

**Supplementary Table 1: Deep sequencing results for viral variants archived in the latent reservoir.**

Patient	HLA Type	Epitope Name	Epitope <sup>1</sup>	Variant <sup>2</sup>	Variation Frequency (%) (PacBio)	Variation Frequency (%) (MiSeq)	Mutation Type <sup>3</sup>
CP05	A*29:02 A*30:01 B*42:01 B*57:01 Cw*06:02 Cw*17:01	RY11	RSLYNTVATLY (A30)	-	0	0	-
		LY9	LYNTVATLY (A29:02)	-	0	0	-
		IW9	ISPRTLNAW (B57:01)	I147L	89.4	92.3	E
		KF11	KAFSPEVIPMF (B57:01)	-	0	0	-
		TL9	TPQDLNTML (B42:01)	Q182A	86.6	88.1	MTND
		TW10	TSTLQEIQGW (B57:01)	T242N	98.4	98.7	E
		QW9	QASQEVKNW (B57:01)	-	0	0	-
CP12	A*01:01 A*29:02 B*44:03 B*57:01 Cw*06:02 Cw*16:01	LY9	LYNTVATLY (A29:02, B44:03)	T81A, V82I	67.1	68.6	MTND
		IW9	ISPRTLNAW (B57:01)	I147L	93	97.3	E
		KF11	KAFSPEVIPMF (B57:01)	-	0	0	-
		TW10	TSTLQEIQGW (B57:01)	T242N	91.3	99.1	E
		QW9	QASQEVKNW (B57:01)	S310T	69.8	72.8	MTND
CP18	A*02:01 A*33:03 B*35:01 B*81:01 Cw*04:01 Cw*18:01	WF9	WASRELERF (B35:01)	-	0	0	-
		SL9	SLYNTVATL (A02:01)	Y79F, V82I, T84V	97.4	98.8	E
		TV9	TLNAWVKVV (A02:01)	-	0	0	-
		TL9	TPQDLNTML (B81:01)	Q182G/A/V	87.6	93.4	MTND
		HA9	HPVHAGPIA (B35:01)	I223V	53.7	66.6	MTND
		PY9	PIIPVGEIY (B35:01)	-	0	0	-
		FK10	FLGKIWPSHK (A0201)	-	0	0	-
CP19	A*23:01 A*68:02 B*15:03 B*58:01 Cw*02:10 Cw*07:18	RY11	RSLYNTVATLY (B58)	V82I, T84V	35.9	24.6	MTND
		VF9	VKVVEEKAF (B15:03)	-	0	0	-
		GHL9	GHQAAMQML (B15)	-	0	0	-
		TW10	TSTLQEIQGW (B58:01)	T242N, G248T	82.9	98.3	E
		QW9	QASQEVKNW (B58:01)	E312D	78.1	97.9	MTND
CP31	A*23:01 A*66:02 B*41:01 B*58:01 Cw*07:18 Cw*08:02	RY11	RSLYNTVATLY (B58)	R76K, T81A	99.5	92.3	E
		KF11	KAFSPEVIPMF (B58:01)	-	0	0	-
		TL9	TPQDLNTML (C08:02)	Q182G, T186L	0	22.9	MTND
		EW10	ETINEEAAEW (B58)	E203D	95.1	69.2	SF
		TW10	TSTLQEIQGW (B58:01)	T242N, G248A	99.1	71.7	E
		QW9	QASQEVKNW (B58:01)	E312D	99	70.4	MTND
CP32	A*34:02 A*68:01 B*44:03 B*53:01 Cw*04:01	LY9	LYNTVATLY (B44:03)	-	0	0	-
		TL9	TPQDLNTML (B53:01)	-	0	0	-
		QW9	QASQEVKNW (B53:01)	S310T	97.2	98.8	E
CP36	A*02:02 A*03:01 B*35:01 B*53:01 Cw*04:01	KK9	KIRLRPGGK (A03:01)	-	0	0	-
		RK9	RLRPGGKKK (A03:01)	K28S	94.5	97.5	MTND
		WF9	WASRELERF (B35:01)	-	0	0	-
		SL9	SLYNTVATL (A02:02)	T84V	98.2	99	E
		TV9	TLNAWVKVV (A02:02)	V159I	81.6	83.4	DR
		EW10	ETINEEAAEW (B53)	-	0	0	-
		HA9	HPVHAGPIA (B35:01)	-	0	0	-
QW9	QASQEVKNW (B53:01)	S310T	70.9	78	MTND		

