

1 **Primary role of type I interferons for the induction of functionally optimal**  
2 **antigen-specific CD8<sup>+</sup> T cells in HIV infection**

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4 **Piccin et al.**

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6 **SUPPLEMENTAL TABLES & FIGURES**

7  
8  
9 **LIST OF SUPPLEMENTARY MATERIAL**

10 **Table S1.** Characteristics of people living with HIV-1.

11 **Table S2.** Mutagenized virus sequences used in this study.

12 **Table S3.** Real-time qPCR primer sequences used in this study.

13 **Table S4.** List of genes.

14 **Figure S1.** Virus production and late RT analysis.

15 **Figure S2.** Memory phenotype of primed CD8<sup>+</sup> T cells.

16 **Figure S3.** Differentially expressed genes in CD8<sup>+</sup> T cells primed with HIV-1 or HIV-2.

17 **Figure S4.** Schematic representation of the *in vitro* priming approach using cognate peptide  
18 and adjuvants.

19 **Figure S5.** Differentially expressed genes in CD8<sup>+</sup> T cells primed in the presence of  
20 proinflammatory cytokines, IFN- $\alpha$ , or cGAMP.

21 **Figure S6.** Impact of cGAMP on CD8<sup>+</sup> T cell priming with ELA in the presence of  
22 proinflammatory cytokines or with ELA20  $\Delta$ env HIV-1.

23 **Figure S7.** Secretion of soluble factors after stimulation of PBMCs with proinflammatory  
24 cytokines or cGAMP.

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**Table S1. Characteristics of people living with HIV-1.**

<b>Donor</b>	<b>Age (yrs)</b>	<b>Sex</b>	<b>Nadir CD4 (cells/<math>\mu</math>L)</b>	<b>CD4 count (cells/<math>\mu</math>L)</b>	<b>CD8 count (cells/<math>\mu</math>L)</b>	<b>Viral load (cp/mL)</b>	<b>Time since diagnosis (yrs)</b>	<b>Time on ART (yrs)</b>
1	36	Male	154	461	941	<40	7	6.5
2	48	Male	195	662	658	<40	17	17
3	36	Male	156	882	1177	<40	14	9
4	55	Male	236	847	613	<40	29	14
5	21	Male	228	331	402	<40	4	4
6	60	Male	-	803	422	<40	25	20
7	36	Male	354	471	322	<40	12	5
8	57	Male	218	911	873	<40	24	21
9	47	Male	274	733	691	<40	13	7
10	50	Male	328	820	723	<40	22	16

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**Table S2. Mutagenized virus sequences used in this study.**

Backbone	Mutation	Original DNA sequence	Mutagenized sequence
pNLAD8	pNLAD8 ELA20	GCA GCT GAC ACA GGA AAC AAC AGC	GCA GCT GAC ACA <b><u>TAC</u></b> <b><u>ACC GCC GCC GAG GAG</u></b> <b><u>CTG GCC GGC ATC GGC</u></b> <b><u>ATC CTG ACC GTG ATC</u></b> <b><u>CTG GGC GTG CTG</u></b> GGA AAC AAC AGC
pNLAD8	pNLAD8 $\Delta$ env	GTG GGT CAC AGT CTA TTA TGG GGT ACC <b><u>TGT GTG GAA AGA AGC</u></b> <b><u>AAC CAC CAC TCT ATT TTG TGC</u></b> <b><u>ATC AGA [...]</u></b> <b><u>AAC ATT AGT AGA</u></b> <b><u>ACA AAA TGG AAT AAC ACT TTA</u></b> <b><u>AAT CAA ATA</u></b> GCT ACA AAA TTA AAA GAA CAA TTT GGG	GTG GGT CAC AGT CTA TTA TGG GGT ACC <b><u>:::</u></b> GCT ACA AAA TTA AAA GAA CAA TTT GGG
pJK7312AS	pJK7312AS ELA20	ACT GCA GAC AAA CCA GCA GCG ACA	ACT GCA GAC AAA <b><u>TAC</u></b> <b><u>ACC GCC GCC GAG GAG</u></b> <b><u>CTG GCC GGC ATC GGC</u></b> <b><u>ATC CTG ACC GTG ATC</u></b> <b><u>CTG GGC GTG CTG</u></b> CCA GCA GCG ACA
pJK7312AS	pJK7312AS $\Delta$ env	GCT TAC TTA ATA TAT TGC ACC AAA TAC <b><u>GTA ACT GTT TTC TAT</u></b> <b><u>GGC GTG CCC GTG TGG AGA AAT</u></b> <b><u>GCA TCC [...]</u></b> <b><u>ACA TAT ATG TAT</u></b> <b><u>TGG CAT AGT AAA GAT AAT AGG</u></b> <b><u>ACT ATT ATA</u></b> AGC TTG AAT AAG TAT TAT AAT TTA ACA	GCT TAC TTA ATA TAT TGC ACC AAA TAC <b><u>:::</u></b> AGC TTG AAT AAG TAT TAT AAT TTA ACA
pNLAD8	pNLAD8 ELA20 $\Delta$ env	Both mutations from pNLAD8 ELA20 and pNLAD8 $\Delta$ env	
pJK7312AS	pJK7312AS ELA20 $\Delta$ env	Both mutations from pJK7312AS ELA20 and pJK7312AS $\Delta$ env	

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**Table S3. Real-time qPCR primer sequences used in this study.**

