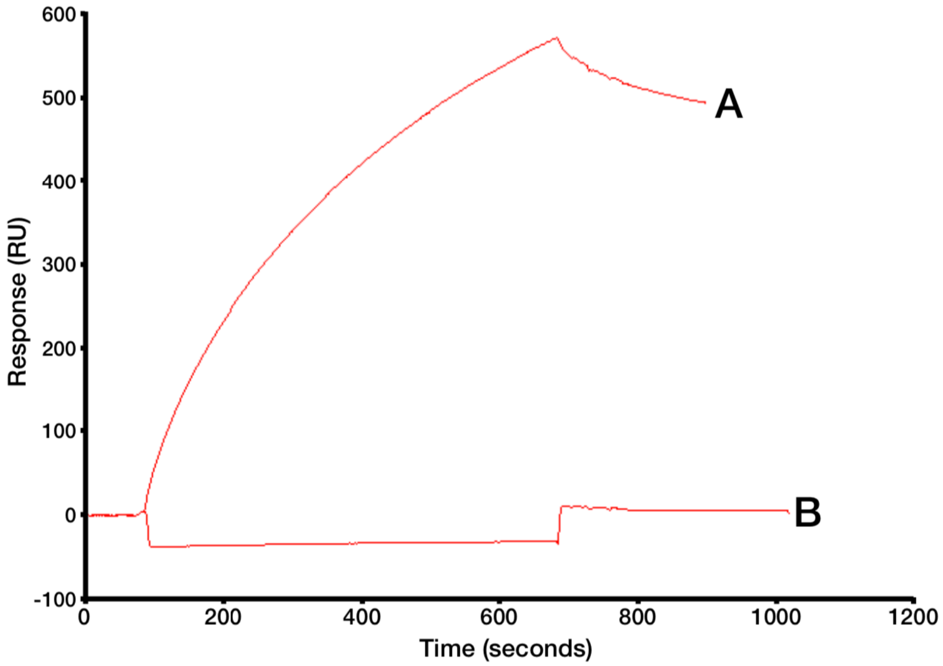

Supplemental figure 1: Confirmation of proper MHC class I complex folding. Binding of assembled MHC class I/β2-microglobulin complexes to W6/32, a monoclonal antibody that recognizes only properly folded MHC class I complexes, was assessed by surface plasmon resonance (SPR). Mamu-A1*002/β2M complexes were prepared as described. After an hour incubation at room temperature, 3 µl of the MHC class I sample was diluted in 87 µl of HBS-EP+ buffer (GE Healthcare, Chicago, IL) and binding of the MHC class I complex to the anti-MHC class I monoclonal antibody W6/32 (ThermoFisher Scientific, Waltham, MA) was analyzed by surface plasmon resonance (SPR). As a control, 10 µl of 2 mg/ml human β2M and 2 µl of 30 mg/ml MHC class I heavy chain were mixed together and diluted with 10 mM MES pH 6.5 to 80 µl. As with the test sample, 3 µl of the control sample was mixed with 87 µl of HBS-EP+ buffer and analyzed by SPR without pre-incubation. SPR analysis was performed on a Biacore X100 instrument (GE), using a CM5 sensor chip with immobilized W6/32 antibody, and a contact time of 600 s and a flow rate of 5 µl/min.

Shown are SPR sensorgrams of interaction between immobilized W6/32 antibody and (A) assembled MHC class I complexes and (B) control MHC class I/β2-microglobulin, indicating that the assembled MHC class I complexes are recognized by and bind W6/32.

Supplemental table I: GenBank accession numbers of SIV and SHIV strains included on the peptide array. All sequences were used without modification; however, the SIVmac239 GenBank entry has a truncated Nef sequence, so a full-length version was manually added.

