

Identification of antigens presented by MHC for vaccines against tuberculosis

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Supplementary data for

Identification of antigens presented by MHC for vaccines against tuberculosis

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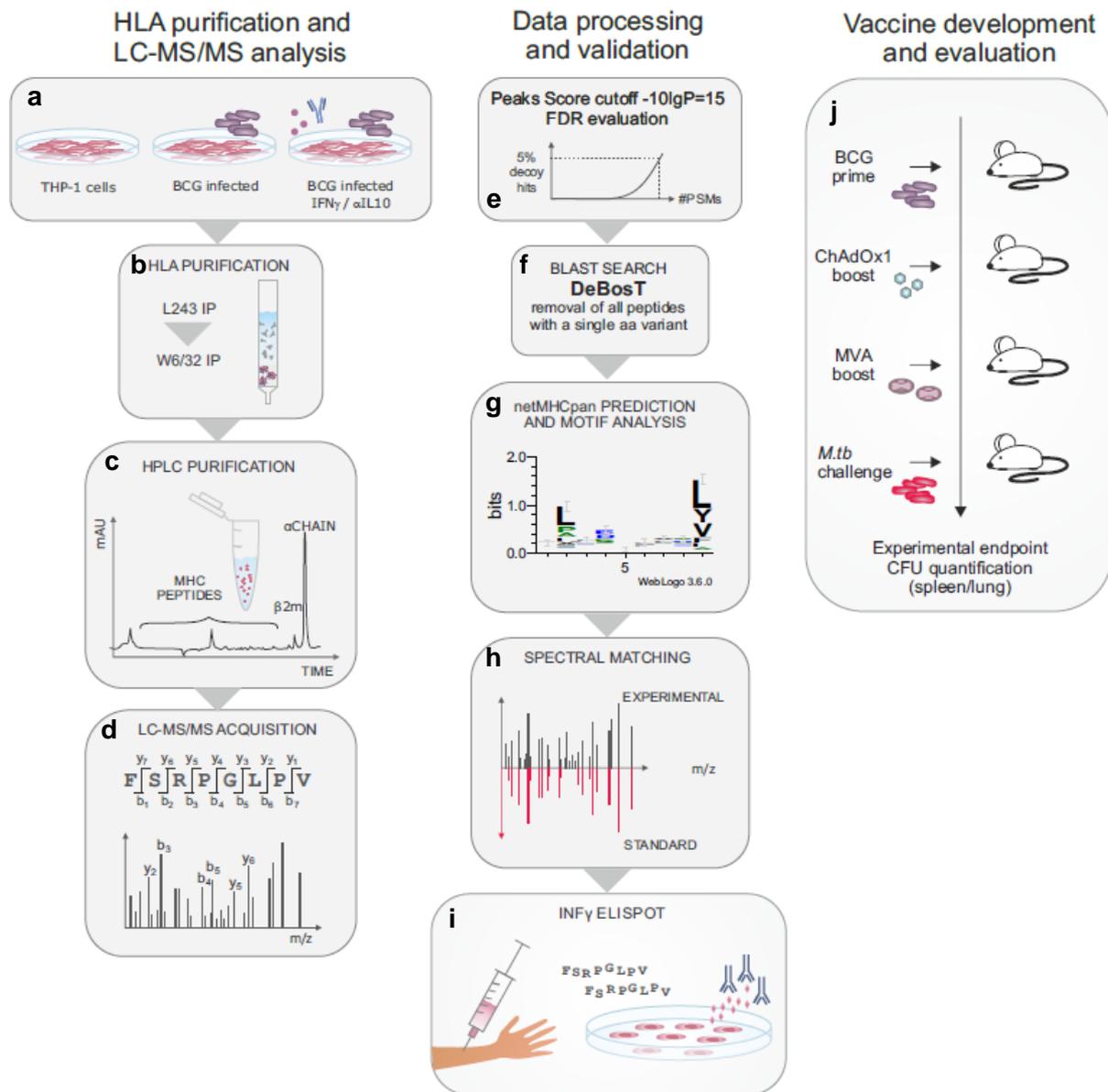
- Equal contributions.