<b>Strain</b>	<b>Amplification</b>	<b>Primer</b>	<b>Sequence</b>	<b>Annealing optimum</b>
Human	$\beta$ -globin	bglobin-f	CCCTTGGACCCAGAGGTTCT	65 °C
		bglobin-r	CGAGCACTTTCTTGCCATGA	65 °C
pJK7312AS	Late RT	hiv2-f2	GCAGGTAGAGCCTGGGTGTTC	65 °C
		hiv2jk-psi-rev	GTTCCGAAGACTCTCACTCTTCTC	65 °C
pNLAD8	Late RT	hiv1-3'U3-fwd	GCATGGAATGGATGACCCTGAGA	65 °C
		hiv1-psi-rev2	CGTCGAGAGATCTCCTCTGGCTTTA	65 °C

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**Table S4. List of genes.**

Gene Symbol	FP	RP	Full Gene Name
<i>ACTB</i>	CCAACCGCGAGAAGATGAC	TAGCACAGCCTGGATAGCAA	actin beta
<i>AKT1</i>	CACACACTCACCGAGAACC	TCGTGGGTCTGGAAAGAGTA	AKT serine/threonine kinase 1
<i>BAG6</i>	GCCTCAGTGGATCCAGCAA	AGAGAAAGCAAGGCCCCAAA	BCL2-associated athanogene 6
<i>BATF</i>	AGCAGTGACTCCAGCTTCA	CTCTTCTGGGCGGCAATAC	basic leucine zipper ATF-like transcription factor
<i>BAX</i>	GGGTTGTCGCCCTTTTCTAC	TCTTGATCCAGCCCAACA	BCL2 associated X, apoptosis regulator
<i>BCL2</i>	ATGTGTGTGGAGAGCGTCAA	GTGCCGGTTCAGGTA CTCA	BCL2 apoptosis regulator
<i>BCL2L1</i>	CTGCCTGCCTTTGCCTAA	CCAAAACACCTGCTCACTCA	BCL2 like 1
<i>BCL6</i>	GATGGAGCATGTTGTGGACAC	AGGAGGCTTGATGGCAGAAA	BCL6 transcription repressor
<i>BECN1</i>	GAGACCCAGGAGGAAGAGACTA	AATCTGCGAGAGACACCATCC	beclin 1
<i>CASP8</i>	GGAAATCTCCAAATGCAAACCTGG	CAGGATGACCCTCTTCTCCAT	caspase 8
<i>CCL3</i>	ATGGCTCTCTGCAACCAGTT	CCGGGAGGTGTAGCTGAAG	C-C motif chemokine ligand 3
<i>CCL3L1</i>	ACGCAGGCAGCAAAGAGTA	ATTGGGAGCAGGTGATGGAA	C-C motif chemokine ligand 3 like 1
<i>CCNH</i>	GAACAGAACTTGCTGTCCAC	CTTCAGATCTGGGTGGTTCA	cyclin H
<i>CCR5</i>	TGAGACATCCGTTCCCTACA	TGGCAGGGCTCCGATGTATA	C-C motif chemokine receptor 5 (gene/pseudogene)
<i>CCR7</i>	GTGGTGGCTCTCCTTGTC	CTGTGGTGTCTCCGATGTA	C-C motif chemokine receptor 7
<i>CD244</i>	AACCACAGCCCTTCTTCAA	GAGCAGGGTTCTGGGCTTTA	CD244 molecule
<i>CD27</i>	CACTACTGGGCTCAGGGAAA	TGCTGGTCACAGTCCTTCA	CD27 molecule
<i>CD300A</i>	GAAAAGCCAGCACCACCAA	TCAAACACCACCGAGGCATA	CD300a molecule
<i>CD38</i>	ACCTCATGTTGTGGTGAA	GTTGCTGCAGTCCTTCTCC	CD38 molecule
<i>CD69</i>	TCACCCATGGAAGTGGTCAA	ACACACTTGTCAGACCCTGTA	CD69 molecule
<i>CD8A</i>	CCATCATGTA CTTCAGCCACTTCG	GCTGCGACGCGATGGT	CD8a molecule
<i>CDC42</i>	GCTGTTGGTAAAACATGTCTCC	AACTGTGACTGCATAGTTGTCA	cell division cycle 42
<i>CDK2</i>	GTTGTACCTCCCCTGGATGAA	ATCCGCTTGTAGGGTCGTA	cyclin dependent kinase 2
<i>CDK4</i>	GACATGTGGAGTGTGGCTGTA	TGGTCGGCTTCAGAGTTTCC	cyclin dependent kinase 4
<i>CDK6</i>	TTGCCCGCATCTATAGTTTCCA	CAAGACTTCGGGTGCTCTGTA	cyclin dependent kinase 6
<i>CDK7</i>	TGAAACTTTGGGCACACCAA	GATGCAAAGGTATTCCAGGGAAA	cyclin dependent kinase 7
<i>CDKN1A</i>	TGGAGACTCTCAGGGTCGAAAA	CGGCGTTTGGAGTGGTAGAA	cyclin dependent kinase inhibitor 1A
<i>CDKN1B</i>	GCAATGCGCAGGAATAAGGAA	TTGGGGAACCGTCTGAAACA	cyclin dependent kinase inhibitor 1B

