SUPPLEMENTAL TABLES

Table S1. ASPE Primers for HIV-1 group M subtype B

Primer no	Type [a]	Sequence (5'-3')	Tag ID [b]	Position [c]
1	M41	Tag- AA GAA AAA ATA AAA GCA TTA RYA GAA ATT TGT RMW GAR A [d]	45	2632 - 2670
2	41L	Tag- AA GAA AAA ATA AAA GCA TTA RYA GAA ATT TGT RMW GAR C	38	2632 - 2670
3	K65	Tag- A AAT CCA TAC AAT ACT CCA GTA TTT GCY ATA AAG AA	12	2708 - 2743
4	65R	Tag- A AAT CCA TAC AAT ACT CCA GTA TTT GCY ATA AAG AG	13	2708 - 2743
5	K70	Tag- CCA GTA TTT GCC ATA AAG AAA AAR RAY RGT ACT AA	18	2724 - 2758
6	70R	Tag- CCA GTA TTT GCC ATA AAG AAA AAR RAY RGT ACT AG	21	2724 - 2758
7	L74	Tag- C ATA AAG AAA AAR GAC AGT ACY ARR TGG AGA AAA Y	67	2735 - 2769
8	74V	Tag- C ATA AAG AAA AAR GAC AGT ACY ARR TGG AGA AAA G	90	2735 - 2769
9	Y115	Tag- A GTA CTR GAT GTR GGT GAT GCA TA	73	2870 - 2893

10	115F	Tag- A GTA CTR GAT GTR GGT GAT GCA TT	62	2870 - 2893
11	Q151	Tag- GG ATT AGR TAT CAR TAC AAT GTR CTY CCA C	29	2971 - 3000
12	151M	Tag- GG ATT AGR TAT CAR TAC AAT GTR CTY CCA A	36	2971 - 3000
13	M184	Tag- AGA AAA CAA AAT CCA GAM ATR GTT ATC TRT CAA TAY A	37	3063 - 3099
14	184V	Tag- AGA AAA CAA AAT CCA GAM ATR GTT ATC TRT CAA TAY G	22	3063 - 3099
15	K219	Tag- ARG TGG GGR TTT WMY ACA CCA GAY A	53	3180 - 3204
16	219Q	Tag- ARG TGG GGR TTT WMY ACA CCA GAY C	44	3180 - 3204
17	219E	Tag- ARG TGG GGR TTT WMY ACA CCA GAY G	96	3180 - 3204
18	L100	Tag- CAA TTA GGA ATA CCA CAY CCH KCA GGR Y	42	2820 - 2847
19	100I	Tag- CAA TTA GGA ATA CCA CAY CCH KCA GGR A	58	2820 - 2847
20	K101	Tag- AA TTA GGA ATA CCA CAY CCH GCA GGR HTA A	55	2821 - 2850
21	101P	Tag- AA TTA GGA ATA CCA CAY CCH GCA GGR HTA CC	89	2821 - 2851

22	101E	Tag- AA TTA GGA ATA CCA CAY CCH GCA GGR HTA G	65	2821 - 2850
23	K103	Tag- GA ATA CCA CAT CCY KCA GGG HTA MAA AAG AAR	19	2827 - 2858
24	103N	Tag- GA ATA CCA CAT CCY KCA GGG HTA MAA AAG AAC	66	2827 - 2858
25	103R	Tag- GA ATA CCA CAT CCY KCA GGG HTA MAA AAG AGA	63	2827 - 2858
26	V106	Tag- A CAT CCY KCA GGG HTA MAA AAG ARV AAA TCA GT	20	2834 - 2866
27	106A	Tag- A CAT CCY KCA GGG HTA MAA AAG ARV AAA TCA GC	39	2834 - 2866
28	106M	Tag- A CAT CCY KCA GGG HTA MAA AAG ARV AAA TCA ATG	75	2834 - 2867
29	Y181	Tag- G CCT TTT AGA AAR SAA AAT CCA GAM ATR GTT ATY TA	9	3056 - 3091
30	181C	Tag- G CCT TTT AGA AAR SAA AAT CCA GAM ATR GTT ATY TG	82	3056 - 3091
31	Y188	Tag- CA GAM ATR GTT ATC TRT CAA TAY RTG GAT GAY TTR TA	83	3076 - 3112
32	188L	Tag- CA GAM ATR GTT ATC TRT CAA TAY RTG GAT GAY TTR TT	93	3076 - 3112
33	G190	Tag- ATA GTT ATY TAT CAA TAC RTG GAT GAY TTR TAT GTW GG	97	3081 - 3118

34	190A	Tag- ATA GTT ATY TAT CAA TAC RTG GAT GAY TTR TAT GTW GC	76	3081 - 3118
35	V32	Tag- CT CTA TTR GAY ACA GGA GCA GAT GAY ACA G	14	2317 - 2346
36	32I	Tag- CT CTA TTR GAY ACA GGA GCA GAT GAY ACA A	48	2317 - 2346
37	I47	Tag- TG CCA GGA ARA TGG AAR CCA ARA ATR A	30	2365 - 2391
38	47V	Tag- G CCA GGA ARA TGG AAR CCA ARA ATR GT	43	2366 - 2392
39	47A	Tag- G CCA GGA ARA TGG AAR CCA ARA ATR GC	78	2366 - 2392
40	L76	Tag- AA ATC TGT GGR CAT ARA GCT RTR GGT ACA GTA T	28	2446 - 2478
41	76V	Tag- AA ATC TGT GGR CAT ARA GCT RTR GGT ACA GTA G	70	2446 - 2478
42	I84	Tag- A GTA TTA RTA GGA CCY ACA CCT GTC AAY A	35	2474 - 2502
43	84V	Tag- A GTA TTA RTA GGA CCY ACA CCT GTC AAY G	77	2474 - 2502
44	L90	Tag- CA CCT GTC AAC ATA ATT GGA AGR AAY CTR T	95	2491 - 2520
45	90M	Tag- CA CCT GTC AAC ATA ATT GGA AGR AAY CTR A	57	2491 - 2520

[a] One primer for each wild-type and one or two primers for each mutant type were designed at 20 mutation loci.

