

Article title: Low-frequency HIV-1 drug resistance mutations in antiretroviral naïve individuals in Botswana.

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Table S1. Comparison of participant characteristics among samples included in analysis and those excluded

Characteristics	Included individuals (n=108)	Excluded individuals (n=423)	P-value
Female, n (%)	107 (99.1)	370 (87.5)	<.001
Male, n (%)	1 (0.9)	53 (12.5)	<.001
Age in years, median (IQR)	27 (24-31)	26 (23-33)	.412
Viral load (log ₁₀ copies/mL), median (IQR)	4.1 (3.5-4.6)	4.2 (3.5-4.6)	.786
CD4 count (cells/mm ³), median (IQR)	365 (225-497)	427 (365-514)	<.01

IQR = (Interquartile ranges: 25th percentile and 75th percentile); Excluded Participants, refers to participants without available amplicons; Included Participants, refers to participant that had available amplicons and included in final analysis.

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Table S2: Comparison of DRMs identified by Sanger sequencing, PASEq and Hydra

PID	PASEq			Hydra			Sanger sequencing		
	NRTI	NNRTI	PI	NRTI	NNRTI	PI	NRTI	NNRTI	PI
P1	None	Y181C (1.25%)	None	None	None	None	None	None	None
P5	None	None	T74P (1.13%)	None	None	None	None	None	None
P7	None	K103N (98.7%), V106M (1.01%)	None	None	K103N(97.8 3%) V106I (7.65%)	None	None	K103N	None
P8	M184V, (2.48%)	E138G (1.31%), M230I (2%)	None	M184I(1.66%)	E138G (1.84%), M230I (2.25%)	None	None	None	None
P9	None	None	M46I (1.65%)	None	None	M46I (1.61%)	None	None	None
P10	None	None		K65R (1.12%)	None	None	None	None	None
P11	None	None	L90M (98.94 %)		None	L90M (99.24%)	None	None	L90 M
P13	K65R (1.7%)	None	None	K65R (2.38%)	None	None	None	None	None
P14	K65R (2%)	None	None	K65R (3.97%)	None	None	None	None	None
P15	K65R (1.23%)	None	None	None	None	None	None	None	None
P16	None	None	M46I (13.85 %)	None	None	M46I (13.9%)	None	None	None
P17	None	P225H (2%)	I84V (3.03%)	None	P225H (2.46%)	I84V (2.64%)	None	None	None
P19	None	E138G (4.65), V108I (11.25%)	N88S (2.78%)	None	V108I(8.15 %)	N88S(4.15 %)	None	None	None
P21	None	None	I84V (1.11%)	None	None		None	None	None
P23	None	None	I50V (1.33%)	None	None	I50V(1.45 %)	None	None	None
P25	M41L	Y188H	None	M41L (36.97%)	Y188H	None	M41	K103N	

	(33.29%)	(1.09%), K103N (97.56%)			(1.06%) K103N (98.8%)		L		
P26	K65R (2.96%)	None	None	K65R (3.74%)	None	None	None	None	None
P27	K65R (2.18%)	None	M46I (2.08%)	None	None	M46I (2.8%)	None	None	None
P28	A62V (98.99%)	None	None	A62V (99.38%)	None	None	A62V	None	None
P29	Q58E (65.68%)	V108I (1.15%)	None	Q58E (70.49%)	None	None	None	None	Q58E
P30	None	E138K (1.12%)	None	None	None	None	None	None	None
P31	F116Y (2.55%)	V108I (3.55%)	None	K65R (1.65%), F116Y (1.98%)	V108I (1.62%)	None	None	None	None
P32	V75I (2.46%)	None	None	V75I (2.64)	None	None	None	None	None
P34	V75I (5.4%)	None	None	K65R (2.56%), V75I (5.03%)	None	None	None	None	None
P36	None	None	M46L (3.38%)	None	None	M46L (3.23%)	None	None	None
P38	K65R (1%)	None	Q58E (99.71 %)	K65R (1.87)	None	Q58E (99.32%)	None	None	Q58E
P41	None	None	M46I (1.66%)	None	None	M46I (1.19%)	None	None	None
P42	K65R (1.14%)	None	None	K65R (1.63%)	None	None	None	None	None
P43	F77L (4.06%)	None	None	F77L (5.39%)	None	None	None	None	None
P44	M184I (2.43%)	None	None	M184I (2.6%)	None	None	None	None	None
P45	None	E138K (2.74%)	None	None	None	None	None	None	None
P46	None	None	M46I (9.1)	None	None	M46I (8.56%)	None	None	None
P47	K65R (1.23%)	None		K65R (1.51%)	None	None	None	None	None
P49	None	None	I50V (1.07%)	None	None	None	None	None	None
P51	None	Y188C (2.231%)	None	None	Y188C (1.69%)	None	None	None	None
P53	None	K103N (7.769%)	None	None	K103N (6.93%)	None	None	None	None
P56	None	None	None	K65R (1.32%)	None	None	None	None	None
P75	None	None	None	K65R (1.04%)	None	None	None	None	None
P85	None	K103N(81 .86%)	None	K103N (71.12%)	None	None	None	K103N	None

