

Supplementary discussion of the possible bias introduced by the use of an ICS assay to screen for T cell responses.

Prior to the ICS assay, the T cells were expanded by *in vitro* culture with a pool of peptides for 8 days in a media supplemented with IL-2 and IL-15. This could potentially introduce a bias in the epitope discovery process since any T cell reactivity that was not maintained under these conditions could have been missed. A priori, we believe that the epitopes discovered here represents the *ex vivo* anti-virus response since it has been demonstrated, at least for CD8⁺ T cells, that acute and transient viral infections generate a stable TcR repertoire (Welsh, PubMed Identifier [9841914](#)). This suggests that the specificities of YFV-specific acute and memory T cell responses are identical. Furthermore, had important responses been missed, one would expect that a strictly reverse immunology approach as the one shown in Supplementary Table III would have identified epitopes missed by the HFRI approach. However, when we compared the two approaches and *ex vivo* tested 34 tetramers based on predicted, but not HFRI, identified peptides, we only identified one of these as an epitope missed by the HFRI approach. Thus, we conclude that we have not systematically missed major epitopes.

Supplementary results and discussion of the performance of the hybrid forward-reverse immunology (HFRI) vs reverse immunology approaches.

Additional opportunities arose for comparing the HFRI and reverse immunology approaches. For donor YF1067, the 27 stimulatory 15mer peptides were submitted to the contemporary NetMHCpan 2.4, which returned 156 submer-HLA-I predictions per stimulatory peptide. For each stimulatory peptide, we retrospectively asked how each of the 19 validated epitopes of donor YF1067 ranked amongst the 156 submers predictions. In 23(≈85%) of the 27 submissions, the number one ranking prediction ended up being validated as an epitope (**Table I**). If one applied the contemporary NetMHCpan 2.4 predictor at a stringent %Rank cut-off of 0.5%, it would have correctly identified 17 (89%) of the 19 epitopes (true positives); missed 2 (false negatives), and erroneously included 14 (false positives) leading to a false positive rate of $14/(14+19) = 42\%$. The current version, NetMHCpan4.0, could have been applied at an even more stringent %Rank cut-off of 0.25%, which would have correctly identified 18 (95%) of the 19 epitopes (true positives); 1 would have been missed (false negative), and 6 would have been erroneously included (false positives) leading to a false positive rate of $6/(6+19) = 24\%$.

Had the predictors been applied, not to the 27 stimulatory peptides, but to the entire YFV proteome, with the above cut-offs and the HLA-A and -B allotypes of YF1067, the number of false positive predictions included by NetMHCpan 2.4 would have been 187, whereas the current NetMHCpan4.0 would have included 158 false positive predictions.

This supports the general conclusion that the present HFRI approach ranks epitope at the very top of the list of candidates while decimating the false discovery rate. It also demonstrates that the current predictors have improved compared to older versions maintaining a high sensitivity while reducing the false positive rate. Nonetheless, there is still room for further improvements.

A

30x30 matrix with columns C1-C30 and rows R1-R30. Cells contain 5-digit numbers. Some cells are highlighted in green, indicating positive responses (e.g., C9, C22, R10, R18).