Virus	Strain/Isolate	Accession No.
SIV	SIVmac239	M33262.1
SIV	pE660.CG7V	JX648291.1
SIV	pE660.CG7G	JX648292.1
SIV	SIVmac251.CM.p3c22	KC522216.1
SIV	SIVmac251.CM.p3d18	KC522217.1
SIV	SIVmac251.CM.p3c20	KC522218.1
SIV	SIVmac251.CM.tb9	KC522219.1
SIV	SIVmac251.CM.p3a6	KC522220.1
SIV	SIVmac251.CM.p3c6	KC522221.1
SIV	SIVmac251.CM.p3d20	KC522222.1
SIV	SIVmac251.CM.p3d1	KC522223.1
SIV	SIVmac251.CM.p3e10	KC522224.1
SIV	SIVmac251.CM.p3c7	KC522225.1
SIV	SIVmac251.CM.p3e9	KC522226.1
SIV	SIVmac251.DB.p1e18	KC522227.1
SIV	SIVmac251.DB.p4e16	KC522228.1
SIV	SIVmac251.DB.p4g16	KC522229.1
SIV	SIVmac251.DB.p1e23	KC522230.1
SIV	SIVmac251.DB.p4a21	KC522231.1
SIV	SIVmac251.DB.p4e11	KC522232.1
SIV	SIVmac251.DB.p1e24	KC522233.1
SIV	SIVmac251.DB.p4f10	KC522234.1
SIV	SIVmac251.DB.p1e19	KC522235.1
SIV	SIVmac251.DB.p4b1	KC522236.1
SIV	SIVmac251.DB.p4e19	KC522237.1
SIV	SIVmac251.DB.p1e22	KC522238.1
SIV	SIVmac251.RD.p3h14	KC522239.1
SIV	SIVmac251.RD.p3i16	KC522240.1
SIV	SIVmac251.RD.p3g16	KC522241.1
SIV	SIVmac251.RD.p3g21	KC522242.1
SIV	SIVmac251.RD.p3j14	KC522243.1
SIV	SIVmac251.RD.p3j17	KC522244.1
SIV	SIVmac251.RD.p3g14	KC522245.1
SIV	SIVmac251.RD.p3j19	KC522246.1
SIV	SIVmac251.RD.tf20	KC522247.1
SIV	SIVmac251.RD.p3f16	KC522248.1
SIV	SIVmac251.RD.p3i17	KC522249.1
SIV	SIVmac251.RD.p3h1	KC522250.1
SIV	SIVmacL28-C1	KU892415.1
SIV	SIVmac746	KU955513.1
SIV	SIVmac766	KU955514.1
SIV	SIVmacCR53	KU955515.1
SIV	SIVmacPBE	KU955516.1
SIV	SIVsmR02012	KU955517.1
SIV	SIVsmR95117	KU955518.1
SIV	SIVsmE660-FL14	JQ864087.1
SIV	SIVsmE660-FL8	JQ864086.1
SIV	SIVsmE660-FL6	JQ864085.1
SIV	SIVsmE660-FL10	JQ864084.1
SIV	SIVsmH635FC	DQ201174.1
SIV	SIVsmH635SB10	DQ201173.1
SIV	SIVsmH635F-L3	DQ201172.1
SIV	SIVsmE543	U72748.2
SIV	SIVmac32H	D01065.1
SIV	SIVMne027	U79412.1
SHIV	SHIV-1157ipd3N4	DQ779174.2
SHIV	pSF257.2	KU521530.1
SHIV	SHIV-89.6P	U89134.1
SHIV	SHIV_DH12_CL8	JN560963.1
SHIV	SHIV_DH12_CL7	JN560962.1
SHIV	SHIV_AD8	JN560961.1
SHIV	pSHIV_AD8_B_ES_3N6	JN560960.1
SHIV	SHIV AD8 B ES 3T7	JN560959.1
SHIV	SHIV-C2/1	AF217181.1
SHIV	SHIV-HXBc2P 3.2	AF041850.1
SHIV	SHIV-4	AF038399.1
SHIV	SHIV-89.6	AF038398.1
SHIV	SHIV-89.6Pcy243	EF672090.1
SHIV	SHIV.B.YU2C	KU958489.1
SHIV	SHIV.C.CH848.dCT	KU958488.1
SHIV	SHIV.C.CH505.dCT	KU958487.1
SHIV	SHIV.D.191859.dCT	KU958486.1
SHIV	SHIV.D.191859	KU958485.1
SHIV	SHIV.A.BG505.dCT	KU958484.1
SHIV	genomic RNA	AB177846.1
SHIV	SHIV_SF162	KF042063.1

