.KR.07.07KY04	.....	.....	.....	.....
B.NL.06.071_00736	.....	.....	.....	.....
B.PE.07.07_2649_w08	.....	.....	.....	.....
B.PY.03.03PY_PSP0115	.....	.....	.....	.....
B.RU.11.11RU_1191	.....	.....	.....	.....
B.TH.07.AA0460_WG11	.....	.....	.....	.....
B.TT.01.01TT_CRC50009	.....	.....	.....	.....
B.WA.94.WA01_00049	.....	.....	.....	.....
B.WA.01.01UAK7167	.....	.....	.....	.....
B.US.11.E538	.....	.....	.....	.....
B.UY.02.02UY_TSU1290	.....	.....	.....	.....
B.VE.10.DEMB10VE001	.....	.....	.....	.....
B.YE.02.02YE507	.....	.....	.....	.....
C.AR.01.ARG0006	.....	.....	.....	.....
C.R.07.DEM07R0003	.....	.....	.....	.....
C.BM.00.00BM07621	.....	.....	.....	.....
C.CN.98.YNRL9840	.....	.....	.....	.....
C.CY.09.CY206	.....	.....	.....	.....
C.ES.07.X2118_2	.....	.....	.....	.....
C.ET.02.02ET_288	.....	.....	.....	.....
C.GE.03.03GEM7003	.....	.....	.....	.....
C.IL.98.98IL5002	.....	.....	.....	.....
C.IN.03.D24	.....	.....	.....	.....
C.IE.00.KER0010	.....	.....	.....	.....
C.MI.99.MIDU101_3	.....	.....	.....	.....
C.MW.93.93MW_965	.....	.....	.....	.....
C.NI.98.98NI_364	.....	.....	.....	.....
C.SO.89.89SM_145	.....	.....	.....	.....
C.TZ.02.CO178	.....	.....	.....	.....
C.US.98.98US_MSC3018	.....	.....	.....	.....
C.UY.01.01UY_011	.....	.....	.....	.....
C.YE.02.02YE511	.....	.....	.....	.....
C.ZA.10.DEMC10Z001	.....	.....	.....	.....
C.ZM.02.02ZM008	.....	.....	.....	.....
D.CO.03.ELT	.....	.....	.....	.....
D.CH.10.DEMD10CH009	.....	.....	.....	.....
D.CY.06.CY103	.....	.....	.....	.....
D.KE.97.ML415_2	.....	.....	.....	.....
D.NR.04.04KB02	.....	.....	.....	.....
D.OL.98.98OL_365	.....	.....	.....	.....
D.TD.99.MNB1	.....	.....	.....	.....
D.TZ.01.A200	.....	.....	.....	.....
D.UG.08.08UG1859	.....	.....	.....	.....
D.UY.02.02UY_TSU1290	.....	.....	.....	.....
D.ZA.98.R1	.....	.....	.....	.....
F1.AO.06.06_AO_ANG125	.....	.....	.....	.....
F1.AR.02.ARG0003	.....	.....	.....	.....
F1.BE.93.VI850	.....	.....	.....	.....
F1.BR.07.07BR044	.....	.....	.....	.....
F1.CY.08.CY222	.....	.....	.....	.....
F1.ES.11.DEMF11BE5001	.....	.....	.....	.....
F1.FT.93.FIN9363	.....	.....	.....	.....
F1.FR.96.96FR_HF411	.....	.....	.....	.....
F1.RD.98.98RD_001	.....	.....	.....	.....
F1.RU.08.D88_045	.....	.....	.....	.....
F2.CH.10.DEMC10CH007	.....	.....	.....	.....
F2.CO.97.CMS3657	.....	.....	.....	.....
G.BE.96.DRCBL	.....	.....	.....	.....
G.CH.10.DEMG10CH008	.....	.....	.....	.....
G.CI.08.08_C1_0084_008	.....	.....	.....	.....
G.CU.99.Cu74	.....	.....	.....	.....
G.ES.09.X2634_2	.....	.....	.....	.....
G.GI.93.03GI_0005	.....	.....	.....	.....
G.HI.93.03HI_HH793_12_1	.....	.....	.....	.....
G.NG.09.09NG_SC62	.....	.....	.....	.....