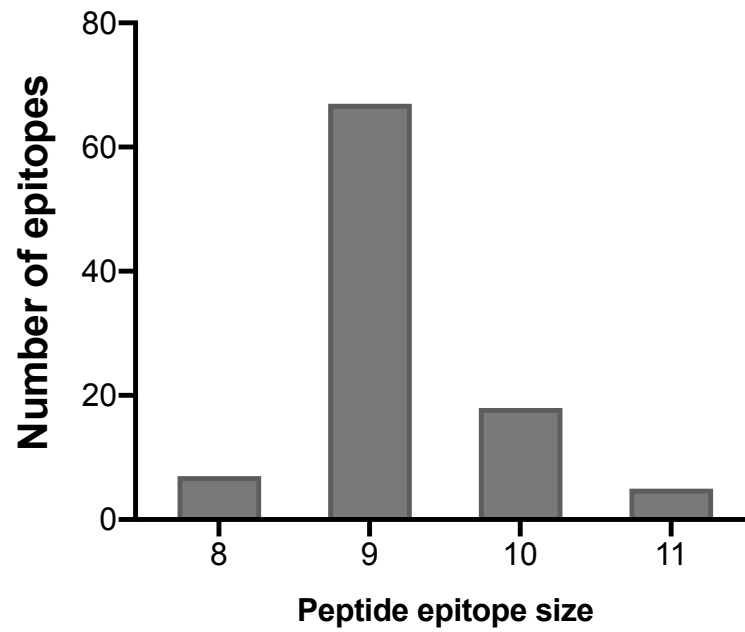
B

30x30 matrix with columns 1-C1 to 1-C15 and 2-C1 to 2-C15. This represents a reorganization of the 30x30 matrix into four 15x15 submatrices.

30x30 matrix with columns 3-C1 to 3-C15 and 4-C1 to 4-C15. This represents another reorganization of the 30x30 matrix into four 15x15 submatrices.

Supplementary Figure S1. Using peptide matrices to screen for peptides containing YFV-derived T cell epitopes
A) The 30x30 matrix approach. The 870 Yellow Fever peptides were organized into a 30x30 matrix. Each 5 digit number in the matrix figure signifies a specific peptide. Row and column peptide pools were made: row pools by mixing the ca. 30 different peptides listed horizontally next to the row number (R1-R30) giving in total 30 different row pools; column pools by mixing the ca. 30 different peptides listed vertically below the column number (C1-C30) giving in total 30 different column pools. This means that every single peptide is present in one specific column and one specific row pool (the oval exemplifies one peptide, 25344, which was present in both column 6 and row 5). The 60 peptide pools (30 row pools and 30 column pools) were used to stimulate the T cells and responses against each row and column pools were evaluated by ELISpot. Theoretically, any given peptide epitope should give rise to a positive response in both a row and a column pool and should therefore be identified as the intersection between the positive row and column pool. The more epitopes, the more positive row and column pools, the more intersections. As exemplified in green, positive responses in both pool R10, R18, C9, and C22, could be due to T cells recognizing two or more of the four peptides (25500, 25738, 25751, and 25751) "located" in the intersection between these row and column pools. Thus, when evaluating T cell responses every intersection of T cell stimulatory column and row pools tentatively identified a T cell epitope-containing peptide for further deconvolution and study.

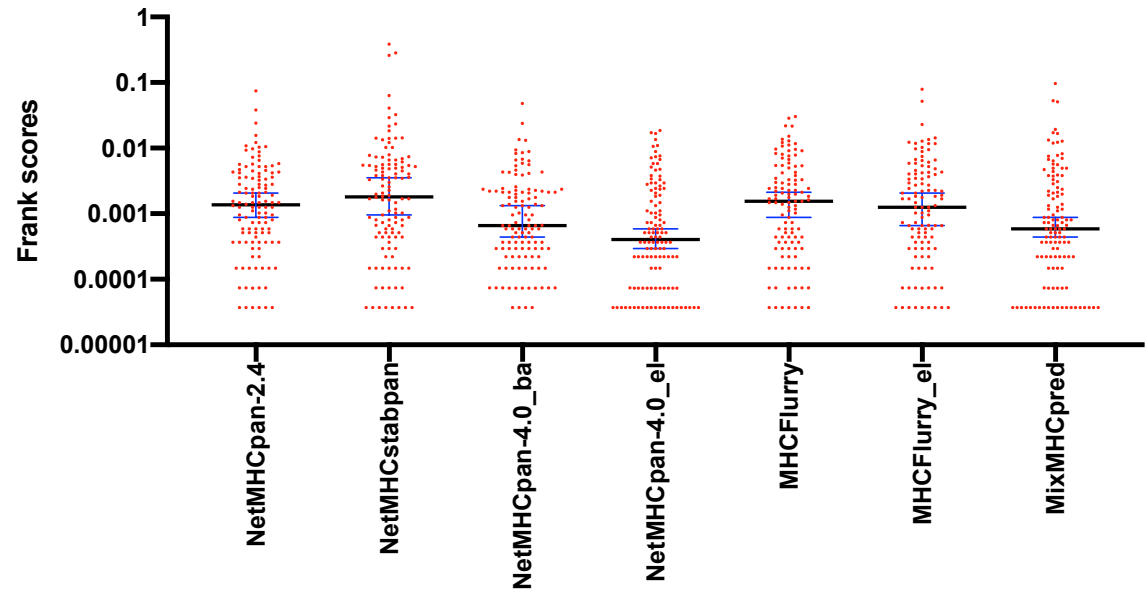
B) The 4x(15x15) matrices approach. The 870 Yellow Fever peptides listed in the 30x30 matrix was reorganized into four 15x15 matrices. Following the same general pooling strategy as for the 30x30 matrix, the 4x(15x15) matrix strategy led to the generation of 4x15 column pools and 4x15 row pools (actually, matrix 4 only contained 14 columns). Per submatrix, every intersection of T cell stimulatory column and row pools tentatively identified a T cell epitope-containing peptide for further deconvolution and study.