<i>CDKN2A</i>	CACCGCTTCTGCCTTTTCA	CCCACATGAATGTGCGCTTA	cyclin dependent kinase inhibitor 2A
<i>CPT1A</i>	TCCATGCCATCCTGCTTTACA	AGTGAATCGTGGATCCCAAA	carnitine palmitoyltransferase 1A
<i>CTLA4</i>	CATGGACACGGGACTCTACA	AATCTGGGTTCCGTTGCCTA	cytotoxic T-lymphocyte associated protein 4
<i>ERCC1</i>	AACCCGGGGCAAATCCAA	CACATTGCGCACGAACTTCA	ERCC excision repair 1, endonuclease non-catalytic subunit
<i>ERCC3</i>	GACTGGAGTCCCTGATGGAA	TGCTTCAAGACCAGCTTGAC	ERCC excision repair 3, TFIIH core complex helicase subunit
<i>ERCC4</i>	CTTCTGGAATCTCTGAGAGCAA	GAGGTGCTGGAGTCAAGAAA	ERCC excision repair 4, endonuclease catalytic subunit
<i>ESRRA</i>	GGAGCGAGAGGAGTATGTTCTAC	CTTCTCGCAGCTGCTCCA	estrogen related receptor alpha
<i>FAS</i>	GCATCTGGACCCTCCTACC	CCTTGGAGTTGATGTCAGTCAC	Fas cell surface death receptor
<i>FASLG</i>	TGGGGATGTTTCAGCTCTTCC	CTGTGTGCATCTGGCTGGTA	Fas ligand
<i>FOXO1</i>	GGTGTCCAGGCTGAGGGTTA	TTCTCTCAGTTCCTGCTGTCA	forkhead box O1
<i>GAPDH</i>	GAACGGGAAGCTTGTCATCAA	ATCGCCCCACTTGATTTTGG	glyceraldehyde-3-phosphate dehydrogenase
<i>GATA3</i>	CACGGTGCAGAGGTACCC	AGGGTAGGGATCCATGAAGCA	GATA binding protein 3
<i>GLS</i>	AAGGCACAGACATGTTGGTA	CACTGGCTGATTCACAAGTCAC	glutaminase
<i>GLS2</i>	TTAGACCCACGGCGTGAA	TCGCCACTATAGGCAGCAA	glutaminase 2
<i>GZMB</i>	CCCCATCCAGCCTATAATCCTAA	CTGGGCCTTGTTGCTAGGTA	granzyme B
<i>GZMK</i>	CACATTTTCATCTGGGCTTCTTAAA	GTGACACTTCTTTCCCTCCA	granzyme K
<i>HIF1A</i>	CAGTCGACACAGCCTGGATA	TTCTTCTGGCTCATATCCCATCAA	hypoxia inducible factor 1 subunit alpha
<i>HK1</i>	TCATTTCCCTGCCAGCAGAC	CGCAGTCTGTTGCCTTAAAACC	hexokinase 1
<i>HLA-DRB1</i>	AGAATGGAGACTGGACCTTCC	GCTCTGTGCAGATTCAGACC	major histocompatibility complex, class II, DR beta 1
<i>ID2</i>	CTCAACACGGATATCAGCATCC	CACACAGTGCTTTGCTGTCA	inhibitor of DNA binding 2
<i>IFITM1</i>	ACACCCTCTTCTTGAAGTGGT	CCAACCATCTTCTGTCCCTA	interferon induced transmembrane protein 1
<i>IFNA1</i>	TGACTCATACACCAGGTCAC	CAGGGGTGAGAGTCTTTGAA	interferon alpha 1
<i>IFNB1</i>	ATGAGCAGTCTGCACCTGAA	GACTGTACTCCTTGGCCTTCA	interferon beta 1
<i>IFNG</i>	ACTGCCAGGACCCATATGTAA	GTTCCATTATCCGCTACATCTGAA	interferon gamma
<i>IFNGR1</i>	AAGCCAGGGTTGGACAAAA	GATATCCAGTTTAGGTGGTCCAA	interferon gamma receptor 1
<i>IL7R</i>	GGAGAAAAGTGGCTATGCTCAA	CTGCGATCCATTCACTTCCA	interleukin 7 receptor
<i>IRF1</i>	AACAAGGATGCCTGTTTGTCC	TGGGATCTGGCTCCTTTTCC	interferon regulatory factor 1
<i>KLRD1</i>	AGCATTACTCCAGGACCCAAC	TAACAGTTGCACCGGTACCC	killer cell lectin like receptor D1
<i>LAG3</i>	TGGAGCCTTTGGCTTTTCC	GAGGGTGAATCCCTTGCTCTA	lymphocyte activating 3