Virus	Strain/Isolate	Accession No.
SIV	SIVmac251.RD.tf1	KC522251.1
SIV	SIVmac251.RD.p3h4	KC522252.1
SIV	SIVmac251.RD.tf5	KC522253.1

Virus	Strain/Isolate	Accession No.
SHIV	SHIVku2	AY751799.1
SHIV	1B3	AF465242.1
SHIV	NHP model of AIDS	BD161892.1

Supplemental table II: Summary of Mamu-A1*001 ELISPOT results. Of the SIVmac239 peptides that strongly bound Mamu-A1*001, we tested the top 90 highest-binding peptides, including 17 peptides corresponding to known epitopes, plus two additional peptides corresponding to known epitopes that were not in the top 90 (indicated by asterisks), by IFN-γ ELISPOT. Shown here are the peptide array binding scores as well as the previously-established IC_{50} values where available (14, 28). We performed IFN-γ ELISPOTs using PBMC from four Mamu-A1*001-positive, SIVmac239-infected rhesus macaques, and the number of animals for which each peptide was positive (bold text) is indicated.

Peptide array ranking	Sequence	Position	Peptide array binding score (fluorescence intensity units)	IC_{50} (nM)	Number of positive ELISPOTs
43	CAPPGYAL*	Env 233-240	8.3685	1.9	0
9	**VTPNYADILL***	**Vif 100-109**	**10.087**	**2.6**	**1**
1621	LGPHYTPKIV*	Pol 147-156	4.3519	3.0	0
59	CAPPGYALL*	Env 233-241	7.7607	5.5	0
35	STPPLVRLV*	Pol 625-633	8.6749	8.7	0
41	**TVPWPNASL***	**Env 620-628**	**8.4253**	**10**	**1**
7	**VTPNYADIL***	**Vif 100-108**	**10.1469**	**12**	**1**
28	STPPLVRL*	Pol 625-632	8.9627	26	0
31	YTPKIVGGI*	Pol 151-159	8.846	26	0
47	LAPVPIPF*	Gag 372-379	8.2514	29	0
44	**STPESANL***	**Tat 28-35**	**8.329**	**43**	**2**
30	LAPVPIPFA*	Gag 372-380	8.8912	50	0
20	LTPEKGWL*	Vif 75-82	9.5103	61	0
16	MTPAERLI*	Pol 961-968	9.6721	77	0
230	**CTPYDINQM***	**Gag 181-189**	**5.517**	**86**	**4**
8	VTPNYADI*	Vif 100-107	10.1361	230	0
2	ITPIGLAPT*	Env 502-510	10.451	286	0
17	LSPRTLNAW*	Gag 149-157	9.6436	355	0
3	SSPPSYFQQT*	Env 726-735	10.4333	-	0
1	LTPKWNNETW	Env 628-637	10.8155	-	0
4	LTPKWNNE	Env 628-635	10.3383	-	0
5	ITPIGLAPTD	Env 502-511	10.2741	-	0
6	ITPIGLAP	Env 502-509	10.2183	-	0
10	SSPPSYFQQ	Env 726-734	9.9876	-	0
11	LTPKWNNET	Env 628-636	9.9236	-	0
12	LTPEKGWLS	Vif 75-83	9.859	-	0
13	SSPPSYFQ	Env 726-733	9.8311	-	0
14	LTPEKGWLST	Vif 75-84	9.8008	6827	0
15	LSPRTLNAWV	Gag 149-158	9.7328	-	0
18	TPEALCDP	Rev 91-98	9.6377	-	0