Supplementary Figure S2. The length distribution of the identified CD8+ T cell epitopes.

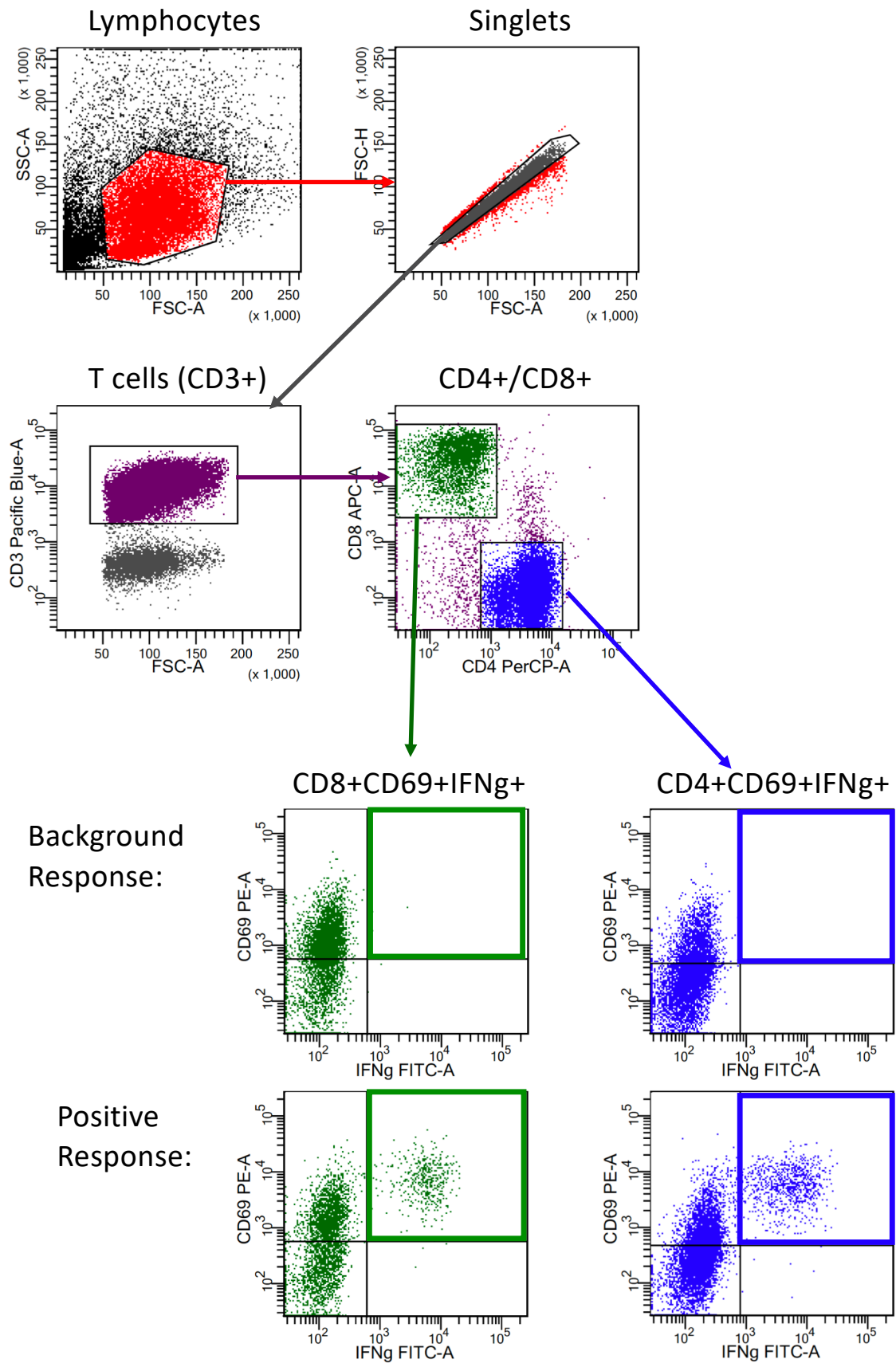
Shown is the number of identified YFV-specific, HLA-class I restricted CD8+ T cell epitopes of 8-, 9-, 10- and 11-mer size for all tetramer validated epitopes.

