

**Supplementary Table 2. The response frequency to unique NAE/AE measured during acute and chronic HIV infection (Longitudinal cohort, N=13)**

Epitope Group	HLA-I restriction	Protein	Predicted epitope <sup>a</sup>	TFV encoding epitope <sup>b</sup>	Tested <sup>c</sup>	Response <sup>d</sup>	
						Acute	Chronic
	A*02	Env	SLFNATAIAV	NLFNTTAAIAV	1	0	1
	A*24	Env	NYTGLIYTL	NYTGIIYTL	1	1	1
	B*44	Gag	AEQASQEVKNW	AEQASQEVKNW	3	2	3
	B*07:02	Gag	GPSHKARIL	GPGHKARIL	1	0	0
	B*35	Gag	NPIIPVGEIY	NPIIPVGEIY	1	0	0
	A*03:01	Gag	RLRPGGKKQ	RLRPGGKKQ	1	0	0
	A*01	Gag	SLFNTVATLY	SLFNTVATLY	2	0	0
	A*11:01	Gag	TLYCVHQK	TMYCVHQK	1	0	1
	A*03:01	Nef	ALDLSHFLK	ALDLSHFLK	2	1	0
	A*03:01	Nef	ALDLSHFLK	ALDLSHFLR	1	0	1
	C*7	Nef	DILDLWIY	DILDLWIY	1	0	0
	A*02	Nef	FLKEKGGLEGL	FLKEMGGLEGL	1	1	1
	A*02	Nef	FLKEKGGLEGL	FLKENGLEGL	1	0	1
	B*07:02	Nef	FPVKPQVPL	FPVKPQVPL	1	1	1
	B*07:02	Nef	FPVKPQVPLR	FPVKPQVPLR	1	0	1
	A*30	Nef	HMAREKHPEYY	HVARELHPEYY	1	0	0
	B*44	Nef	KEKGGLEGLIH	KEMGGLEGLIH	1	0	1
	B*44	Nef	KEKGGLEGLIH	KENGGLEGLIH	1	0	1
<b>AE</b>	C*07:02	Nef	KRQEILDLWVY	KRQEILDLWVY <sup>1</sup>	1	0	1
	A*23:01	Nef	RFPLTFGWCF	RFPLTFGWCF	1	1	1
	B*07:02	Nef	RPMTFKGAL	RPMTFKGAL	1	1	0
	B*07:02	Nef	TPGPGTRYPL	TPGPGTRYPL	1	0	1
	B*07	Nef	VPVEPEKVEEA	VPMEPEKIEEA	1	0	0
	B*07	Nef	VPVEPEKVEEA	VPMEPEKVEEA	1	0	0
	B*44	Pol	AELQKQGQGQW	AELQKQGQGQW	1	1	1
	A*03:01	Pol	AIFQC <sup>C</sup> SMTK	AIFQC <sup>C</sup> SMTK	2	0	0
	C*04	Pol	AYFLLKLA	AYFLLKLA	2	0	1
	B*44:03	Pol	EDMNLPGRW	EDMNLPGRW	1	0	0
	B*44	Pol	IDKAQEEHEKY	IDKAQEDHEKY	1	0	1
	B*44:02	Pol	IDKAQEEHEKY	IDKAQEEHEKY	1	0	0
	A*30	Pol	ILKEPVHGVYY	ILKEPVHGVYY	1	0	0
	A*30	Pol	NIQKFRVYY	NLQKFRVYY	1	0	0
	A*03:01	Pol	QIYPGIKVK	QIYPGIKVK	1	1	1
	B*35	Pol	VPLDKDFRKY	VPLDKDFRKY	1	0	0
	A*02:01	Vpr	ALIRILQQL	ALLRSLQQL	1	0	1
	B*07	Vpr	FPRPWLHGL	FPRMWLHGL	1	0	1
	B*07:02	Vpr	FPRPWLHGL	FPRVWLHGL	1	0	0
	A*02	Env	SLLNATAIAV	NLLNTTAAIAV	1	1	1
	A*02	Env	SLLNATAIAV	SLLNATAIAV	1	0	0
	A*03:01	Env	TVYYGVPVWK	TVYYGVPVWK	1	1	0