Peptide array ranking	Sequence	Position	Peptide array binding score (fluorescence intensity units)	IC_{50} (nM)	Number of positive ELISPOTs
19	MTPAERLINM	Pol 961-970	9.6144	-	0
21	MTPAERLIN	Pol 961-969	9.4925	-	0
22	FSSPPSYFQQ	Env 725-734	9.3375	-	0
23	**TPESANLGE**	**Tat 29-37**	**9.2769**	**-**	**3**
24	FSSPPSYFQ	Env 725-733	9.2663	-	0
25	FSSPPSYF	Env 725-732	9.2264	-	0
26	TPEALCDPTE	Rev 91-100	9.196	-	0
27	SPPSYFQQ	Env 727-734	8.9673	-	0
29	YTPKIVGGIG	Pol 151-160	8.9392	-	0
32	LSPRTLNA	Gag 149-156	8.7839	-	0
33	MSPSYVKY	Vpx 62-69	8.7662	6381	0
34	TPESANLG	Tat 29-36	8.7261	-	0
36	APVPIPFA	Gag 373-380	8.6296	-	0
37	**STPESANLGE**	**Tat 28-37**	**8.4623**	**-**	**3**
38	STPPLVRLVF	Pol 625-634	8.4394	-	0
39	MSPSYVKYR	Vpx 62-70	8.4364	-	0
40	TPESANLGEE	Tat 29-38	8.43	-	0
42	TPAERLIN	Pol 962-969	8.374	-	0
45	TPEALCDPT	Rev 91-99	8.2987	-	0
46	LAPVPIPFAA	Gag 372-381	8.2954	-	0
48	APVPIPFAA	Gag 373-381	8.2434	-	0
49	**YSFPDPPTDT**	**Rev 58-67**	**8.0926**	**-**	**1**
50	SPPSYFQQT	Env 727-735	8.0737	-	0
51	MSPSYVKYRY	Vpx 62-71	8.0661	1378	0
52	VPWPNASL	Env 621-628	8.0275	-	0
53	TTVPWPNASL	Env 619-628	8.0263	-	0
54	VPWPNASLTP	Env 621-630	8.0239	-	0
55	**STPESANLG**	**Tat 28-36**	**7.9503**	**-**	**3**
56	YSFPDPPT	Rev 58-65	7.8633	-	0
57	LSPLCITM	Env 104-111	7.8383	-	0
58	TPLDLAIQ	Rev 67-74	7.8137	-	0
60	VPIPFAAA	Gag 375-382	7.7329	-	0
61	TVPWPNAS	Env 620-627	7.6856	-	0
62	TPAERLINM	Pol 962-970	7.6717	-	0
63	VPWPNASLT	Env 621-629	7.6711	-	0
64	**ISTPPLVRL**	**Pol 624-632**	**7.6681**	**-**	**1**

Peptide array ranking	Sequence	Position	Peptide array binding score (fluorescence intensity units)	IC_{50} (nM)	Number of positive ELISPOTs
65	**QTNPYPTGPG**	**Rev 22-31**	**7.6257**	**-**	**1**
66	**ISTPPLVRLV**	**Pol 624-633**	**7.5903**	**-**	**1**
67	SPRTLNAW	Gag 150-157	7.5645	-	0
68	QTNPYPTGP	Rev 22-30	7.5606	-	0
69	TPIGLAPT	Env 503-510	7.5415	-	0
70	TVPWPNASLT	Env 620-629	7.5259	-	0
71	SPAIFQYT	Pol 364-371	7.5057	-	0
72	SPPSYFQQTH	Env 727-736	7.4898	-	0
73	TPAERLINMI	Pol 962-971	7.4785	-	0
74	VPIPFAAAQ	Gag 375-383	7.3507	-	0
75	LTACQGVGGP	Gag 348-357	7.3473	-	0
76	TPLDLAIQQ	Rev 67-75	7.3364	-	0
77	YSFPDPPTD	Rev 58-66	7.325	-	0
78	VFSSPPSYFQ	Env 724-733	7.2631	-	0
79	SPAIFQYTM	Pol 364-372	7.2564	-	0
80	TPINIFGRN	Pol 189-197	7.2498	-	0
81	QTNPYPTG	Rev 22-29	7.2488	-	0
82	TPIGLAPTD	Env 503-511	7.2413	-	0
83	VPIPFAAAQQ	Gag 375-384	7.2296	-	0
84	TTVPWPNAS	Env 619-627	7.2289	-	0
85	VFSSPPSYF	Env 724-732	7.2109	-	0
86	APPGYALL	Env 234-241	7.2054	-	0
87	SLTPKWNNET	Env 627-636	7.1852	-	0
88	IPPSRSML	Vpr 94-101	7.182	7576	0
89	**NTPEALCDPT**	**Rev 90-99**	**7.1785**	**-**	**1**
90	LSPLCITMR	Env 104-112	7.1633	-	0