Frank scores by different predictors of 120 unbiased epitopes



AUC	0.99636	0.98743	0.99755	0.99797	0.99631	0.99604	0.99562
Median Frank score	0.00136	0.00180	0.00066	0.00040	0.00154	0.00125	0.00059
Wilcoxon matched-pairs signed rank test. p-value	0.0001	<0.0001	0.0102	NA	<0.0001	<0.0001	0.0156

Supplementary Figure S3. The Yellow Fever proteome of 3411 aa is submitted to the various indicated predictors along with the HLA-I restriction elements used by the epitopes discovered by the HFRI approach, and the bindings of all 13610 possible 8-11mer peptides per HLA-I are predicted. Per predictor, the median Frank scores (the frequencies of False Positive predictions) of the 120 HFRI discovered epitopes is determined. The median Frank is indicated by black bars and the +/- 95% CI is indicated by blue error bars. For illustrative purposes, the perfect predictions with a Frank score of 0 has been recoded to a Frank score of 0.000037 and are clearly visible as the bottom line of symbols.



Supplementary Figure S4: Gating strategy for intracellular cytokine staining (ICS). Initially a lymphocyte gate is set based on FSC-A/SSC-A, then the singlets are gated based on FCS-A/FCS-H before the CD3+ T cells are gated. Within the gated CD3+ T cell population the CD4+ and CD8+ T cells are gated. The gated CD4+ and CD8+ T cell are then analysed in a CD69/IFN γ plot and the responding T cells CD4+CD69+IFN γ + and CD8+CD69+IFN γ +, respectively, can be determined. Illustrated here are background plots (no stimulation) and positive response plots (stimulated with a peptide epitope) for both CD4+CD69+IFN γ + and CD8+CD69+IFN γ +

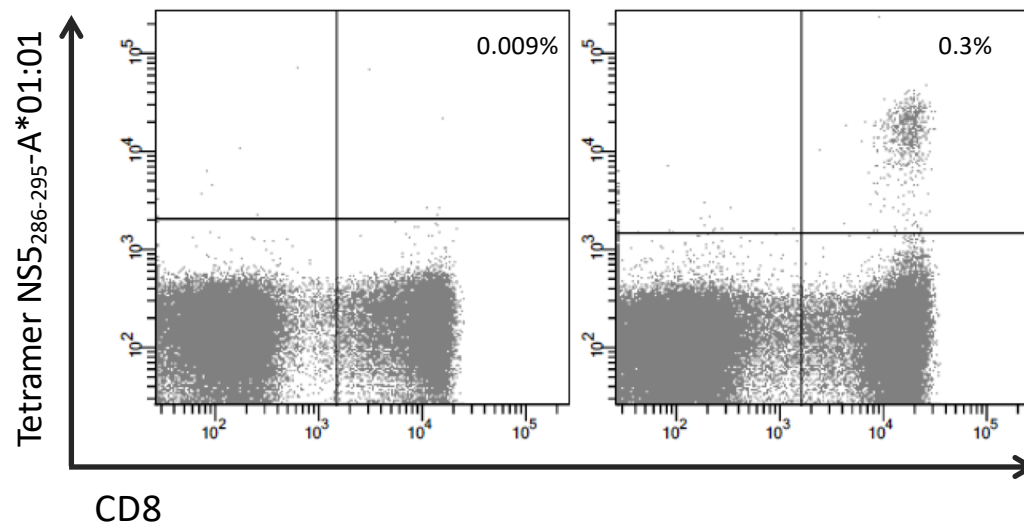


Figure S5: HLA-A*01:01 positive donor stained for the dominant HLA-A1*01:01 epitope, NS5286-295. PBMCs from the donor before vaccination (left plot) and after Yellow Fever vaccination (right plot) were stained with anti CD3-Pacific Blue, CD8-PerCp, and PE labeled NS5286-295-A1*01:01 tetramer. Shown is CD3 gated T cells and the percentage given is tetramer +CD8+ T cells.