P94	M46L (44.49%)	None	None	None	None	M46L (47.43%)	None	None	M46 L
P101	None	None	None	K65R (2.7%)	None	None	None	None	None

DRMs = drug resistance mutations; NNRTI = non nucleoside reverse transcriptase inhibitor; NRTI = nucleoside reverse transcriptase inhibitor; PI = protease inhibitor; PID = patient identification; PAsEq = polymorphism analysis sequencing; None means no drug resistance mutations detected.

Table S3: Detailed ART regimens for individuals with follow-up data (n=82)

PID	Year of ART initiation	Initiation regimen
P1	2014	ATRIPLA *
P3	2014	ATRIPLA*
P4	2014	ATRIPLA *
P5	2015	ATRIPLA *
P6	2015	ATRIPLA*
P8	2015	ATRIPLA*
P9	2016	ATRIPLA*
P10	2015	ATRIPLA
P11	2015	ATRIPLA*
P12	2015	ATRIPLA*
P13	2015	ATRIPLA*
P14	2015	ATRIPLA *
P16	2015	ATRIPLA *
P17	2015	ATRIPLA*
P18	2016	DTG + Truvada
P19	2015	ATRIPLA*
P20	2016	DTG + Truvada
P21	2015	ATRIPLA*
P22	2015	ATRIPLA
P23	2015	ATRIPLA*
P26	2017	DTG + Truvada
P29	2015	ATRIPLA
P30	2015	ATRIPLA*
P31	2015	ATRIPLA*
P32	2012	ATRIPLA
P33	2015	ATRIPLA
P34	2015	ATRIPLA
P35	Missing initiation dates	Missing initiation regimen
P36	2015	ATRIPLA*
P37	2015	ATRIPLA*
P39	2015	ATRIPLA
P41	2015	ATRIPLA
P42	2015	ATRIPLA
P46	2015	ATRIPLA*
P47	2017	DTG + Truvada
P48	2015	ATRIPLA
P49	2015	ATRIPLA*
P50	2015	ATRIPLA*
P51	2016	ATRIPLA
P52	2016	ATRIPLA
P53	2012	ATRIPLA *
P54	2018	DTG +Truvada
P55	2015	ATRIPLA
P56	2017	DTG + Truvada
P57	2015	ATRIPLA
P58	2015	ATRIPLA

P59	2016	DTG + Truvada
P60	2016	ATRIPLA *
P61	Missing initiation dates	Missing initiation regimen
P62	2015	ATRIPLA*
P63	2015	ATRIPLA *
P64	2016	DTG + Truvada
P65	2016	ATRIPLA *
P68	2016	ATRIPLA*
P69	2015	ATRIPLA*
P70	2015	ATRIPLA
P71	2016	DTG + Truvada *
P73	2016	DTG + Truvada *
P74	2012	ATRIPLA *
P75	2016	ATRIPLA
P76	2012	ATRIPLA *
P77	2017	DTG + Truvada
P78	2013	ATRIPLA
P79	2016	DTG + Truvada *
P80	2016	DTG + Truvada
P81	2017	DTG +Truvada *
P82	2012	ATRIPLA
P83	2014	ATRIPLA
P84	2014	ATRIPLA *
P86	2018	DTG +Truvada
P87	2015	ATRIPLA
P89	2018	ATRIPLA
P91	2016	DTG + Truvada *
P93	2015	ATRIPLA
P95	2015	ATRIPLA *
P97	Missing initiation dates	Missing initiation regimen
P98	2015	ATRIPLA
P99	2017	DTG + Truvada
P100	2015	ATRIPLA *
P101	2016	DTG + Truvada *
P102	2015	ATRIPLA
P103	2015	ATRIPLA

PID = Patient identification; ATRIPLA = TDF+FTC+EFV; DTG = dolutegravir; Truvada = TDF+FTC; * Inferred initiation regimen based on initiation dates. Bold = Individuals who experienced virological failure (n=12).