Forward primer PBS 5'-TAGCAGTGGCGCCCGA-3'

	5' LTR US end	Lys tRNA primer binding site	Packaging loops begin		
B.FR.83.HXB2	TTTAGTCAGTGTGG.AAAATCT	TAGCAGTGGCGCCCGA	CAGGGACC.TGAAAGGAAAG	GGAAACCAAGGG	AGCTCTCTCGAC.GCA..GGACTCGGCTGCTG...AAGCGC.GCACGGCAAGAGCGGAGGGGG...G
G.PT.x.PT3386	-C-AA...A				..GTGC.AAAAGTT...A.CG...A.CG...A.CG...
G.AE.93.SE9105_G6165	..G-CTT...				..GTGC.AAAAGTT...A.CG...A.CG...A.CG...
H.BE.93.V1991	..T...				..T...A.AA...A.CG...A.CG...A.CG...
H.BE.93.V1997	..T...				..T...A.AA...A.CG...A.CG...A.CG...
H.CF.98.056	..T...				..T...A.AA...A.CG...A.CG...A.CG...
H.BE.98.08GBAC4801	..Y...				..GTGC.AAAAGTT...A.CG...A.CG...A.CG...
J.D.97.1.97DC_KT147	..T...				..T...A.AA...A.CG...A.CG...A.CG...
J.CH.04.04CMU11421	..T...				..T...A.AA...A.CG...A.CG...A.CG...
J.SE.93.SE9280_7887	..T...				..T...A.AA...A.CG...A.CG...A.CG...
J.E.94.SE9173_7822	..T...				..T...A.AA...A.CG...A.CG...A.CG...
K.CO.97.0728_G07811	..T...				..T...A.AA...A.CG...A.CG...A.CG...
K.CH.96.96CM_HP533	..T...				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.AF.07.569M	..T...				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.CN.09.1119	..T...				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.HK.04.HK003	..T...				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.JP.x.DR0492	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.TH.04.BM1	..T...				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.TH.09.AA1113_MG11	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.TH.98.CM248	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
01.AE.VN.98.98VND15	..C..CA..TC				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.CH.08.D89288CM001	..G...				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.ES.06.F1261	..C..A.TT.A..A				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.FR.91.D1263	..GG..C..G				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.GH.03.03GH181AG	..G..A.T...AA				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.IR.x.POC_44951	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.NC.x.IBNG	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.SN.98.98SE MP1211	..G...				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.US.06.062_7696_FL01	..C..A.TT.A..A				..T...A.AA...A.CG...A.CG...A.CG...
02.AG.UZ.02.02UCB65	..G..G..CAGTGTG				..T...A.AA...A.CG...A.CG...A.CG...
03.AB.RU.97.KAL153_2	..T...				..T...A.AA...A.CG...A.CG...A.CG...
04.cpx.CY.94.94CY032_3	..T...				..T...A.AA...A.CG...A.CG...A.CG...
05.DF.BE.x.VT1310	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
06.cpx.AU.96.BFP90	..T...				..T...A.AA...A.CG...A.CG...A.CG...
07.BC.CN.98.98CM009	..G..G..CAGTGTG				..T...A.AA...A.CG...A.CG...A.CG...
08.BC.CN.06.06BC085	..G..A..AG..A				..T...A.AA...A.CG...A.CG...A.CG...
09.cpx.GH.96.96GH2911	..CC				..T...A.AA...A.CG...A.CG...A.CG...
10.CO.TZ.96.96TZ_BF061	..TA..C..T				..T...A.AA...A.CG...A.CG...A.CG...
11.cpx.CH.99.99C91_1816	..C...				..T...A.AA...A.CG...A.CG...A.CG...
12.FR.AR.99.ARA159	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
13.cpx.CU.96.96CM_1849	..C...TGT...A				..T...A.AA...A.CG...A.CG...A.CG...
14.BG.ES.05.X1870	..C..A.TC..CCCT				..T...A.AA...A.CG...A.CG...A.CG...
15.01B.TH.99.99TH_MU2079	..C..T..A..G				..T...A.AA...A.CG...A.CG...A.CG...
16.AZD.KR.97.97KR004	..C..T..A..G				..T...A.AA...A.CG...A.CG...A.CG...