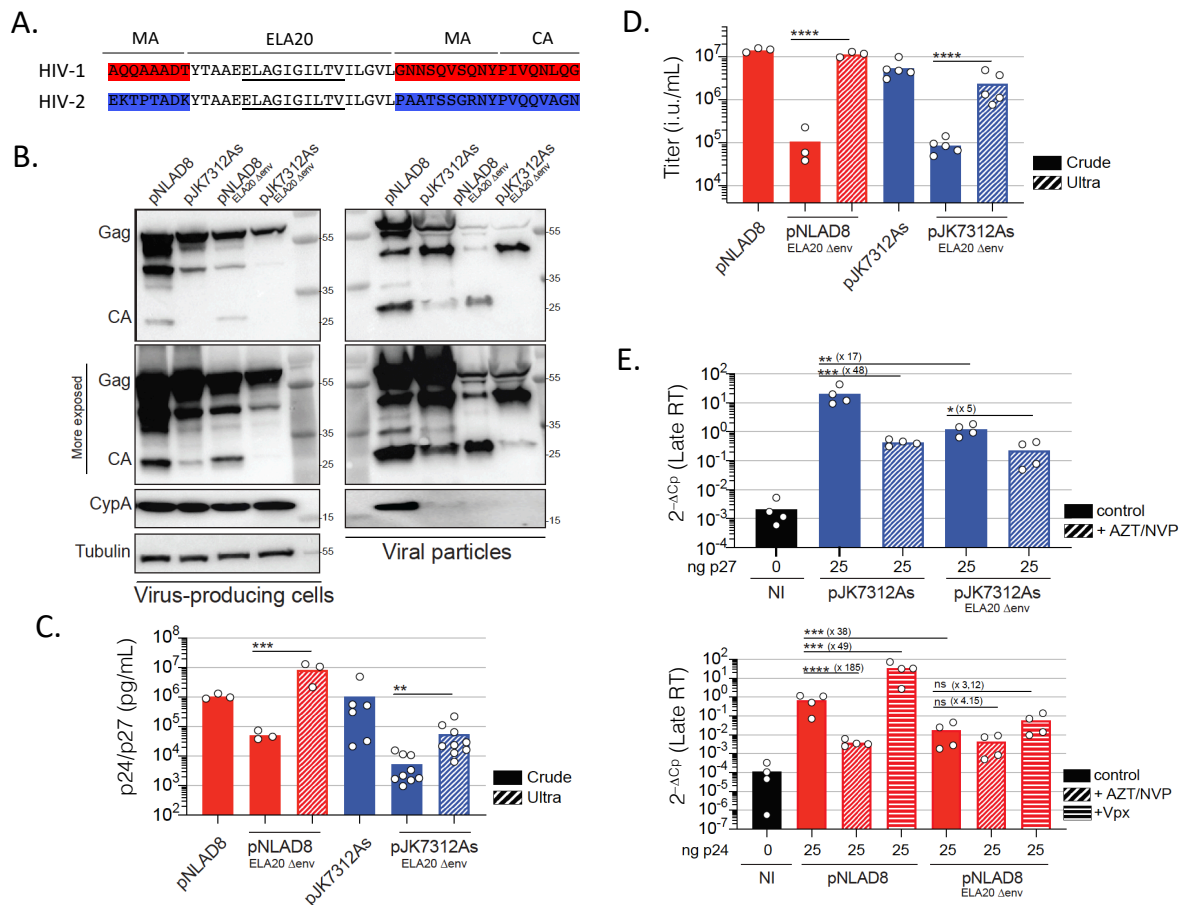
<i>LAMP1</i>	TCCAGGCTTTCAAGGTGGAA	CCACAGCGATGGGGATCA	lysosomal associated membrane protein 1
<i>LEF1</i>	AAGAAAGTGCAGCTATCAACCA	GCTGTCTTTCTTTCCGTGCTA	lymphoid enhancer binding factor 1
<i>MIF</i>	TGCCATCATGCCGATGTTCA	GGTGAGCTCGGAGAGGAAC	macrophage migration inhibitory factor
<i>MLST8</i>	TGCAGGCTACGACCACAC	TGTGACCTCCAAGGCATTCA	MTOR associated protein, LST8 homolog
<i>MTOR</i>	CCAAACCCAGGTGTGATCAA	TCCTCATTTCCAGGCCACTA	mechanistic target of rapamycin kinase
<i>MX1</i>	ATGCTACTGTGGCCAGAAA	GGCGCACCTTCTCCTCATA	MX dynamin like GTPase 1
<i>MYC</i>	CCTGGTGCTCCATGAGGA	CCTGCCTCTTTCCACAGAAA	MYC proto-oncogene, bHLH transcription factor
<i>NDUFA5</i>	ACCAACTTCAAGGCGGTCAA	TGGCTCCCATAGTTTCCATTCC	NADH:ubiquinone oxidoreductase subunit A5
<i>NFATC1</i>	TCCTCTCCAACACCAAAGTCC	AGGATTCCGGCACAGTCAA	nuclear factor of activated T cells 1
<i>NT5E</i>	ATGAACGCCCTGCGCTAC	GTGGCTCGATCAGTCCTTCC	5'-nucleotidase ecto
<i>OAS1</i>	TACCCTGTGTGTGTGCCAA	AGAGGACTGAGGAAGACAACC	2'-5'-oligoadenylate synthetase 1
<i>OPA1</i>	CCAAAGTAGACCTGGCAGAGAA	TCATTGGGAAGAGCTTTCCTTCA	OPA1, mitochondrial dynamin like GTPase
<i>PCNA</i>	TCTGAGGGCTTCGACACCTA	CATTGCCGGCGCATTTTAGTA	proliferating cell nuclear antigen
<i>PDCD1</i>	GCAGCCTGGTGCTGCTA	GTGCGCCTGGCTCCTA	programmed cell death 1
<i>PFKM</i>	AGGAAGAATGTGCTTGGTCAC	CGCCCATCTTAGTGGCAA	phosphofructokinase, muscle
<i>PKM</i>	CGGGTGAACCTTGGCATGAA	CATCCGGTCAGCACAAATGAC	pyruvate kinase M1/2
<i>POLR2A</i>	CTCGCCTCTTCTACTCCAACA	ATGGAGTCCCAATGCCAATA	RNA polymerase II subunit A
<i>PRDM1</i>	CCTGGTACACACGGGAGAAAA	TTGAGATTGCTGGTGCTGCTA	PR/SET domain 1
<i>PRF1</i>	CATCTGTGTAGCCGCTTCTCTA	TGCCAGGAGGAGCAGAC	perforin 1
<i>PRKAA1</i>	CCAACATGCTGCACCAGAA	AGAATAACCCCACTGCTCCA	protein kinase AMP-activated catalytic subunit alpha 1
<i>PRKCA</i>	ACCATCCGCTCCACACTAAA	AGTCGTGGTCTTTGTCTGAA	protein kinase C alpha
<i>RHOA</i>	GTGCCACAGTGTGAGAA	TGTGTCCACAAAGCCAAC	ras homolog family member A
<i>RICTOR</i>	CTTCCGTGTCGGAGGTTTATA	ACACAGCCTCTGCTTCTTCA	RPTOR independent companion of MTOR complex 2
<i>RPTOR</i>	GCTCAGAGCTGGAGGATGAA	AGGGTCCACACCAACATTCA	regulatory associated protein of MTOR complex 1
<i>RUNX1</i>	ACCACAGAGCCATCAAATCAC	CGGGCTTGGTCTGATCATCTA	RUNX family transcription factor 1
<i>SH2D1A</i>	GAAGTCCTCAGCTAGAAGTACACA	GGGCTTTCAGGCAGACATCA	SH2 domain containing 1A
<i>SLC2A1</i>	ATTGTGGGCATGTGCTTCC	AGAACCAGGAGCACAGTGAA	solute carrier family 2 member 1
<i>SLC2A3</i>	CCGTCCGACTCTTCGTCAA	TAAAGCAGCCACCAAGTGACA	solute carrier family 2 member 3
<i>STAT3</i>	GGAAATAATGGTGAAGGTGCTGAAC	CCGAGGTCAACTCCATGTCAAA	signal transducer and activator of transcription 3