Patient	HLA Type	Epitope Name	Epitope <sup>1</sup>	Variant <sup>2</sup>	Variation Frequency (%) (PacBio)	Variation Frequency (%) (MiSeq)	Mutation Type <sup>3</sup>
CP38	A*03:01	KK9	KIRLRPGGK (A03:01)	K26R	10.4	13.1	E
	A*24:02	RK9	RLRPGGKKK (A03:01)	K26R, K28Q	75.4	78.7	E
	B*44:02	KW9	KYKLVKLVV (A24:02)	K28Q,K30R,I34L	98.3	99.4	E
	B*81:01	TL9	TPQDLNTML (B81:01)	Q182G/S, T186L	95.7	99.4	MTND
	Cw*05:01	RL11	RDYVDRFYKTL (B44:02)	-	0	0	-
	Cw*18:01	AW11	AEQASQEVKNW (B44:02,Cw5)	S310T	12.5	12.3	MTND
CP39	A*03:01	KK9	KIRLRPGGK (A03:01)	-	0	0	-
	A*03:01	RK9	RLRPGGKKK (A03:01)	K28Q	94.7	98.6	E
	A*29:02	LY9	LYNTVATLY (A29:02)	Y79F, V82I, T84V, Y86F	99	98.6	E
	B*07:02	SV9	SPRTLNAWV (B07:02)	-	0	0	-
	B*15:16	TV9	TLNAWVKVV (A02:01)	-	0	0	-
	Cw*07:02	TL9	TPQDLNTML (B07:02)	-	0	0	-
Cw*14:02	HA9	HPVHAGPIA (B7)	-	0	0	-	
	GL9	GPGHKARVL (B07:02)	-	0	0	-	
CP40	A*02:02	KK9	KIRLRPGGK (A03:01)	K18R	39.8	40.4	MTND
	A*03:01	RK9	RLRPGGKKK (A03:01)	K28T/R	89.5	91.1	DR
	B*15:16	RL10	RPGGKKKYKL (B51:01)	K28T/R, K30R	91.8	92.4	MTND
	B*51:01	SL9	SLYNTVATL (A02:02, Cw14)	Y79F, T81A, V82I, T84V	99.4	99.3	E
	Cw*14:02	TV9	TLNAWVKVV (A02:02)	V159I	3.4	4.2	DR
CP42	A*02:01	KK9	KIRLRPGGK (A03:01)	-	0	0	-
	A*02:01	RK9	RLRPGGKKK (A03:01)	K28Q	97.5	98.9	E
	A*03:01	SL9	SLYNTVATL (A02:01)	Y79F, V82I	98.3	98.7	E
	B*07:02	SV9	SPRTLNAWV (B07:02)	-	0	0	-
	B*38:01	TV9	TLNAWVKVV (A02:01)	-	0	0	-
	Cw*07:02	TL9	TPQDLNTML (B07:02)	-	0	0	-
	Cw*12:03	HA9	HPVHAGPIA (B7)	-	0	0	-
		GL9	GPGHKARVL (B07:02)	-	0	0	-
	FK10	FLGKIWPSHK (A02:01)	-	0	0	-	
CP47	A*02:01	SL9	SLYNTVATL (A02:01)	Y79F,T81A,V82I,T84V	92.3	96.4	E
	A*25:01	QW11	QAISPRTLNAW (A25:01)	I147L	96.5	96.5	DR
	B*18:01	TV9	TLNAWVKVV (A02:01)	-	0	0	-
	Cw*07:01	EW10	ETINEEAAEW (A25:01)	-	0	0	-
	Cw*12:03	FRK10	FRDYVDRFYK (B18:01)	-	0	0	-
		FK10	FLGKIWPSHK (A02:01)	-	0	0	-
CP48	A*33:03	LY9	LYNTVATLY (B44:03)	T81A, V82I, T84V	94.2	98.7	MTND
	A*37:01	RL11	RDYVDRFYKTL (B44)	-	0	0	-
	B*44:03	AW11	AEQASQEVKNW (B44)	S310T	24.5	27.8	MTND
CP49	A*01:01	GK9	GGKKKYKLV (B08:01)	-	0	0	-
	A*01:01	EV9	ELRSYNTV (B08:01)	R76K, Y79F	99.2	98.5	MTND
	A*02:01	SL9	SLYNTVATL (A02:01)	Y79F	99.2	98.5	E
	B*08:01	VQV9	VQNLQGMV (B13)	L138M	97	97.3	MTND
	B*13:02	TV9	TLNAWVKVV (A02:01)	-	0	0	-
	Cw*06:02	GII1	GQMREPRGSDI (B13)	-	0	0	-
	Cw*07:01	EI8	EIYKRWII (B08:01)	-	0	0	-
		DL9	DCKTILKAL (B08:01)	-	0	0	-
		RI9	RQANFLGKI (B13)	-	0	0	-
	FK10	FLGKIWPSHK (A02:01)	-	0	0	-	
CP50	A*03:01	KK9	KIRLRPGGK (A03:01)	-	0	0	-
	A*30:04	RK9	RLRPGGKKK (A03:01)	K28Q	91.8	94	E
	B*35:01	WF9	WASRELERF (B35:01)	-	0	0	-
	B*49:01	RY11	RSYNTVATLY (A30)	R76K	97.4	98.5	IE
	Cw*04:01	HA9	HPVHAGPIA (B35:01)	-	0	0	-
	Cw*07:01	PY9	PPIPVGEIY (B35:01)	-	0	0	-