17.BF.AR.99.ARA038	..T...				..T...A.AA...A.CG...A.CG...A.CG...
18.cpx.CU.99.99C76	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
19.cpx.CU.99.CU7	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
20.BG.CU.99.CU103	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
21.AZD.HE.99.99HE003	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
22.01A1.CH.01.01CH_0001BBY	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
23.BG.CU.03.CB118	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
24.BG.ES.08.X2456_2	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
25.cpx.CH.02.02C1	..C..GT...A				..T...A.AA...A.CG...A.CG...A.CG...
26.AU.CO.02.02CD_PBT0047	..T...				..T...A.AA...A.CG...A.CG...A.CG...
27.cpx.FR.04.04CD_FR_K25	..C..A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
28.BF.BR.99.BRFPM2000	..T...				..T...A.AA...A.CG...A.CG...A.CG...
29.BF.BR.01.BRFPM16704	..T...TG...				..T...A.AA...A.CG...A.CG...A.CG...
31.BC.BR.04.04BR142	..T...G..C				..T...A.AA...A.CG...A.CG...A.CG...
32.06A1.EE.01.EE0369	..T...A...A				..T...A.AA...A.CG...A.CG...A.CG...
33.01B.ID.07.07IK189_C	..T...				..T...A.AA...A.CG...A.CG...A.CG...
34.01B.TH.99.09R247BP	..T...				..T...A.AA...A.CG...A.CG...A.CG...
35.AD.AF.07.07AD	..T...				..T...A.AA...A.CG...A.CG...A.CG...
36.cpx.CH.00.00CMNYU030	..T...				..T...A.AA...A.CG...A.CG...A.CG...
37.cpx.CH.00.00CMNYU026	..T...				..T...A.AA...A.CG...A.CG...A.CG...
38.BF1.UY.03.UY03_3389	..TAG...				..T...A.AA...A.CG...A.CG...A.CG...
39.BF.BR.04.04BR0179	..TAG...				..T...A.AA...A.CG...A.CG...A.CG...
40.BF.BR.05.05BRR1055	..TAG...				..T...A.AA...A.CG...A.CG...A.CG...
42.BF.LU.03.LU0F_05_03	..Y...				..T...A.AA...A.CG...A.CG...A.CG...
43.02G.SA.03.111223	..C..A.G...A				..T...A.AA...A.CG...A.CG...A.CG...
44.BF.CL.00	..C..G..G...A				..T...A.AA...A.CG...A.CG...A.CG...
45.cpx.FR.04.04FR_AUK	..C..A...A				..T...A.AA...A.CG...A.CG...A.CG...
46.BF.BR.07.07BR_FPS625	..T...				..T...A.AA...A.CG...A.CG...A.CG...
47.BF.ES.08.LU2	..TAG...TGTG				..T...A.AA...A.CG...A.CG...A.CG...
48.01B.MY.07.07MYKT021	..C..A.G...A				..T...A.AA...A.CG...A.CG...A.CG...
49.cpx.GM.03.N26677	..T...C...A				..T...A.AA...A.CG...A.CG...A.CG...
51.01B.SG.11.11SG_HM021	..T...				..T...A.AA...A.CG...A.CG...A.CG...
52.01B.MY.03.03MYL018_1	..T...				..T...A.AA...A.CG...A.CG...A.CG...
53.01B.MY.11.11FR164	..T...ATA				..T...A.AA...A.CG...A.CG...A.CG...
54.01B.MY.09.09MY00823	..T...				..T...A.AA...A.CG...A.CG...A.CG...
55.01B.CN.10.10NC5102056	..T...				..T...A.AA...A.CG...A.CG...A.CG...
0.BE.07.AN170	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.CH.91.MYPS180	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.CH.98.98CA184	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.FR.92.VAU	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.SN.99.99SE MP1299	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.US.19.LTN	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
0.US.97.97US080692A	..AGACTGAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
N.CH.02.D100131	..C..GGACTGAGTGA				..T...A.AA...A.CG...A.CG...A.CG...
N.CH.04.04CM_1015_04	..GG..CTGAGTA				..T...A.AA...A.CG...A.CG...A.CG...