<i>TBX21</i>	GGGCGTCCAACAATGTGAC	CCGTCGTTACCTCAACGATA	T-box transcription factor 21
<i>TCF7</i>	CTGCACATGCAGCTATACCC	TGGATTCTTGGTGCTTTTCCC	transcription factor 7
<i>TERT</i>	CCAGAACGTTCCGCAGAGAAAA	ACGCTGAACAGTGCCTTCAC	telomerase reverse transcriptase
<i>TFAM</i>	GAAGACTGTAAAGGAAAACCTGGAA	CATTTGTTCTTCCAAGACTTCA	transcription factor A, mitochondrial
<i>TNF</i>	CCCAGGGACCTCTCTAATCA	ATGGGCTACAGGCTTGTCAC	tumor necrosis factor
<i>TNFSF10</i>	AGAAGGAAGGGCTTCAGTGAC	CCTGGACCTCCATCATAGCC	TNF superfamily member 10
<i>TP53</i>	GACTGTACCACCATCCACTACA	AAAGCTGTTCCGTCCCAGTA	tumor protein p53
<i>VHL</i>	TGTTTAGGGCAAACATCACAA	AAAATGCCACCACCTTCTCC	von Hippel-Lindau tumor suppressor
<i>XCL1</i>	ACTGCCGGTTAGCAGAATCAA	CCCATGTGGCTTGTGGATCA	X-C motif chemokine ligand 1
<i>XPC</i>	CTCTGCTCGAGATGATGAGGAA	ACAATACCAGCCGGGTCAA	XPC complex subunit, DNA damage recognition and repair factor

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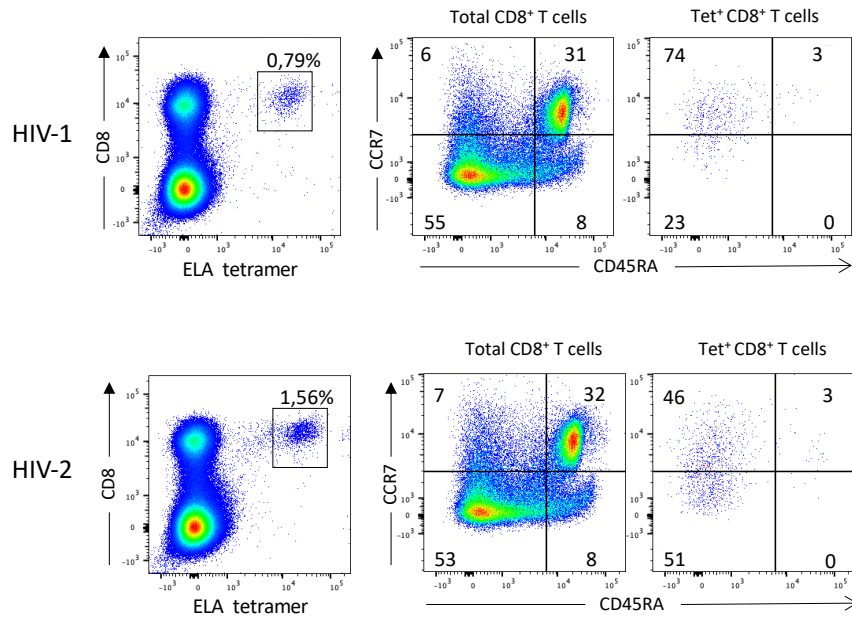