Proteom position	Protein position	Sequence	HLA restriction	Predicted affinity (%RANK)	Stability (t _{1/2} ; h)	Responders /donor tested	Tetramer validated (%CD8 ⁺ T cells)	Reference
YFV_pp61-69	CapsidC (61-69)	ITAHLLKRLW	B*57:01	0.05	9.0	3/11	0.01-0.02	
YFV_pp64-72	CapsidC (64-72)	HLKRLWKML	B*08:01	0.30	0.5	8/42	0.03-0.30	
YFV_pp102-110	ER anchor (1-9)	SHDVLTVQF	B*38:01	0.40	1.6	7/7	0.02-0.20	
YFV_pp103-110	ER anchor (2-9)	HDVLTVQF	B*37:01	3.00	19.4	2/2	0.02-0.50	
YFV_pp331-339	EnvE (46-54)	ETVAIDRPA	A*68:02	0.18	15.8	2/2	0.10-0.40	
YFV_pp453-460	EnvE (168-175)	QEVEFIGY	B*18:01	0.08	4.1	13/14	0.01-0.70	
YFV_pp471-479	EnvE (186-194)	TAVDFGNSY	B*35:01	0.25	2.7	9/23	0.01-0.10	
YFV_pp485-494	EnvE (200-209)	TESWIVDRQW	B*44:02	0.15	NA	33/35	0.01-1.50	(PMID:28386132) ¹
YFV_pp485-494	EnvE (200-209)	TESWIVDRQW	B*44:03	0.13	NA	8/12	0.03-0.20	
YFV_pp486-494	EnvE (201-209)	ESWIVDRQW	B*57:01	0.30	1.9	13/15	0.01-0.20	
YFV_pp492-500	EnvE (207-215)	RQWAQDLTL	B*40:02	0.40	2.4	2/7	0.01-0.20	
YFV_pp492-500	EnvE (207-215)	RQWAQDLTL	B*13:02	0.40	2.4	4/4	0.05-0.30	(PMID:28386132) ¹
YFV_pp500-510	EnvE (215-225)	LPWQSGSGGVW	B*53:01	0.03	NA	3/3	0.20-0.30	
YFV_pp500-510	EnvE (215-225)	LPWQSGSGGVW	B*35:01	0.20	2.9	12/22	0.01-0.20	
YFV_pp511-519	EnvE (226-234)	REMHHLVEF	B*37:01	0.03	19.8	3/3	0.01-0.30	
YFV_pp511-519	EnvE (226-234)	REMHHLVEF	B*40:01	0.05	1.5	19/30	0.01-0.80	
YFV_pp517-525	EnvE (232-240)	VEFEPHAA	B*40:02	0.80	12.1	6/7	0.01-0.10	
YFV_pp517-525	EnvE (232-240)	VEFEPHAA	B*50:01	0.10	3.8	2/3	0.10-0.20	
YFV_pp569-577	EnvE (284-292)	RVKLSALTL	B*07:02	1.50	4.8	5/41	0.03-0.40	(PMID: 22039500) ²
YFV_pp569-578	EnvE (284-293)	RVKLSALTLK	A*03:01	0.25	36.3	29/39	0.01-0.20	
YFV_pp651-660	EnvE (366-375)	EVNPPFGDSY	A*25:01	0.13	3.1	2/11	0.03-0.10	
YFV_pp651-660	EnvE (366-375)	EVNPPFGDSY	A*26:01	0.13	1.5	3/10	0.02-0.03	
YFV_pp729-737	EnvE (444-452)	GLFGGLNWI	A*02:01	0.30	5.1	12/89	0.01-0.10	(PMID: 22039500) ²
YFV_pp759-767	EnvE (474-482)	SMSMLVGV	A*02:01	0.30	16.4	27/95	0.01-0.10	
YFV_pp802-810	NS1 (24-32)	DSDDWLNKY	A*01:01	0.05	1.4	40/53	0.01-0.20	