N.CH.06.U14842	..C..AGACTGAGTGA				..T...A.AA...A.CG...A.CG...A.CG...
N.CH.05.YBF106	..C..AGACTGAGTGA				..T...A.AA...A.CG...A.CG...A.CG...
N.CH.97.YBF106	..CA...A.T.A..A				..T...A.AA...A.CG...A.CG...A.CG...
N.FR.11.N1_FR_2011	..TAG..C..A...A				..T...A.AA...A.CG...A.CG...A.CG...
P.CH.06.U14788	..CTAG..C..A...A				..T...A.AA...A.CG...A.CG...A.CG...
P.FR.09.RF09	..GA..G.TAA..CA				..T...A.AA...A.CG...A.CG...A.CG...
CPZ.CO.06.BF1167	..C..ATA..TGA..AGA				..T...A.AA...A.CG...A.CG...A.CG...
CPZ.CO.05.SIVcpzMT145	..-TAGTCAAG				..T...A.AA...A.CG...A.CG...A.CG...
CPZ.GA.08.GAB1	..AG..G.TAA..A				..T...A.AA...A.CG...A.CG...A.CG...
CPZ.TD.06.SIVcpzTAN13	..A..AAGTAG				..T...A.AA...A.CG...A.CG...A.CG...
CPZ.US.05.US_Mdr1Lyn	..A..AAGTAG				..T...A.AA...A.CG...A.CG...A.CG...

Reverse primer PBS 5'-TCTCTCTCCTTCTAGCCTCCGC-3'

	GC . . . GACTGGTGTAGTACGCCAAAAA . . . . . TTTTGACTGCGGGAGG . . . . . CTAGAAGG . . . . . AGAGAG . . . . .	Packaging loops end	Gag and Gag-Pol start	
B. FR. 83. HBX2	GC . . . GACTGGTGTAGTACGCCAAAAA . . . . . TTTTGACTGCGGGAGG . . . . . CTAGAAGG . . . . . AGAGAG . . . . .		TGGGTCCGAGAGCTAGTATTAAAGCGGGGAGAATAGATCGATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAAG	867
Gag			M G A R A S V L S G G E L D R W E K I R L R P G G K	
A1.AU.03.P51044 Day0	.....	.....	.....	74
A1.CH.03.H117 CH-BID V3538	.....	.....	.....	78
A1.E5.06.X117	.....	.....	.....	119
A1.IT.02.60800	.....	.....	.....	878
A1.KE.06.06KEC51 001	.....	.....	.....	409
A1.RU.11.11RU0939	.....	.....	.....	409
A1.RW.07.pR463F	.....	.....	.....	888
A1.SE.95.SEB538	.....	.....	.....	72
A1.TZ.01.A341	.....	.....	.....	72
A1.UA.01.01UADN139	.....	.....	.....	72
A1.VG.07.p191845	.....	.....	.....	906
A1.X.09.0425AK162B1	.....	.....	.....	299
A2.CO.07.07CDK1049	.....	.....	.....	214
A2.CH.01.01CM 1445MV	.....	.....	.....	72
A2.CY.94.94CY017_41	.....	.....	.....	236
B.AR.04.04AR143170	.....	.....	.....	74
B.AU.04.P51039 Day174	.....	.....	.....	78
B.BD.09.DEMB0900001	.....	.....	.....	236
B.BR.06.06BR1119	.....	.....	.....	281
B.CA.07.07C1191_03	.....	.....	.....	288
B.CH.04.HIV-CH BID V4488	.....	.....	.....	78
B.CH.10.DEMB10CN002	.....	.....	.....	231
B.CO.01.PC0001	.....	.....	.....	72
B.CU.99.Cu19	.....	.....	.....	408
B.CY.09.CY266	.....	.....	.....	78
B.DE.94.HIV-DE BID V4131	.....	.....	.....	78
B.DK.07.PHWL 011	.....	.....	.....	236
B.DO.05.05DO 1608B4	.....	.....	.....	72
B.E5.09.P2149	.....	.....	.....	72
B.FR.08.DEMB08FR002	.....	.....	.....	223
B.GE.03.03GEMZ004	.....	.....	.....	72
B.HT.05.05HT 19389	.....	.....	.....	72
B.JM.05.05JM 1018	.....	.....	.....	72