Patient and	HLA Type	Epitope Name	Epitope <sup>1</sup>	Variant <sup>2</sup>	Variation Frequency (%) (PacBio)	Variation Frequency (%) (MiSeq)	Mutation Type <sup>3</sup>
AP01	A*02:01 A*03:01 B*35:01 B*44:02 Cw*04:01 Cw*05:01	KK9	KIRLRPGGK (A03:01)	-	0	0	-
		RK9	RLRPGGKKK (A03:01)	K28Q	3.4	4.3	E
		WF9	WASRELERF (B35:01)	-	0	0	-
		SL9	SLYNTVATL (A02:01)	T84V	94.4	98.7	E
		TV9	TLNAWVKVV (A02:01)	-	0	0	-
		HA9	HPVHAGPIA (B35:01)	I223P	95.2	94.7	MTND
		PY9	PPIPVGIEY (B35:01)	-	0	0	-
		RL11	RDYVDRFYKTL (B44:02)	-	0	0	-
		AW11	AEQASQEVKNW (B44:02,Cw5)	N315G	96.5	94.9	MTND
AP03	A*24:02 A*24:07 B*15:02 B*27:05 Cw*01:02 Cw*03:03	FK10	FLGKIWPSHK (A02:01)	-	0	0	-
		IK9	IRLRPGGKK (B27:05)	K26N	66.1	61.5	MTND
		KW9	KYKCLKHIVW (A24:02)	K28Q	29.5	36.4	E
		VL8	VIPMFSAL (C01:02)	-	0	0	-
		KK10	KRWIILGLNK (B27:05)	R264K, L268M	25	25.8	E
		YL9	YVDRFYKTL (C03:03)	-	0	0	-
AP04	A*02:01 A*24:02 B*14:01 B*35:01 Cw*04:01 Cw*15:05	KW9	KYKCLKHIVW (A24:02)	K30Q/R	50.4	52.9	MTND
		WF9	WASRELERF (B35:01)	F44Y	7.7	7	MTND
		SL9	SLYNTVATL (A02:01)	V82I	11.7	12.3	E
		TV9	TLNAWVKVV (A02:01)	V159I	7.6	6.9	DR
		HA9	HPVHAGPIA (B35:01)	-	0	0	-
		PY9	PPIPVGIEY (B35:01)	-	0	0	-
		CC9	CRAPRKKGC (B14)	K411R	70.5	79.2	MTND
		FK10	FLGKIWPSHK (A02:01)	I437L	7.7	6.9	MTND
AP05	A*02:01 B*07:02 B*51:01 Cw*01:02 Cw*07:02	RL10	RPGGKKKYKL (B51:01)	K28Q	95.8	98.7	MTND
		SL9	SLYNTVATL (A02:01)	-	0	0	-
		SV9	SPRTLNAWV (B07:02)	-	0	0	-
		TV9	TLNAWVKVV (A02:01)	V159I	99.2	98.5	DR
		VL8	VIPMFSAL (Cw01:02)	-	0	0	-
		TL9	TPQDLNMTL (B07:02)	-	0	0	-
		HA9	HPVHAGPIA (B7)	H219P, I223V	99.4	98.7	MTND
		GL9	GPGHKARVL (B07:02)	R361K	6.1	18.3	MTND
AP07	A*02:07 A*33:03 B*46:01 B*58:01 Cw*01:02 Cw*03:02	FK10	FLGKIWPSHK (A02:01)	H441N	97.2	98.1	MTND
		RY11	RSLYNTVATLY(B58)	-	0	0	-
		VL8	VIPMFSAL(Cw01:02)	S173T	96.6	97.2	DR
		TW10	TSTLQEIQIGW(B58:01)	-	0	0	-
		YL9	YVDRFYKTL(A02:07)	-	0	0	-
		QW9	QASQEVKNW(B58)	-	0	0	-
AP08	A*02:01 A*03:01 B*07:02 Cw*07:02	KK9	KIRLRPGGK (A03:01)	-	0	0	-
		RK9	RLRPGGKKK (A03:01)	R28Q	96.1	98.7	E
		SL9	SLYNTVATL (A02:01)	-	0	0	-
		SV9	SPRTLNAWV (B07:02)	-	0	0	-
		TV9	TLNAWVKVV (A02:01)	-	0	0	-
		TL9	TPQDLNMTL (B07:02)	Q182S	93.1	96.5	MTND
		HA9	HPVHAGPIA (B7)	-	0	0	-
		GL9	GPGHKARVL (B07:02)	-	0	0	-
FK10	FLGKIWPSHK (A02:01)	-	0	0	-		