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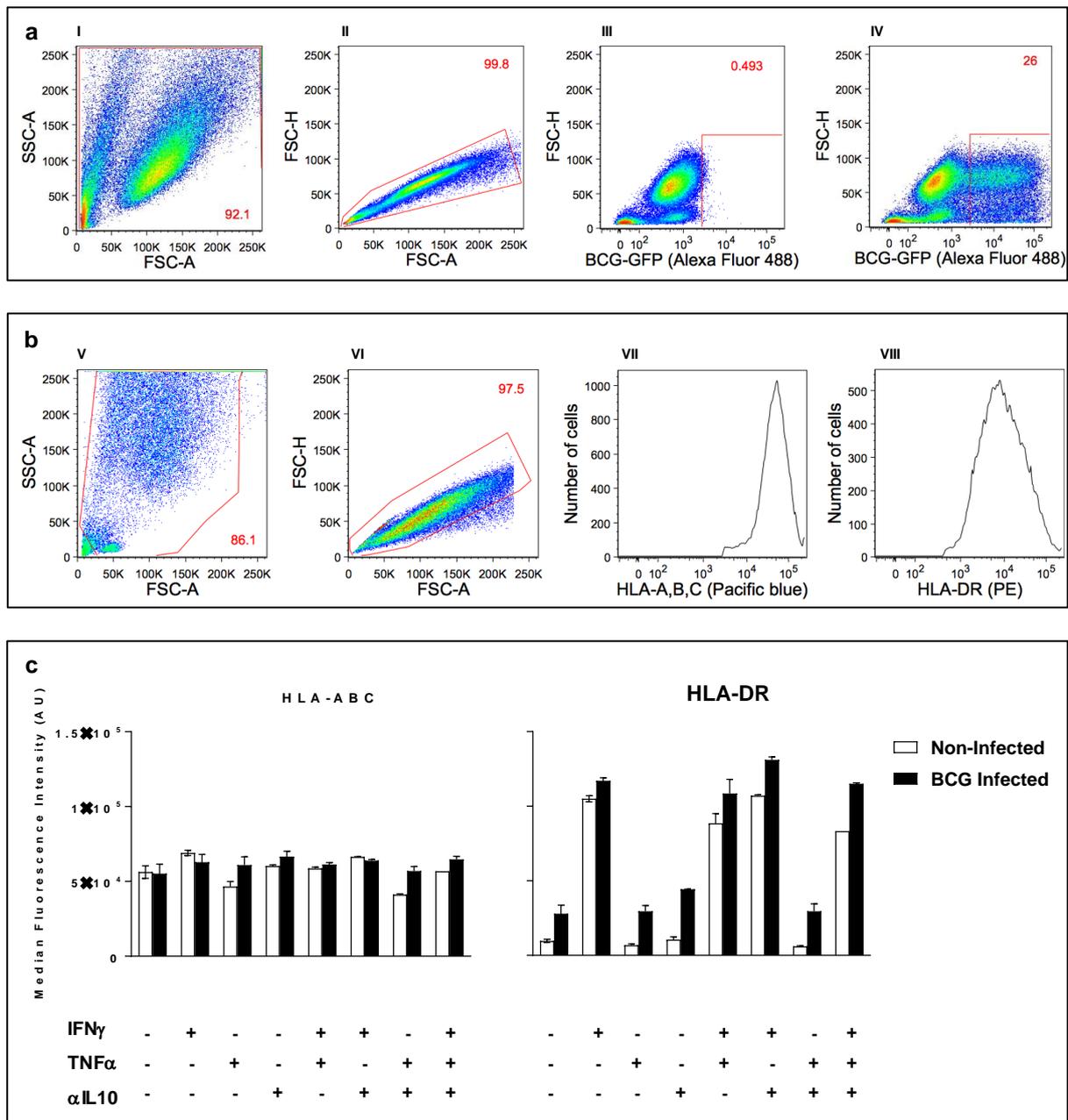
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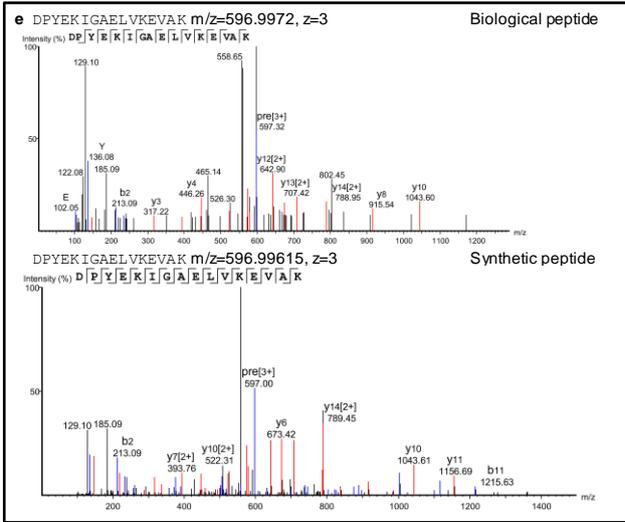
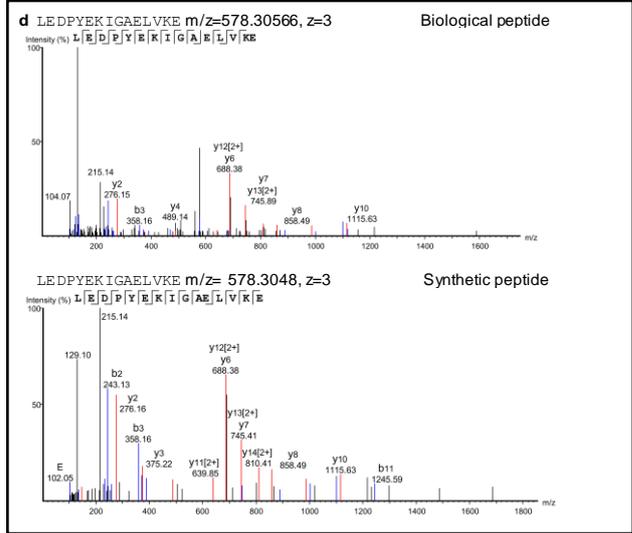
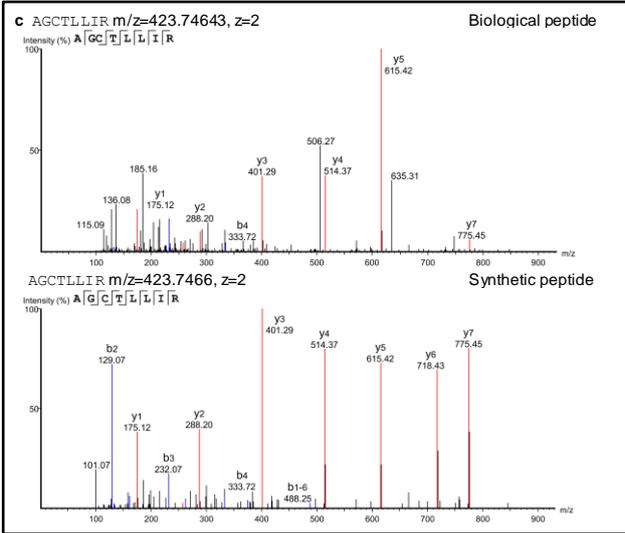
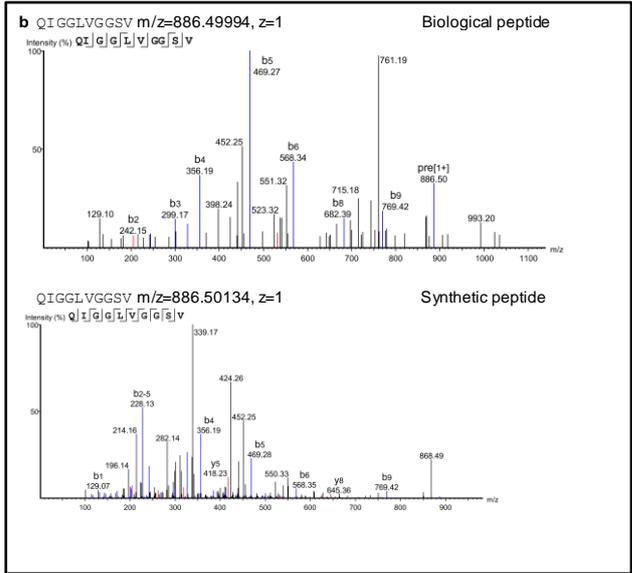
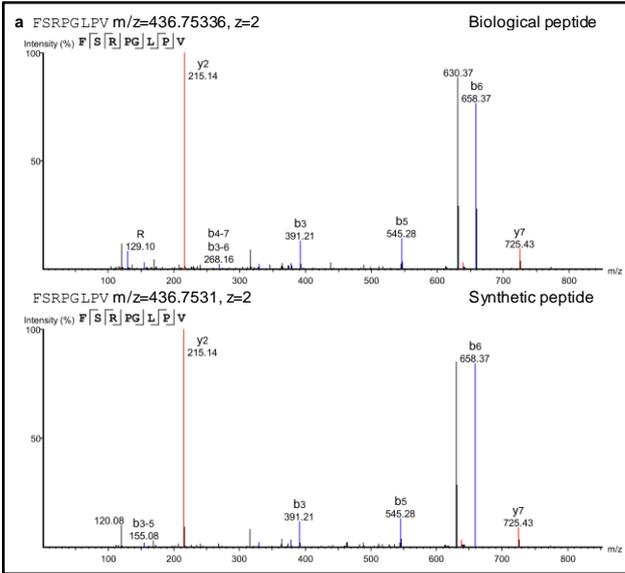
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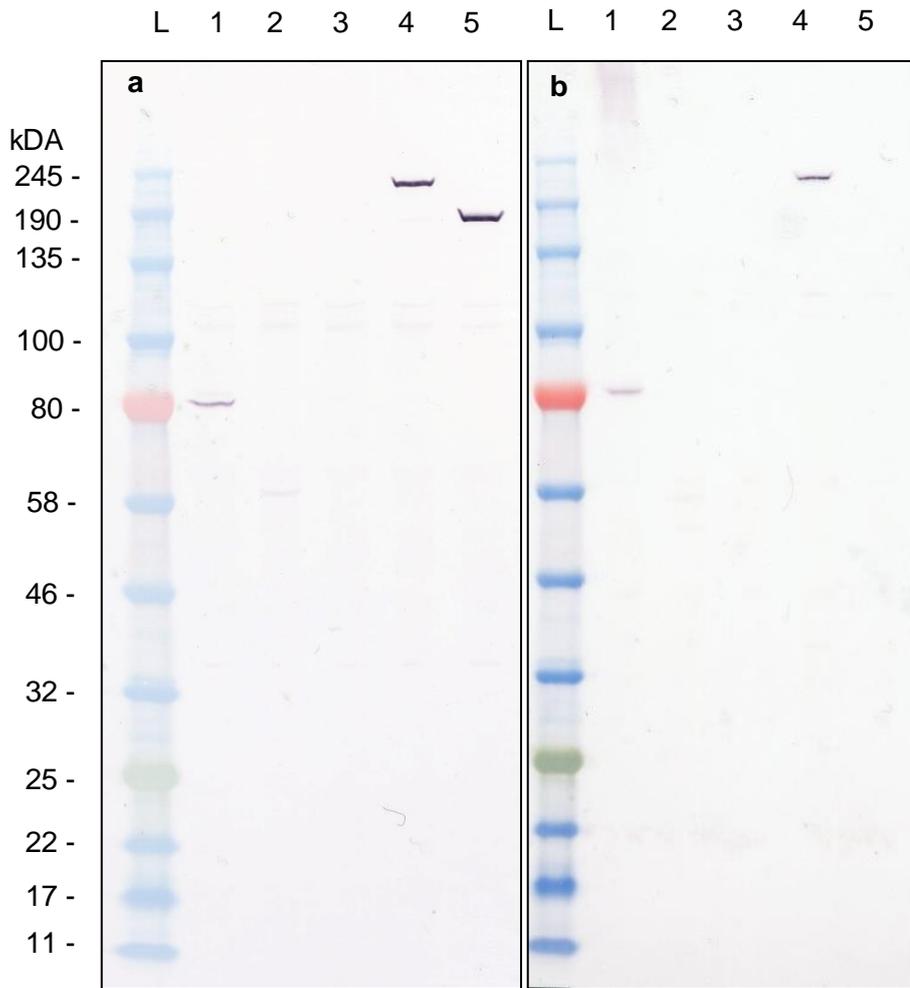
Supplementary Figure 1 Immunopeptidomics pipeline for MHC class-I and class-II peptide identification by mass spectrometry and bioinformatics. **a** to **d** Sample preparation and mass spectrometry. **e** to **i** Data analysis and peptide identification. **a** THP-1 cells were differentiated with 20nM PMA to macrophage-like cells and infected with BCG-GFP, alive or heat-killed, at a MOI 10, with or without pre-treatment with IFN γ and anti-IL10. **b** THP-1 cells were harvested, lysed and total proteins collected. HLA molecules were purified by immunoprecipitation with monoclonal antibody against HLA-DR (clone L243), followed by monoclonal antibody against pan-HLA class-I (clone W6/32). **c** Peptides bound to the HLA groove were released from the HLA groove after 10% acetic acid denaturation of the α -chains and β -2-microglobulin, and separated by HPLC, using a C18 preparative column and a gradient of acetonitrile in formic acid 0.1% (v/v). **d** The HPLC fraction containing peptides were concentrated and injected in the LC-MS/MS for PSM identification. **e** PSMs with Peaks score higher than 15 were selected. **f** PSMs identified as *Mycobacterium bovis* BCG were blasted against the human proteome using the DeBosT algorithm. Peptides with one amino acid different from human were excluded. Peptides with two or more amino acids different from human were selected. **g** Peptides with higher netMHC rank were prioritized. **h** Selected peptides sequences were confirmed by spectral match validation. **i** Immunogenicity evaluated by IFN- γ ELISPOT against PBMC from BCG-vaccinated volunteers, *M.tb* latently infected subjects or patients with tuberculosis disease. **j** Vaccine efficacy evaluated in murine aerosol *M.tb* challenge experiment.