B.JP.05.05DR0538	.....	.....	.....	871
B.KR.07.07KY74	.....	.....	.....	333
B.NL.00.071_00736	.....	.....	.....	392
B.PE.07.07.2649 wq8	.....	.....	.....	279
B.PY.03.03PY PSP0115	.....	.....	.....	411
B.RU.11.11RU0939	.....	.....	.....	219
B.TH.07.AA0403 wG11	.....	.....	.....	72
B.TT.01.01TT CRC50069	.....	.....	.....	72
B.TW.90.TW075 19649	.....	.....	.....	866
B.UA.01.01UAKY167	.....	.....	.....	790
B.US.11.E538	.....	.....	.....	72
B.UY.02.02UY T5U1290	.....	.....	.....	219
B.VE.10.DEMB10VE001	.....	.....	.....	72
B.YE.02.02YE507	.....	.....	.....	72
C.AR.01.ARG4006	.....	.....	.....	72
C.BR.07.DEMB07BR003	.....	.....	.....	234
C.BW.00.00BW017	.....	.....	.....	78
C.CN.98.YNRL9840	.....	.....	.....	78
C.CY.09.CY266	.....	.....	.....	316
C.E5.07.X2118_2	.....	.....	.....	72
C.EI.02.02EI 288	.....	.....	.....	72
C.GE.03.03GEMZ033	.....	.....	.....	213
C.LL.98.98LL5002	.....	.....	.....	888
C.IN.03.D24	.....	.....	.....	72
C.KE.00.KER2010	.....	.....	.....	246
C.MH.99.MHDU013_3	.....	.....	.....	78
C.MJ.95.95MJ 365	.....	.....	.....	72
C.SN.90.90SE 364	.....	.....	.....	72
C.SO.89.89SOF 145	.....	.....	.....	72
C.TZ.02.C0178	.....	.....	.....	72
C.US.98.98US MSC3018	.....	.....	.....	A
C.UY.01.TRA3011	.....	.....	.....	72
C.VE.02.02VE511	.....	.....	.....	72
C.ZA.10.DEMC10ZAB01	.....	.....	.....	231
C.ZH.02.02ZH188	.....	.....	.....	866
D.CO.03.E11	.....	.....	.....	413
D.CO.10.DEMC10CM009	.....	.....	.....	78
D.CY.06.CY163	.....	.....	.....	333
D.DE.97.ML415_2	.....	.....	.....	836
D.KR.04.04KR048	.....	.....	.....	866
D.SN.90.SE365	.....	.....	.....	85
D.TD.99.MW011	.....	.....	.....	72
D.TZ.01.A280	.....	.....	.....	72
D.VE.00.01VE1959	.....	.....	.....	883
D.YE.02.02YE516	.....	.....	.....	72
D.ZA.90.R1	.....	.....	.....	213
F1.AB.06.AB 06 ANG125	.....	.....	.....	0
F1.AE.03.ARE933	.....	.....	.....	170
F1.BE.93.V1850	.....	.....	.....	272
F1.BR.07.07BR044	.....	.....	.....	630
F1.CY.08.CY266	.....	.....	.....	78
F1.E5.11.DEMF110E5001	.....	.....	.....	218
F1.FI.93.FIN9363	.....	.....	.....	208
F1.FR.96.96FR 04111	.....	.....	.....	906
F1.R0.96.BCI R07	.....	.....	.....	323
F1.RU.08.D08 845	.....	.....	.....	72
F1.RU.10.DEMB10RUCM007	.....	.....	.....	72
F2.CH.37.CHS365	.....	.....	.....	72
G.BE.96.DRCBL	.....	.....	.....	852
G.CH.10.DEMG10CM008	.....	.....	.....	251
G.CO.05.CX 2084_08	.....	.....	.....	104
G.CU.99.CU74	.....	.....	.....	480
G.E5.09.X2634_2	.....	.....	.....	344
G.GH.03.03GH1756	.....	.....	.....	410
G.H.03.H031756	.....	.....	.....	269
G.H.03.H031756	.....	.....	.....	74
G.MG.09.09MG SC62	.....	.....	.....	74