	B*07	Env	IPRRIRQGL	VPVRIRQGL	1	0	0
	A*11:01	Gag	ACQGVGGP <u>G</u> HK	ACQGVGGPGHK	1	0	1
	B*44	Gag	AEIQKQGQ <u>G</u> QW	AEIQKQGQGQW	1	1	0
	B*08:01	Gag	IYKR <u>W</u> IL	IYKRWIL	2	0	1
	A*03:01	Gag	<u>K</u> IRLRPGGK	KIRLRPGGK	2	0	0
	A*24:02	Gag	KY <u>K</u> LKHIVW	KYKLKHIVW	1	0	1
	A*03:01	Gag	RLRPGG <u>K</u> KK	RLRPGGKKK	2	0	2
	A*30	Gag	RLRPGG <u>K</u> KKY	RLRPGGKKKY	1	0	0
	A*03:01	Gag	RLRPGG <u>K</u> KKYK	RLRPGGKKKYR	1	0	1
	B*52:01	Gag	RMYSPT <u>S</u> ILDI	RMYSPTSILDI	1	1	0
	A*01	Gag	SLY <u>N</u> TVATLY	SLYNTVATLY	1	0	0
	A*03:01	Nef	A <u>V</u> DLSHFLK	AVDLSHFLK	1	1	0
	C*07	Nef	KRQ <u>D</u> ILD <u>L</u> W <u>Y</u>	DILDWVY	2	0	0
	B*07:02	Nef	FPV <u>R</u> PQVPL	FPVRPQVPL	1	1	1
NAE	B*07:02	Nef	FPV <u>R</u> PQVPLR	FPVRPQVPLR	2	0	0
	A*30:02	Nef	GY <u>F</u> PDWQNY	GYFPDWQNY	1	0	0
	B*07:02	Nef	RP <u>M</u> TYK <u>G</u> AL	RPMTYK <u>G</u> AL	3	1	3
	A*23:01	Nef	RY <u>P</u> L <u>T</u> FGW <u>C</u> F	RYPLCFGWCF	1	1	1
	A*24:02	Nef	RY <u>P</u> L <u>T</u> FGWCF	RYPLTFGW	1	0	1
	C*03:02	Nef	SL <u>L</u> HPMS <u>Q</u> HGM	TLLHPMSQHGM	1	0	0
	B*07:02	Nef	TPG <u>P</u> G <u>I</u> RYPL	TPGPGIRYPL	1	1	0
	B*35:01	Nef	V <u>P</u> LR <u>P</u> MTYKGA	VPLRPMTYKAA	1	1	1
	B*15:03	Pol	<u>G</u> HKAIGTVL	GHKAIGTVL	1	1	0
	B*15:10	Pol	IL <u>K</u> EPVHG <u>V</u> Y	ILKEPVHGVY	1	1	0
	B*58:01	Pol	I <u>T</u> TESIV <u>I</u> W	ITTESIVIW	1	0	0
	A*03:01	Pol	QI <u>Y</u> A <u>G</u> IK <u>V</u> K	QIYAGIKVK	1	1	1
	B*15:03	Pol	R <u>K</u> A <u>K</u> IIR <u>D</u> Y	RKAKIIRDY	1	1	1
	B*07:02	Pol	SP <u>A</u> IFQ <u>S</u> SM	SPAIFQSSM	1	0	1
	B*51:01	Pol	TA <u>F</u> T <u>I</u> PS <u>I</u>	TAFTIPSI	1	1	0
	A*30	Rev	KT <u>V</u> RLIK <u>F</u> LY	KTVRLIKRLY	1	0	0
	B*07	Rev	R <u>P</u> A <u>E</u> PV <u>P</u> L <u>Q</u> L	RFEEPVPLQL	1	0	0
	B*07:02	Rev	R <u>P</u> A <u>E</u> PV <u>P</u> L <u>Q</u> L	RPAEPVPLQL	2	1	1
	B*07	Vif	H <u>P</u> RI <u>S</u> SE <u>V</u> HI	HPRISSQVYI	1	0	1

<sup>a</sup> Predicted NAE or AE. The polymorphic site is underlined and the adaptation at that site is shown in red/underlined

<sup>b</sup> NAE or AE encoded in TFV sequence for each patient

<sup>c</sup> Number of patients tested for the corresponding epitope at both stages of infection

<sup>d</sup> Number of patients responding to the corresponding epitope at each stage of infection