Supplementary Figure 2 Infection and MHC activation of human macrophages. **a** Gating strategy to determine the rate of infection in THP-1 cells. Cells were acquired and plotted on side scatter-area (SSC-A) versus forward scatter-area (FSC-A) to define the population, 92.1% of events (I). Cells were subsequently gated for singlets using forward scatter-height (FSC-H) versus FSC-A, 99.8% of cells (II). Gated cells were plotted using FSC-H versus Alexa Fluor 488, to determine the percentage of GFP-negative events, 0.493%, representing uninfected cells (III) and compared to GFP-positive events, 26%, cells infected with a BCG expressing GFP (IV). In this representative example, non-infected sample contained 86,000 events and the infected sample contained 89,000 events. For each experiment, triplicates were used to calculate the rate of infection. **b** Gating strategy to quantify MHC activation in human monocyte derived macrophages. Single-stained and unstained mouse beads were used to calculate compensations. Samples containing 50,000 cells were acquired, plotted and gated for singlets as described in **a** (V and VI, respectively). Gated events were plotted in histograms, number of cells versus Pacific blue, to determine the distribution of the fluorescence intensity of HLA-A,B,C (VII). Gated events were also plotted in histograms, number of cells versus PE, to determine the distribution of the fluorescence intensity of HLA-DR (VIII). The fluorescence intensity of the histograms represent the surface marker expression. **c** Expression of HLA-A,B,C and HLA-DR in human monocyte derived macrophages stimulated with IFN γ , TNF α , anti-IL10, alone or in combination and infected with BCG. The columns represent the average and the error bars represent the standard deviation. Each condition was tested in duplicate or triplicate except the triple positive stimulated non-infected cells, with one replicate. No statistical test was performed due to low number of replicates.