48 **Figure S1. Virus production and late RT analysis.**



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50 (A) Insertion of the ELA20 sequence into HIV-1 and HIV-2. (B) Western blot of Gag, capsid  
51 (CA), cyclophilin A (CypA), and tubulin in virus-producing 293FT cells and VLPs. Data are  
52 representative of three independent experiments. (C) Concentrations of p24 or p27 in crude  
53 preparations of pNLAD8 (n = 3) or pJK7312As (n = 6) and crude or ultracentrifuged  
54 preparations of pNLAD8 ELA20 Δenv (n = 3) or pJK7312As ELA20 Δenv (n = 9), respectively.  
55 Each dot represents one experiment. Bars indicate mean values. \*\*p < 0.01, \*\*\*p < 0.001  
56 (unpaired repeated measures ANOVA). (D) Titers of crude pNLAD8 (n = 3) or pJK7312As (n  
57 = 5) on 293FT cells and crude or ultracentrifuged pNLAD8 ELA20 Δenv (n = 3) or pJK7312As  
58 ELA20 Δenv (n = 5) on GHOST X4R5 cells. Each dot represents one experiment. Bars indicate  
59 mean values. \*\*\*\*p < 0.0001 (unpaired repeated measures ANOVA). (E) Quantification of  
60 pJK7312As or pJK7312As ELA20 Δenv (top, n = 4) and pNLAD8 or pNLAD8 ELA20 Δenv  
61 late RT products (bottom, n = 4) 24 h after infection of MDDCs. Cells were left untreated or  
62 treated with azidothymidine (AZT) and nevirapine (NVP) at the time of the infection. SIVmac  
63 VLPs were added to provide Vpx. NI, no infection. Each dot represents one experiment. Bars  
64 indicate mean values. \*\*\*p < 0.001, \*\*\*\*p < 0.0001, ns = not significant (paired repeated  
65 measures ANOVA using log-transformed data).

66 **Figure S2. Memory phenotype of primed CD8<sup>+</sup> T cells.**



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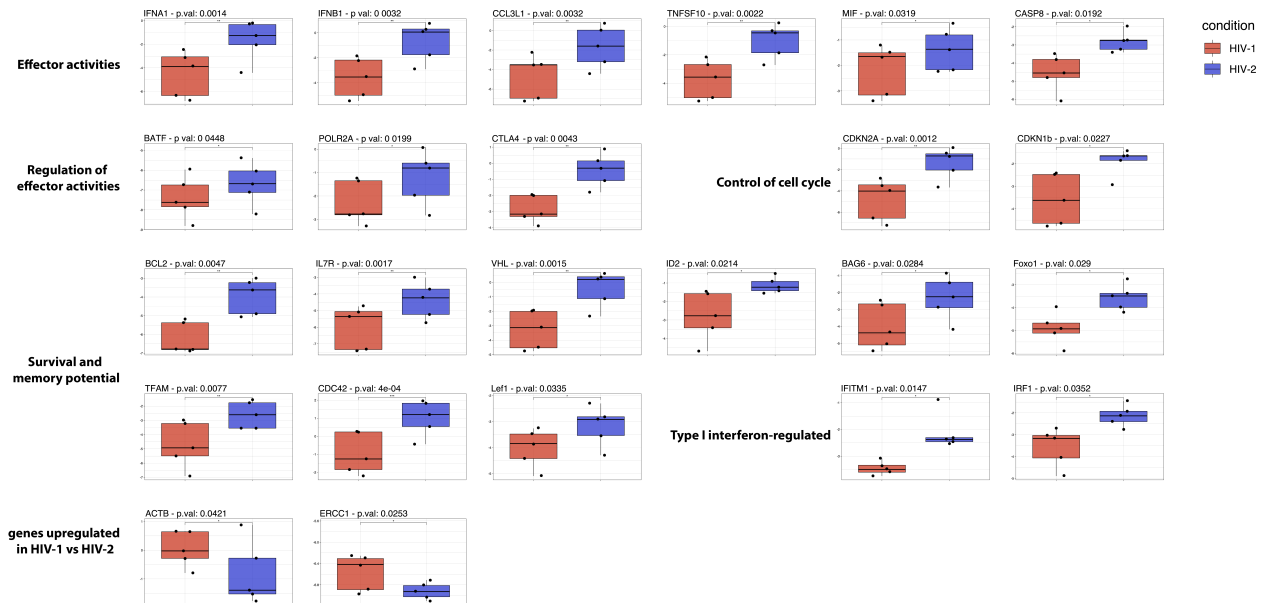
68 Representative flow cytometry plots showing the expression of CCR7 and CD45RA among  
69 ELA-specific CD8<sup>+</sup> T cells primed in the presence of ELA20  $\Delta$ env HIV-1 (top) or ELA20  $\Delta$ env  
70 HIV-2 (bottom). Numbers indicate percentages in the drawn gates.

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73 **Figure S3. Differentially expressed genes in CD8<sup>+</sup> T cells primed with HIV-1 or HIV-2.**