Supplemental table III: Comparison of Mamu-A1*001 binding to known SIVmac239 epitopes and the equivalent SIVmac251 sequences. Sequences with amino acid changes between viruses are indicated in bold. Only one sequence was considered “high binding” in SIVmac239 but not in SIVmac251 as the result of a position three proline to leucine substitution.

SIVmac239 epitope	SIVmac239 intensity	SIVmac239 top 192	SIVmac251 sequence	SIVmac251 intensity	SIVmac251 top 192
ITPIGLAPT	10.45	Yes	ITPIGLAPT	10.45	Yes
SSPPSYFQQT	10.43	Yes	SSPPSYFQQT	10.43	Yes
VTPNYADIL	**10.15**	**Yes**	**VTPDYADIL**	**10.04**	**Yes**
VTPNYADI	**10.14**	**Yes**	**VTPDYADI**	**9.52**	**Yes**
VTPNYADILL	**10.09**	**Yes**	**VTPDYADILL**	**9.80**	**Yes**
MTPAERLI	9.67	Yes	MTPAERLI	9.67	Yes
LSPRTLNAW	9.64	Yes	LSPRTLNAW	9.64	Yes
LTPEKGWL	**9.51**	**Yes**	**LTPERGWL**	**9.38**	**Yes**
STPPLVRL	8.96	Yes	STPPLVRL	8.96	Yes
YTPKIVGGI	8.85	Yes	YTPKIVGGI	8.85	Yes
STPPLVRLV	8.67	Yes	STPPLVRLV	8.67	Yes
TVPWPNASL	8.43	Yes	TVPWPNASL	8.43	Yes
CAPPGYAL	8.37	Yes	CAPPGYAL	8.37	Yes
STPESANL	**8.33**	**Yes**	**TTPESANL**	**8.72**	**Yes**
LAPVPIPF	8.25	Yes	LAPVPIPF	8.25	Yes
CAPPGYALL	7.76	Yes	CAPPGYALL	7.76	Yes
ASTPESANL	**6.71**	**Yes**	**ATTPESANL**	**7.43**	**Yes**
QSPGGLDKGL	**6.46**	**Yes**	**QSLGGLGKGL**	**4.26**	**No**
VVPGFQAL	6.21	Yes	VVPGFQAL	6.21	Yes
GSPAIFQYTM	6.21	Yes	GSPAIFQYTM	6.21	Yes
QVPSLQYLA	6.04	Yes	QVPSLQYLA	6.04	Yes
GSPAIFQYT	5.91	Yes	GSPAIFQYT	5.91	Yes
CTPYDINQM	5.52	No	CTPYDINQM	5.52	No
YVPCHIRQI	4.85	No	YVPCHIRQI	4.85	No
GPPPPPPPGL	4.83	No	GPPPPPPPGL	4.83	No
QVPKFHLPV	4.77	No	QVPKFHLPV	4.77	No
IYPGIKTKHL	4.53	No	IYPGIKTKHL	4.53	No
RIPERLERW	4.50	No	RIPERLERW	4.50	No
QNPIPVGNI	4.41	No	QNPIPVGNI	4.41	No
LGPHYTPKIV	4.35	No	LGPHYTPKIV	4.35	No
DPPTNTPEAL	4.22	No	DPPTNTPEAL	4.22	No
HLPRELIFQV	4.20	No	HLPRELIFQV	4.20	No
VNPTLEEMLT	4.05	No	VNPTLEEMLT	4.05	No