Supplementary Figure 3 Spectral Match Validation. HLA-associated peptide sequences were synthesized and measured by LC-MS/MS under identical conditions as the experimentally identified peptide sequences. Both the biological and the synthetic peptides were plotted relative to each other to illustrate the spectral match. Fragment ions are labelled in the spectra and the regarding molecular fragment is indicated in the peptide sequence above each spectrum. Ions are labelled as follows: b: singly charged N-terminal fragment ion; y: singly charged C-terminal fragment ion; o: loss of H₂O; p: parent peptide ion. The mass to charge ratio [m/z] of the precursor ionized peptide and the charge status is shown for each spectrum. Fragment mass spectra for five peptides validated. Examples of MHC-I validated peptides: **a** fbpA⁴⁴⁻⁵¹ FSRPGLPV, **b** iniC¹⁹¹⁻²⁰⁰ QIGGLVGGSV, **c** mmpL¹²³⁹⁶⁻⁴⁰³ AGCTLLIR, and MHC-II validated nested peptides: **d** groL²⁶¹⁻⁷⁵ LEDPYEKIGAEVLVKE. **e** groL²⁶³⁻⁷⁸ DPYEKIGAEVLVKEVAK.



Supplementary Figure 4 Expression of antigens by viral vectors. Expression of selected antigens in HeLa cells infected ChAdOx1 (a) and MVA (b) expressing each antigen. L – Ladder Broad Range (11-245 kDa) NEB #P7712. Lane 1 - GLFT2 (71.52 kDa), 2 - Rv0341 (43.93 kDa), 3 - Infected with irrelevant ChAdOx1, 4 - fas D1 (184.68 kDa), 5 - fas D2 (141.79 kDa).

Supplementary Table 1 HLA Genotyping of THP-1 cells

Locus	Allele	Allele	Interpreted	
HLA-A	*02:01-604	-	A	2
HLA-B	*15:11/15/209N/305/367	-	B	75
HLA-C	*03:03/13/18/20N-316N	-	Cw	9
HLA-DRB1	*01:01/05/07-14/16-73	*15:01/12/13/16/20/22-128	DR	1 15
HLA-DRB3				
HLA-DRB4				
HLA-DRB5	*01:01-05/08N/10N/14-18		DR	51
HLA-DQB1	*06:02/14/47/68/70/72-147	*05:01/07/11/12/18/20-63	DQ	6 5
HLA-DPB1	*04:02	*02:01	DP	

The Histocompatibility and Immunogenetics Report was produced by the Transplant Immunology & Immunogenetics, Oxford Transplant Centre, The Churchill Hospital, Oxford, UK.