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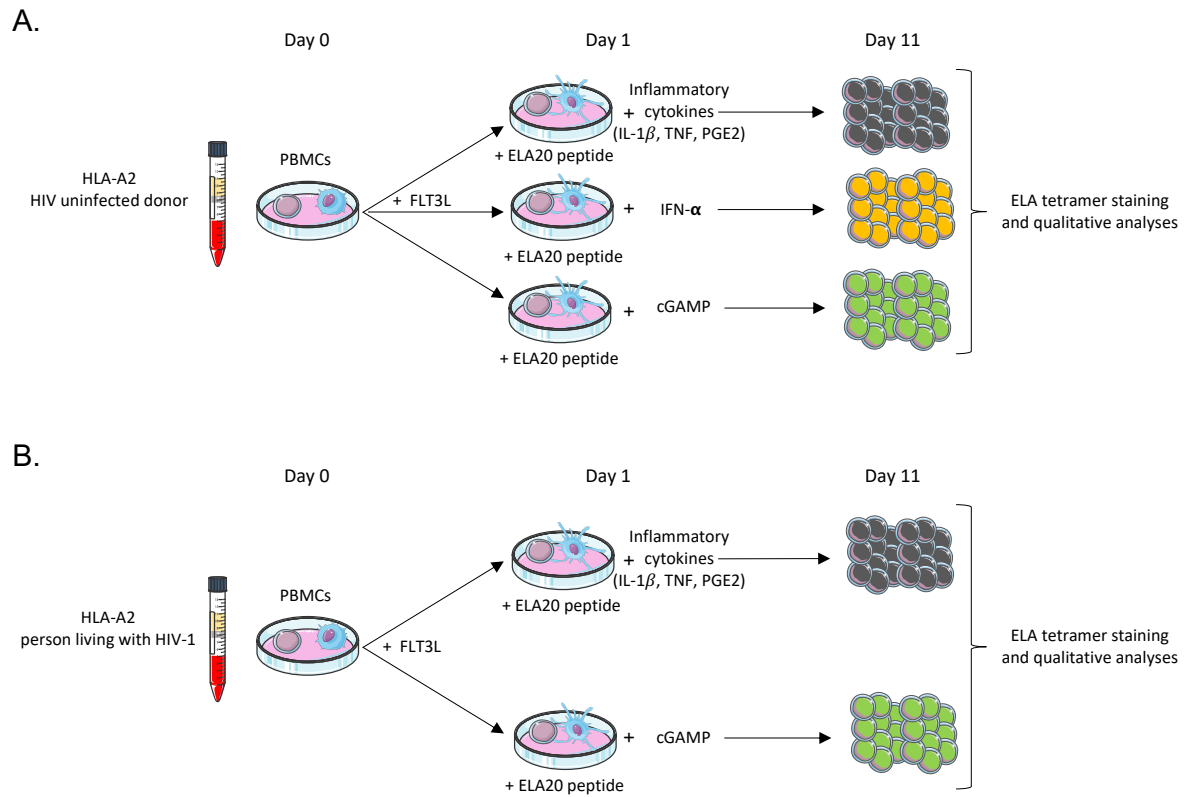
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77 Plots show genes that were differentially expressed between ELA-specific CD8<sup>+</sup> T cells primed  
78 with ELA20  $\Delta$ env HIV-1 (red) and ELA-specific CD8<sup>+</sup> T cells primed with ELA20  $\Delta$ env HIV-  
79 2 (blue). Each dot represents one donor. Results are plotted as  $\log_2 2^{-\Delta\text{ct}}$  normalized to *GAPDH*.  
80 Data are shown as median  $\pm$  IQR. Samples lacking a *GAPDH* signal were excluded from the  
81 analysis. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$  (pairwise t-test).

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84 **Figure S4. Schematic representation of the *in vitro* priming approach using cognate**  
85 **peptide and adjuvants.**  
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88 **(A)** Priming conditions using HIV-uninfected HLA-A2<sup>+</sup> donor PBMCs. **(B)** Priming conditions  
89 using HLA-A2<sup>+</sup> PBMCs from PLWH.

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92 **Figure S5. Differentially expressed genes in CD8<sup>+</sup> T cells primed in the presence of**  
 93 **proinflammatory cytokines, IFN- $\alpha$ , or cGAMP.**



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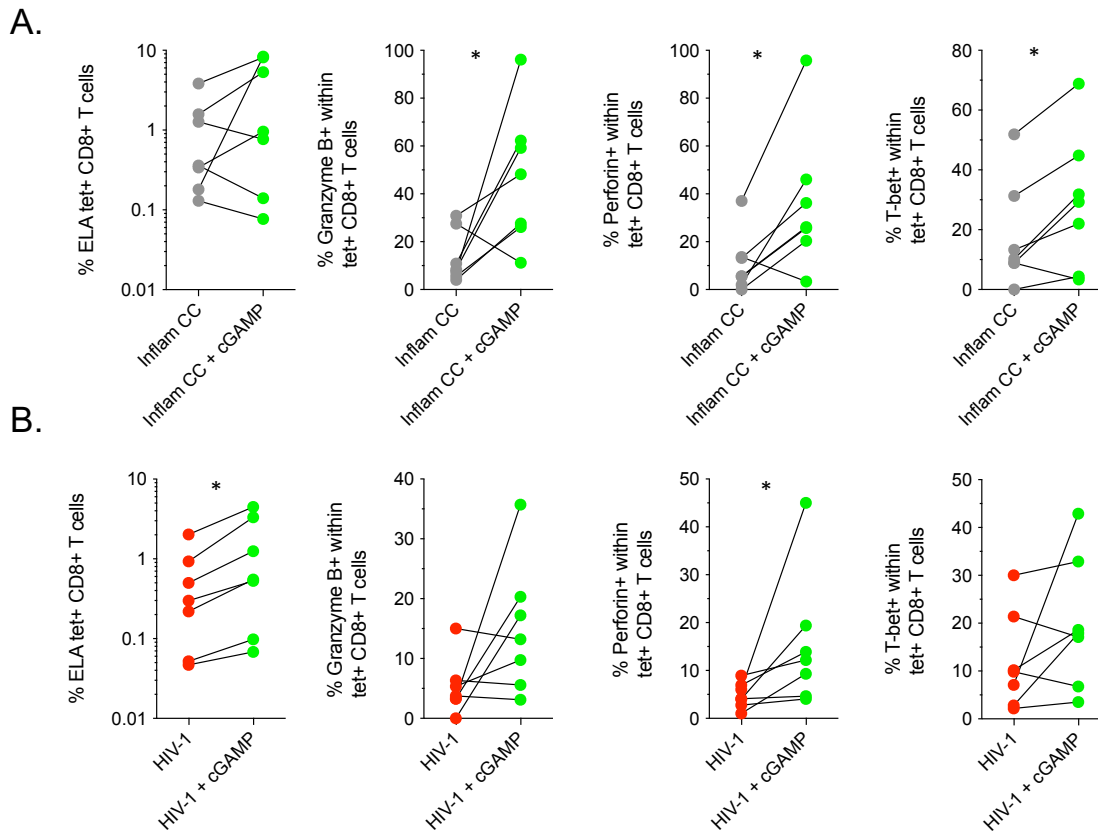
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96 Plots show genes that were differentially expressed among ELA-specific CD8<sup>+</sup> T cells primed  
 97 in the presence of proinflammatory cytokines (IL-1 $\beta$ , TNF, and PGE2, n = 7), IFN- $\alpha$  (n = 7),  
 98 or cGAMP (n = 7). Each dot represents one donor. Results are plotted as  $\log_2(-\Delta ct)$  normalized  
 99 to *GAPDH*. Data are shown as median  $\pm$  IQR. Samples lacking a *GAPDH* signal were excluded  
 100 from the analysis. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001 (pairwise t-test).