[b] Each Tag matches with one of the MagPlex®-TAG™ Microspheres.

[c] Positions are based on HXB2 sequence. All ASPE primers begin upstream of the mutation of interest.

[d] Bases different from the subtype C ASPE primers were underlined (Zhang G, Cai F, Zhou Z, DeVos J, Wagar N, Diallo K, Zulu I, Wadonda-Kabondo N, Stringer JS, Weidle PJ, Ndongmo CB, Sikazwe I, Sarr A, Kagoli M, Nkengasong J, Gao F, Yang C. 2013. Simultaneous Detection of Major Drug Resistance Mutations in the Protease and Reverse Transcriptase Genes for HIV-1 Subtype C by Use of a Multiplex Allele-Specific Assay. Journal of clinical microbiology 51:3666-3674.)

Table S2. Comparison of drug resistance mutations identified by the Sanger sequencing with those identified by the MAS assay

No.	**ID** [a]	**Drug resistance Mutations** [b]	
		Sanger sequencing	**MAS**
1	HN1	K70KR, K103N, Y115F, M184V, K219Q	K70KR, K103N, Y115F, M184V, K219Q
2	HN2	None	None
3	HN8	K103R	K103R
4	HN11	K101E, K103R	K101E, K103R
5	HN13	M41L, K70R, K101E, M184V, K219E	M41L, K70R, K101E, **K103KN**, M184V, K219E
6	HN14	K103R	K103R
7	HN15	Y181C, M184MV	**K65KR**, Y181C, M184MV
8	HN16	None	None
9	HN17	None	None
10	HN18	None	None
11	HN19	K103R	K103R
12	HN20	K101KE, Y181YC, M184MV	K101KE, Y181YC, M184MV
13	HN21	None	None
14	HN24	None	None
15	HN27	None	None
16	HN32	L100I, K103N, Y115F, Q151M, M184V, K219E	L100I, K103N, **Y115YF**, Q151M, M184V, K219E
17	HN34	**M41L**[c], K103R, M184V, G190A	K103R, M184V, G190A
18	HN37	None	None

19	HN38	K103KN	K103KN
20	HN39	None	None
21	HN40	None	None
22	HN42	None	None
23	HN45	None	None
24	HN47	L74LV, L100IL, K103N, M184MV	L74LV, L100IL, K103N, M184MV
25	HN48	K103N, M184V	K103N, **M184MV**
26	HN50	None	None
27	HN59	None	None
28	HN63	M184V, **Y188L**[c]	M184V
29	HN68	None	None
30	HN70	None	None
31	HN71	K70R, Y181YC, M184V, **K219E**[c]	K70R, Y181YC, M184V
32	HN72	None	None
33	HN74	None	None
34	HN75	K103R	K103R
35	HN76	None	None
36	HN79	K103KR	K103KR
37	HN80	L74V	L74V
38	HN81	K70R, **Y181C**[c], M184V, K219Q	K70R, M184V, K219Q
39	HN82	None	None
40	HN83	None	None
41	HN85	K103KR	K103KR
42	HN86	K103R, V106A, M184V	K103R, V106A, M184V
43	HN89	K103R	K103R

44	HN90	None	None
45	HN91	None	None
46	HN93	M41ML, K70R, K103N, M184V, G190A	M41ML, K70R, K103N, M184V, G190A
47	HN96	None	None
48	HN97	K70KR, L74LV, K103N, M184MV, K219KE	**V32VI**[d], **I47IV**[d], K70KR, L74LV, K103N, M184MV, K219KE
49	HN98	None	None
50	HN100	**K70KR**[c], K103N, Y181C, M184V, **K219KE**	K103N, Y181C, M184V
51	HN101	K103KN, V106VM	**K101KE**, K103KN, V106VM
52	HN102	None	None
53	HN103	M184MV, K103N	M184MV, **K103KN**
54	HN104	K103N	K103N
55	HN106	K103N, M184MV	K103N, M184MV
56	HN107	None	None
57	HN109	K103R	K103R
58	HN110	K103R	K103R
59	HN111	None	None
60	HN112	None	None
61	HN113	None	None
62	HN114	M41L, K70R, K101E, Y181C, M184V, G190A	**L90M**[d], M41L, K70R, K101E, Y181C, M184V, G190A
63	HN115	None	None
64	HN117	M184MV	M184MV

65	HN118	K101E, K103R	K101E, K103R
66	HN119	None	None
67	HN120	K103R	K103R
68	HN122	None	None
69	HN123	K103R, Y181YC	K103R, Y181YC

[a] Subject identifier (ID).

[b] Major mutations that confer resistance to protease and reverse transcriptase inhibitors. Discordant drug resistance mutations are shown in bold.

[c] Indeterminate results by the MAS assay.

[d] Protease inhibitor (PI) mutations.