Supplementary Table 2 MHC-I peptide identification

Peptide identification		Antigen identification			HLA-peptide binding		Experimental details		
Sequence	n	UniProt	Name	Symbol	netMHC best hit	netMHC best score	Experiment number	Sample	Peaks score (-10*log10(Pvalue))
<i>Peptides identified in different experiments</i>									
FSRFGLELV	8	A1KQD8/ A1KJU9/ A0A0H3M0R3	Diacylglycerol acyltransferase/mycolyltransferase Ag85A/ Diacylglycerol acyltransferase/mycolyltransferase Ag85B/ Secreted antigen 85-c fbpC (85C)	fbpA/ fbpB/ fbpC	HLA-C*03:13	2.3986	4 3 4	CYT HKBCG B CYT HKBCG A CYT HKBCG	24.81 22.84 22.77
QIGGLVGGSV	10	A0A0H3M1A8	Isoniazid inducible gene protein iniC	iniC	HLA-A*02:01	14.7788	4 2 4	CYT HKBCG B DAY7 A CYT LIVEBCG A	23.29 17.89 16.49
IGAGAIIVAA	10	A0A0H3MFF6	Probable conserved integral membrane protein [second part]	BCG_2410	HLA-C*03:03	12.5346	4 2 2	CYT LIVEBCG A CYT LIVEBCG A DAY7 A	18.47 15.91 18.45
LDSRQFERY	9	A0A0H3M738	Polyketide synthetase mbtD	mbtD	HLA-B*15:15	5.9146	2 1 4	DAY1 A DAY7 B CYT HKBCG B	15.37 18.11 15.62
GIGAGAAVL	9	A0A0H3MCA7	Probable conserved transmembrane protein	BCG_3967	HLA-C*03:13	2.2331	4 2	CYT HKBCG B DAY7 A	18.11 15.62
<i>Peptides identified in more than 1 sample</i>									
LAASLLSRV	9	A0A0H3MAQ2	Galactofuranosyl transferase	BCG_3870c	HLA-C*03:03	1.0334	1 1	DAY1 B DAY1 A	28.16 21.06
AGCTLLIR	8	A0A0H3M689	Probable conserved transmembrane transport protein mmpL12	mmpL12	HLA-B*15:15	89	3 3	NOCYT HKBCG CYT LIVEBCG	24.98 22.93
ASSVFAPAL	9	A0A0H3M6D2	Putative conserved integral membrane transport protein	BCG_2476c	HLA-C*03:13	0.3975	4 4 4	CYT LIVEBCG B NOCYT HKBCG B NOCYT LIVEBCG B	21.49 18.66 17.25
<i>Peptides identified in the same antigen</i>									
PALMVLGR	9	A0A0H3M5L6	Probable conserved transmembrane transport protein mmpL14	mmpL14	HLA-A*02:01	55	1	DAY1 A	19.01
PAIAGATF	8	A0A0H3M5L6			HLA-B*15:11	3.1917	2	DAY1 A	16.62
GIETELATL	9	A0A0H3MFR6	Probable fatty acid synthase fas	fas	HLA-A*02:01	2.6087	3	NOCYT LIVEBCG	18.48
ADLVVIVGGA	10	A0A0H3MFR6			HLA-A*02:01	10.5071	2	DAY1 A	15.68
VTVNATPD	8	A0A0H3M7L7	Probable polyketide synthase pks12	pks12	HLA-B*15:11	65	4	NOCYT LIVEBCG A	16.06
VNGPSAVVV	9	A0A0H3M7L7			HLA-C*03:13	6.804	4	NOCYT LIVEBCG B	15.77
<i>Peptides identified once</i>									
LHVEQLQTI	9	A0A0H3M9J8	Probable conserved transmembrane protein	BCG_3501c	HLA-C*03:13	4.0392	2	DAY1 A	23.68
LFAPLDDHS	9	A0A0H3M7I5	Putative transposase	BCG_2830	HLA-A*02:01	38	2	DAY7 A	23.28
ALAAAAAGVT	10	A0A0H3M9Q7	Probable Sn-glycerol-3-phosphate-binding lipoprotein ugpB [first part]	ugpBa	HLA-A*02:01	3.9356	4	CYT HKBCG A	21.36
LAADALVVKV	10	A0A0H3MC70	Transposase for insertion sequence element IS1081	BCG_2532c	HLA-C*03:03	3.611	2	DAY7 B	19.45
LAPPADPA	9	A0A0H3M8Z9	Possible resuscitation-promoting factor rpfA	rpfA	HLA-C*03:03	2.641	2	DAY7 A	19.45
LAEIYQGEV	9	A0A0H3M6G7	Methionine synthase	metH	HLA-C*03:03	4.9093	2	DAY1 A	19.15
AADAHRAGV	10	A0A0H3MCA7	Probable conserved transmembrane protein	BCG_3967	HLA-C*03:03	5.5597	2	DAY1 A	19.08
TLHEVPVL	8	A0A0H3MAQ0	Uncharacterized protein	BCG_3864c	HLA-A*02:01	2.5974	4	CYT LIVEBCG A	18.5
TMIEYYLHE	9	A0A0H3MFH1	Uncharacterized protein	BCG_2427c	HLA-A*02:01	6.55	2	DAY7 A	18.25
EDCHFCSQSG	10	A1KJ05	Biotin synthase	bioB	HLA-B*15:15	95	2	DAY7 A	17.68
EHADWIVDIGP	11	A0A0H3M4F7	UvrABC system protein A	uvrA	HLA-A*02:01	80	2	DAY7 B	17.58
LSIPSVVIP	9	A0A0H3M5L1	PPE family protein	PPE24	HLA-C*03:03	12.3553	2	DAY7 A	17.47
APEAVDLLVQLA	12	A0A0H3MFU7	Conserved hypothetical alanine leucine valine rich protein	BCG_2582c	HLA-A*02:01	32.4138	2	DAY1 A	17.31
TIGGVADHLAT	11	A1KM20	1-deoxy-D-xylulose-5-phosphate synthase	dxs	HLA-A*02:01	42.75	2	DAY1 B	17.1
ADGTDGKGGGG	13	A0A0H3M617	PE-PGRS family protein	PE_PGRS27	HLA-B*15:15	97.5	4	NOCYT LIVEBCG A	17.07
PSGSGTPLVSY	11	A0A0H3M520	Probable fatty-acid-CoA ligase fadD24	fadD24	HLA-B*15:15	19.9571	2	DAY1 B	16.89
AQVRASVTY	9	A1KF53	R2-like ligand binding oxidase	BCG_0270	HLA-B*15:15	0.0538	2	DAY1 B	16.76
WDCAAVNV	8	A0A0H3MC94	Uncharacterized protein	BCG_1242c	HLA-C*03:03	50.3846	3	CYT HKBCG	16.59
GPAPFAALS	8	A0A0H3MGQ7	Phenolphthiocerol synthesis type-I polyketide synthase ppsD	ppsD	HLA-B*15:11	19.3043	4	CYT LIVEBCG B	16.51
ITNVSIPAI	9	A0A0H3M207	PPE family protein	PPE8	HLA-C*03:03	0.5682	2	DAY7 A	16.41
PATASFAYA	9	A0A0H3MA86	PPE family protein	PPE4	HLA-C*03:03	23.942	4	CYT LIVEBCG A	16.18
GGGLSSPVI	9	A0A0H3M376	PE-PGRS family protein	PE_PGRS14	HLA-C*03:13	9.0088	2	DAY7 A	15.86
PSSGRITVAGV	11	A0A0H3MDE4	Probable 'component linked with the assembly of cytochrome' transport transmembrane ATP-binding protein ABC transporter cydD	cydD	HLA-A*02:01	70	3	CYT HKBCG	15.86
AAIEERLSR	9	A0A0H3M1D1	Uncharacterized protein	BCG_0405c	HLA-B*15:11	7.0108	4	NOCYT HKBCG A	15.7
DFVSILDVRW	10	A0A0H3MF71	Sulfurtransferase	sseB	HLA-C*03:13	6.8816	2	DAY7_B	15.57
RTLFRVFP	8	A0A0H3M2S6	Conserved transmembrane transport protein mmpL3	mmpL3	HLA-C*03:13	7.4497	3	CYT HKBCG	15.38
DYSDAGLYL	9	A0A0H3M5F4	Aminotransferase	BCG_1241	HLA-B*15:11	2.9928	2	DAY1 A	15.34
PATLAAALP	9	A0A0H3M9A8	Probable membrane protein	BCG_1061c	HLA-C*03:03	58.4091	2	DAY7 A	15.24
HPVLVDRFLED	11	A0A0H3MCS3	Carbamoyl-phosphate synthase large chain	carB	HLA-C*03:13	68.75	4	CYT HKBCG A	15.01