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103 **Figure S6. Impact of cGAMP on CD8<sup>+</sup> T cell priming with ELA in the presence of**  
 104 **proinflammatory cytokines or with ELA20  $\Delta$ env HIV-1.**  
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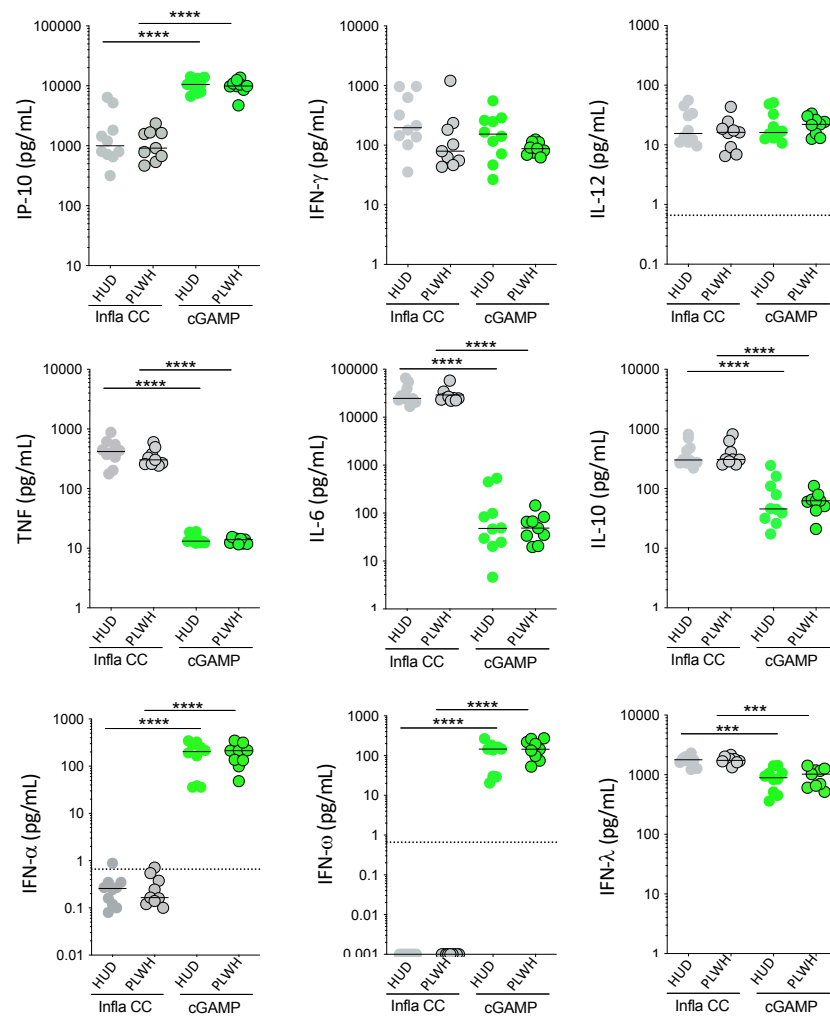


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108 Expression of granzyme B, perforin, and T-bet among ELA-specific CD8<sup>+</sup> T cells primed with  
 109 ELA20 in the presence of proinflammatory cytokines (IL-1 $\beta$ , TNF, and PGE2) (A) or ELA20  
 110  $\Delta$ env HIV-1 in the absence or presence of cGAMP (B). Each connected dot represents one  
 111 donor (n = 7). \*p < 0.05 (Wilcoxon signed rank test).

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113 **Figure S7. Secretion of soluble factors after stimulation of PBMCs with proinflammatory**  
 114 **cytokines or cGAMP.**



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 116 Concentrations of various chemokines/cytokines in culture supernatants 3 days after  
 117 stimulation of PBMCs from HUDs (n = 8) (A) or PLWH on ART (n = 8) (B) with  
 118 proinflammatory cytokines (IL-1 $\beta$ , TNF, and PGE2) or cGAMP. Each dot represents one  
 119 donor. Bars indicate median values. \*\*\*p < 0.001, \*\*\*\*p < 0.0001 (Mann-Whitney U test).