Patient	HLA Type	Epitope Name	Epitope <sup>1</sup>	Variant <sup>2</sup>	Variation Frequency (%) (PacBio)	Variation Frequency (%) (MiSeq)	Mutation Type <sup>3</sup>
AP09	A*03:01 A*11:01 B*08:01 B*14:02 Cw*07 Cw*08	KK9	KIRLRPGGK (A03:01)	-	0	0	-
		RK9	RLRPGGKKK (A03:01)	-	0	0	-
		GK9	GGKKKYKLK (B08:01)	-	0	0	-
		EV9	ELRSLYNTV (B08:01)	R76K, V82I	98.9	98.9	IE
		EI8	EIYKRWII (B08:01)	-	0	0	-
		DA9	DRFYKTLRA(B14:02)	-	0	0	-
		DL9	DCKTILKAL (B08:01)	-	0	0	-
		AK11	ACQGVGGPGHK(A11:01)	G357S	98	99.1	SF
		CC9	CRAPRKKGC (B14)	-	0	0	-
AP10	A*01:01 A*02:01 B*08:01 B*15:01 Cw*03 Cw*07	GK9	GGKKKYKLK (B08:01)	-	0	0	-
		EV9	ELRSLYNTV (B08:01)	-	0	0	-
		SL9	SLYNTVATL (A02:01)	-	0	0	-
		TV9	TLNAWVKVV (A02:01)	-	0	0	-
		EI8	EIYKRWII (B08:01)	-	0	0	-
		GLY9	GLNKIVRMY(B15:01)	-	0	0	-
		DL9	DCKTILKAL (B08:01)	-	0	0	-
		FK10	FLGKIWPSHK (A02:01)	G435R	31.7	51.6	MTND
		RL10	RPGGKKKYKL (B51:01)	-	0	0	-
AP11	A*02:01 B*35:01 B*51:01 Cw*02:02 Cw*04:01	WF9	WASRELERF (B35:01)	-	0	0	-
		SL9	SLYNTVATL (A02:01)	-	0	0	-
		TV9	TLNAWVKVV (A02:01)	-	0	0	-
		HA9	HPVHAGPIA (B7)	-	0	0	-
		PY9	PPIPVGEIY (B35:01)	-	0	0	-
		FK10	FLGKIWPSHK (A02:01)	G435R	2.1	6.7	MTND
		RL10	RPGGKKKYKL (B51:01)	-	0	0	-
AP12	A*01:01 A*03:01 B*07:02 Cw*07	KK9	KIRLRPGGK (A03:01)	-	0	0	-
		RK9	RLRPGGKKK (A03:01)	-	0	0	-
		SV9	SPRTLNAWV (B07:02)	R150K	2.7	5.6	MTND
		TL9	TPQDLNTML (B07:02)	-	0	0	-
		HA9	HPVHAGPIA (B7)	-	0	0	-
		GL9	GPGHKARVL (B07:02)	-	0	0	-
		GL9	GPGHKARVL (B07:02)	-	0	0	-

<sup>1</sup>Each patient's relevant optimal Gag epitopes are based on reported information in the HIV Molecular Immunology Database, Los Alamos National Laboratory (<http://www.hiv.lanl.gov/content/immunology/index.html>) according to the HLA type.

<sup>2</sup>Sequences from each subject were aligned to the reference HIV-1 clade B consensus Gag sequence. Variants were determined by the differences from the reference sequence.

<sup>3</sup>Mutation Type abbreviations: **MTND**: mutation type not determined; **E**: documented escape; **IE**: inferred escape; **DR**: diminished response; **SF**: susceptible form.