Supplementary Table 3 MHC-II peptide identification

Peptide identification		Antigen identification			HLA-peptide binding		Experimental details		
Sequence	n	Accession	Name	Symbol	netMHCpan best hit	netMHCpan best score	Experiment number	Sample ID	Peaks score (-10log10(Pvalue))
<i>Nested peptides identified in different experiments</i>									
KAPAKKAAAK	10	A1KFU9	Heparin-binding hemagglutinin	hbhA	HLA-DRB5*01:01	44	3	CYT HKBCG	21.26
KAPAKKAAAKVTQK	15				HLA-DRB5*01:01	21	4	NOCYT HKBCG A	24.92
AAAKKAPAKKAAAKK	15				HLA-DRB5*01:01	17	3	CYT LIVEBCG	17.24
KKAAAKKAPAKKAAAKK	17				HLA-DRB5*01:01	12	4	NOCYT LIVEBCG A	28.56
KKAAAKKAPAKKAAAKK	17						4	NOCYT LIVEBCG B	17.03
AKKAAAPAKKAAAKK	20				HLA-DRB5*01:01	12	4	NOCYT LIVEBCG A	17.73
<i>Nested peptides</i>									
DPYEKIGAEIVK	12	A1KFR2	60 kDa chaperonin 2	groL2	HLA-DRB1*01:01	12	4	CYT HKBCG A	68.08
DPYEKIGAEIVKEVA	15				HLA-DRB1*01:01	13	4	CYT HKBCG A	46.93
DPYEKIGAEIVKEVAK	16				HLA-DRB1*01:01	17	4	CYT HKBCG A	49.14
EDPYEKIGAEIVKE	14				HLA-DRB1*01:01	16	4	CYT HKBCG A	45.4
LEDPYEKIGAEIVKE	15				HLA-DRB1*01:01	16	4	CYT HKBCG A	30.75
NGEELYLILSARDVLA	15	A1KPA9	10 kDa chaperonin	groS	HLA-DRB1*01:01	1.9	4	CYT LIVEBCG A	68.22
YLILSARDVLA	11				HLA-DRB1*01:01	0.9	4	CYT LIVEBCG A	41.23
QGGAGGMGGS GADNA	15	A0A0H3M9Q3	PE-PGRS family protein	PE_PGRS54	HLA-DRB1*01:01	95	4	NOCYT LIVEBCG A	24.29
GGAGGMGGS GADNA	14				HLA-DRB1*01:01	95	4	NOCYT HKBCG B	15.83
AGGMGGS GADNA	12				HLA-DRB1*01:01	95	4	NOCYT LIVEBCG A	18.32
GAGDGDGANFASG	15	A0A0H3M3G6	PE-PGRS family protein	PE_PGRS23	HLA-DRB1*01:01	95	4	NOCYT LIVEBCG B	16.03
GAGDGDGANFASGGAGG	19				HLA-DRB1*01:01	95	4	NOCYT LIVEBCG A	21.42
<i>Peptides identified in more than 1 sample</i>									
KAK (+43.99) GHLDAGAK	11	A0A0H3MAB5	Glyceraldehyde-3-phosphate dehydrogenase	gap	HLA-DRB5*01:01	75	4	CYT LIVEBCG A	31.54
K (+43.99) AKGHLDAGAK							4	CYT LIVEBCG A	27.16
DEETLQGYITR	11	A0A0H3MCS3	Carbamoyl-phosphate synthase large chain	carB	HLA-DRB1*01:01	65	2	DAY1	21.07
							2	DAY7	20.96
<i>Peptides identified in the same antigen</i>									
AGANGVA V G A P	11	A0A0H3M617	PE-PGRS family protein	PE_PGRS27	HLA-DRB1*01:01	95	2	DAY1	23.01
AGDGGAPGDGAN	13	A0A0H3M617	PE-PGRS family protein	PE_PGRS27	HLA-DRB1*01:01	95	4	NOCYT LIVEBCG B	17.49
LQDM (+15.99) AILTGGQVIS	14	A1KFR2	60 kDa chaperonin 2	groL2	HLA-DRB1*01:01	8	4	CYT HKBCG A	35.36
AQTGVYEDLLAAGVADPVK	19	A1KFR2	60 kDa chaperonin 2	groL2	HLA-DRB1*01:01	35	4	CYT LIVEBCG A	35.11
KAPAKKAPAKASSETSAAKGGS	21	A1KGI7	50S ribosomal protein L22	rplV	HLA-DRB5*01:01	85	4	NOCYT LIVEBCG B	21.12
PAKKAAPAKA	11	A1KGI7	50S ribosomal protein L22	rplV	HLA-DRB5*01:01	38	4	CYT LIVEBCG A	16.31
<i>Peptides identified once</i>									
S (+14.02) GQIKTGAPARSE	13	A1KHG1	Enolase	eno	HLA-DRB5*01:01	30	4	CYT HKBCG A	42.78
ANRAELKALIASNLLGQNT	19	A0A0H3M8U4	PPE family protein	PPE50	HLA-DRB1*01:01	5	4	CYT LIVEBCG A	39.94
DTNYHYLVPEIGFS	14	A1KHS4	5-methyltetrahydropteroyltryptophan methyltransferase	metE	HLA-DRB1*01:01	6	4	CYT HKBCG A	31.61
GAGGKAGLLFGSGGA	15	A0A0H3MB82	PE-PGRS family protein	PE_PGRS13	HLA-DRB1*01:01	85	4	NOCYT LIVEBCG A	28.99
PGGGGAGGGGAAANTDS	18	A0A0H3M903	PE-PGRS family protein	PE_PGRS15	HLA-DRB1*01:01	95	4	NOCYT HKBCG B	27.9
AKVINISVT	9	A0A0H3MC87	Possible secreted alanine and proline rich protease	BCG_3941c	HLA-DRB1*01:01	23	4	NOCYT HKBCG A	25.85
APMRPPRS	8	A0A0H3MDJ5	Possible integral membrane efflux protein efpA	efpA			3	CYT LIVEBCG	25.82
KLVANSLIK	9	A0A0H3M5J1	Probable serine protease htrA	htrA	HLA-DRB5*01:01	1.5	4	CYT HKBCG A	21.53
KAPAKKTPAKGAKSAPPKPA	20	A0A0H3MC68	Possible histone-like protein hns	hns	HLA-DRB5*01:01	80	4	NOCYT LIVEBCG B	21.46
AVDPYAI G V P	10	A0A0H3M602	Probable dehydrogenase	BCG_1493	HLA-DRB1*15:01	80	2	DAY7	21.32
GANGAPGTTSTSGGN	15	A0A0H3M1W6	PE-PGRS family protein	PE_PGRS7	HLA-DRB1*01:01	95	2	DAY7	20.82
RVGIVSNDP	9	A0A0H3M2X4	Probable molybdopterin biosynthesis protein moeA1	moeA1	HLA-DRB1*01:01	75	4	CYT HKBCG A	20.64
ALAILDVTGV	10	A0A0H3M5J7	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	murE	HLA-DRB1*01:01	4.5	4	NOCYT HKBCG A	20.61
RVGIDAEAGPT	11	A0A0H3M564	Histidinol dehydrogenase	hisD	HLA-DRB1*01:01	95	4	CYT LIVEBCG A	19.9
GTGGNASATGT	11	A0A0H3MI A6	PE-PGRS family protein	PE_PGRS53	HLA-DRB1*01:01	95	4	CYT HKBCG A	19.84
GGWLLDGGGAGGSG	14	A0A0H3M8Q1	PE-PGRS family protein	PE_PGRS9	HLA-DRB1*01:01	55	2	DAY1	19.62
TAELLGAMSEA	11	A1KM16	Uroporphyrinogen decarboxylase	hemE	HLA-DRB1*01:01	36	4	NOCYT LIVEBCG B	19.55

Continued in next page

Supplementary Table 3 MHC-II peptide identification - continued

Sequence	n	Accession	Name	Symbol	netMHCpan best hit	netMHCpan best score	Experiment number	Sample ID	Peaks score (-10*log10(Pvalue))
<i>Peptides identified once</i>									
AAIAAGTTIVL	12	A0A0H3MAU4	Probable conserved transmembrane protein	BCG_3906c	HLA-DRB1*01:01	11	2	DAY7	19.15
RLGVDLAEV	9	A0A0H3MIH3	Probable acyl-CoA dehydrogenase fadE34	fadE34	HLA-DRB1*01:01	55	3	CYT LIVEBCG	19.13
LGRGLLGLI	9	A0A0H3MDN2	Signal recognition particle receptor FtsY	ftsY	HLA-DRB1*01:01	20	2	DAY7	18.42
TELDEVTVNGLHP	12	A0A0H3M178	Replicative DNA helicase	dnaB	HLA-DRB1*01:01	90	4	CYT LIVEBCG A	18.41
EINSARLYV	9	A0A0H3M207	PPE family protein	PPE8	HLA-DRB1*15:01	28	3	CYT HKBCG	18.25
KMAAAGCGRIVLNSRTQPTQKMRET	25	A1KQG0	Phthioceranic/hydroxyphthioceranic acid synthase	pkS2	HLA-DRB5*01:01	43	4	NOCYT HKBCG A	18.11
KPLEVVVFHHRPERYQFS	18	A0A0H3M332	Probable transcriptional regulatory protein (Probably gntR-family)	BCG_0845c	HLA-DRB5*01:01	31	4	NOCYT HKBCG B	17.98
DIPNISDEVLADL	13	A1KEG7	DNA-directed RNA polymerase subunit beta	rpoB	HLA-DRB1*01:01	90	4	CYT HKBCG A	17.97
GDYEGLWGL	9	A0A0H3M8U0	PPE Family protein [first part]	PPE55a	HLA-DRB1*01:01	80	3	NOCYT LIVEBCG	17.95
FGAPERMVQNT	11	A0A0H3M155	Possible conserved membrane protein	BCG_0323	HLA-DRB1*01:01	95	4	NOCYT HKBCG B	17.9
PPVIAAVPRK	10	A0A0H3MJ54	Putative lipase lipE	lipE	HLA-DRB5*01:01	2.5	4	NOCYT LIVEBCG B	17.81
AAELSRDLDFRAR	13	A0A0H3M6E7	Probable transmembrane serine/threonine-protein kinase j pknJ	pknJ	HLA-DRB1*15:01	65	4	CYT HKBCG A	17.7
TPTPRNAAGA	10	A0A0H3MAK2	Possible transcriptional regulatory protein	BCG_0526	HLA-DRB1*01:01	95	4	CYT HKBCG A	17.52
VTLASILPVLAA	11	A0A0H3M5J6	Possible nitrate/nitrite transporter narK2	narK2	HLA-DRB1*01:01	2.5	4	NOCYT HKBCG A	17.49
PVKAKLAPVP	10	A0A0H3M812	Possible transmembrane protein	BCG_0465c	HLA-DRB1*01:01	36	2	DAY7	17.37
HGGSGNGGGSGGSGGS	16	A0A0H3MHS0	PE_PGRS50 protein	PE_PGRS50	HLA-DRB1*01:01	95	4	NOCYT HKBCG B	17.25
KADLAAEH	8	A0A0H3MJE7	Putative ferredoxin-dependent glutamate synthase [NADPH] (Large subunit) gltB	gltB			4	NOCYT LIVEBCG B	17.21
HESALLVSLGGA	12	A0A0H3M4I3	Possible long-chain acyl-CoA synthase	BCG_1721	HLA-DRB1*01:01	28	4	NOCYT LIVEBCG B	17.11
IARQRRRFR	9	A1KPR5	Uncharacterized tRNA/rRNA methyltransferase BCG_3644c	BCG_3644c	HLA-DRB5*01:01	3	4	NOCYT LIVEBCG A	17.06
VVFLAYSQARWRDS	15	A0A0H3M9W9	Conserved hypothetical alanine and arginine rich protein	BCG_2938	HLA-DRB5*01:01	3	4	NOCYT LIVEBCG B	17.05
IIVAVVVGPA	10	A0A0H3M5I7	Uncharacterized protein	BCG_2160	HLA-DRB1*01:01	11	4	CYT HKBCG A	16.85
LPQDAIRWAALVALVAIGA	19	A0A0H3M9U0	Possible integral membrane C-type cytochrome biogenesis protein dipZ	dipZ	HLA-DRB1*01:01	22	4	CYT LIVEBCG A	16.77
GLVWQIYRPR	12	A0A0H3M0K6	Probable conserved transmembrane protein	BCG_0082	HLA-DRB1*15:01	4	4	CYT HKBCG A	16.44
GGAGGIGGSAVLFGAGG	17	A0A0H3M4W3	PE-PGRS family protein	PE_PGRS29	HLA-DRB1*01:01	90	4	NOCYT LIVEBCG A	16.32
KPNPIGVGLME	11	A0A0H3MBW3	Probable conserved two-domain membrane protein	BCG_3788	HLA-DRB1*01:01	80	4	NOCYT HKBCG B	16.32
KGGTGKSTIAAALTLAAGGRK	23	A0A0H3MIR0	Probable anion transporter atpase	BCG_3738	HLA-DRB5*01:01	4.5	4	NOCYT HKBCG A	16.29
PTYAFQRQ	8	A0A0H3M4G9	Probable polyketide synthase pkS8	pkS8			3	CYT LIVEBCG	16.26
APLLAELIRGGAALSRVRHFGD	22	A0A0H3MAM8	Uncharacterized protein	BCG_3838	HLA-DRB1*01:01	3	4	CYT HKBCG A	16.23
DGALTGGMC	9	A1KM20	1-deoxy-D-xylulose-5-phosphate synthase	dxs	HLA-DRB1*01:01	75	4	NOCYT LIVEBCG B	16.22
DITLPMPPRWTQV	13	A0A0H3M0J7	Secreted proline rich protein MTC28 (PROLINE RICH 28 kDa ANTIGEN)	mtc28	HLA-DRB1*01:01	45	2	DAY7	16.1
GTQAKLAVIRVP	12	A0A0H3M833	Probable exported protease	BCG_2240c	HLA-DRB5*01:01	27	2	DAY7	16.04
TALMVVRIE	9	A0A0H3M2H3	Possible two component sensor kinase	BCG_0897	HLA-DRB5*01:01	20	4	CYT HKBCG A	15.84
VTVAPAMT	8	A0A0H3MCS3	Carbamoyl-phosphate synthase large chain	carB			4	NOCYT HKBCG A	15.8
PGLAGLQALQR	11	A0A0H3M9W7	Putative cation transporter P-type atpase ctpJ	ctpJ	HLA-DRB1*01:01	6.5	4	CYT LIVEBCG A	15.77
RLLVIALKHNVI	12	A0A0H3M6I2	Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex	pdhC	HLA-DRB1*15:01	1	4	CYT HKBCG A	15.76
GKPALLRPV	9	A0A0G2Q9D4	Beta sliding clamp	dnaN_1	HLA-DRB1*01:01	38	2	DAY1	15.75
VTSGVGVAGVGVLLG	16	A0A0H3M793	Probable oxidoreductase	BCG_0116	HLA-DRB1*01:01	80	4	NOCYT LIVEBCG B	15.74
AAHAEGAAGLA	11	A0A0H3M5P8	PPE family protein	PPE28	HLA-DRB1*01:01	75	2	DAY7	15.66
RAAARRI GTAASVSVFE	17	A0A0H3MA06	Possible oxidoreductase	BCG_0234	HLA-DRB1*01:01	24	3	CYT LIVEBCG	15.66
PAPVVVEVDLLD	12	A0A0H3M8A6	Fatty-acid-CoA ligase fadD26	fadD26	HLA-DRB1*15:01	80	2	DAY7	15.61
EGLLSYLPQGGQ	12	A1KP90	Putative S-adenosyl-L-methionine-dependent methyltransferase BCG_3469	BCG_3469	HLA-DRB1*15:01	7	4	CYT LIVEBCG A	15.54
YVRVGKNGPY	10	A0A0H3MA36	DNA topoisomerase 1	topA	HLA-DRB5*01:01	19	3	CYT HKBCG	15.41
DGPLGGI SPVGFKPEGV	17	A0A0H3MFP8	Integral membrane indolylacetylinoitol arabinosyltransferase embA	embA	HLA-DRB1*01:01	90	4	NOCYT HKBCG A	15.41
HGLDEVV IGMPHRGRNLNVLN	21	A1KI36	Multifunctional 2-oxoglutarate metabolism enzyme	kgd	HLA-DRB5*01:01	23	4	NOCYT HKBCG B	15.39
PAKAAAARPATKAPAKKATARR	23	A0A0H3M7X4	Probable DNA-binding protein HU homolog hupB	hupB	HLA-DRB5*01:01	29	4	CYT HKBCG A	15.36
TPEQLSRFE	9	A0A0H3MFR6	Probable fatty acid synthase fas	fas	HLA-DRB1*01:01	95	3	NOCYT LIVEBCG	15.35
SGLLGLDGFNA	12	A0A0H3M7N8	PE-PGRS family protein	PE_PGRS3	HLA-DRB1*01:01	5	4	NOCYT HKBCG B	15.25
LASEMPECQAGI GVAAGQ	18	A0A0H3MA33	Possible adenylate cyclase	BCG_1381c	HLA-DRB1*01:01	85	4	NOCYT LIVEBCG B	15.23
LSLTPEDWIA	10	A0A0H3MC15	Integral membrane indolylacetylinoitol arabinosyltransferase embB	embB	HLA-DRB1*01:01	65	4	CYT HKBCG A	15.16
GLGDHTTAVLSLTRA	16	A0A0H3M3X1	Probable conserved transmembrane protein	BCG_1520c	HLA-DRB5*01:01	39	4	CYT HKBCG A	15.08
VHRTGPGFM	9	A0A0H3M485	Probable enoyl-CoA hydratase echA5	echA5	HLA-DRB5*01:01	28	4	NOCYT HKBCG A	15.07

The common amino acids of nested peptides are presented in bold.
N/D - Not determined.

Supplementary Table 4 Description of the HLA types of human samples used in this study

Volunteer	HLA match	Time point
<i>BCG Vaccinated</i>		
39	A2/Cw9/DR15/DR51	D14
10	A2	D14
12	DR15/DR51	D14
38	A2/DR15/DR51	D14
41	DR1	D14
117	A2	D14
<i>Latently Infected Volunteers</i>		
9	DR15/DR51	W52
11	B75	Screening
14	A2	W52
16	DR15/DR51	W52
17	A2/DR15/DR51	W52
25	DR51	Screening
28	DR15/DR51	Screening

D14 - Day 14. W52 - Week 52.