YFV_pp883-891	NS1 (105-113)	SRIRDGLQY	B*27:02	0.80	9.0	1/1	0.05-0.05	
YFV_pp884-893	NS1 (106-115)	RIRDGLQYGW	A*32:01	0.40	107.9	15/18	0.02-0.10	
YFV_pp884-893	NS1 (106-115)	RIRDGLQYGW	B*57:01	0.40	6.3	9/15	0.01-0.10	
YFV_pp885-893	NS1 (107-115)	IRDGLQYGW	B*27:02	1.00	2.4	1/1	0.40-0.40	
YFV_pp894-902	NS1 (116-124)	KTWGKNLVF	A*32:01	0.03	32.1	19/19	0.10-2.80	(PMID:28386132) ¹
YFV_pp894-902	NS1 (116-124)	KTWGKNLVF	B*58:01	0.25	9.3	3/3	0.20-0.40	
YFV_pp894-902	NS1 (116-124)	KTWGKNLVF	B*57:01	0.10	5.3	14/15	0.02-0.80	(PMID:25674793) ¹
YFV_pp945-953	NS1 (167-175)	VYMDAVFEY	A*29:02	0.08	39.1	3/9	0.03-0.10	
YFV_pp945-953	NS1 (167-175)	VYMDAVFEY	A*24:02	0.80	32.8	7/33	0.01-0.20	(PMID 23338234) ³
YFV_pp970-978	NS1 (192-200)	KSAHGSPTF	B*58:01	0.13	13.7	2/3	0.10-0.10	
YFV_pp983-991	NS1 (205-213)	HEVNGTWMI	B*40:01	0.13	1.2	2/31	0.02-0.03	
YFV_pp1002-1010	NS1 (224-232)	CEWPLTHTI	B*49:01	0.01	11.7	2/3	0.05-0.05	
YFV_pp1002-1010	NS1 (224-232)	CEWPLTHTI	B*40:01	0.40	0.9	6/26	0.02-0.80	
YFV_pp1114-1123	NS1 (336-345)	RPRKTHESHL	B*07:02	0.03	4.8	19/44	0.01-0.20	
YFV_pp1114-1124	NS1 (336-346)	RPRKTHESHLV	B*07:02	0.10	3.0	12/44	0.01-0.20	
YFV_pp1119-1127	NS1 (341-349)	HESHLVRSW	B*44:02	0.05	NA	30/33	0.02-0.40	
YFV_pp1119-1127	NS1 (341-349)	HESHLVRSW	B*44:03	0.05	NA	9/13	0.10-0.30	
YFV_pp1131-1140	NS2A (1-10)	GEIHAVPFGL	B*40:01	0.01	1.5	22/28	0.01-0.50	
YFV_pp1131-1141	NS2A (1-11)	GEIHAVPFGLV	B*40:01	0.25	1.2	13/31	0.01-0.30	
YFV_pp1134-1143	NS2A (4-13)	HAVPFGLVSM	B*35:08	0.80	13.5	2/2	1.30-9.70	(PMID: 11853408) ⁴ ; (PMID:19740333) ⁵
YFV_pp1134-1143	NS2A (4-13)	HAVPFGLVSM	B*35:03	0.80	7.7	6/6	0.20-4.50	(PMID: 11853408) ⁴ ; (PMID:19740333) ⁵
YFV_pp1134-1143	NS2A (4-13)	HAVPFGLVSM	B*35:01	0.40	7.0	22/24	0.10-1.70	(PMID: 11853408) ⁴ ; (PMID:19740333) ⁵ ; (PMID:28386132) ¹
YFV_pp1200-1207	NS2A (70-77)	DAMYMALI	B*51:01	0.80	17.3	13/18	0.03-2.20	
YFV_pp1227-1234	NS2A (97-104)	SPRERLVL	B*07:02	0.01	4.1	4/44	0.01-0.02	
YFV_pp1227-1236	NS2A (97-106)	SPRERLVLT	B*07:02	0.03	1.8	40/44	0.02-4.00	
YFV_pp1317-1325	NS2A (187-195)	SMQKTIPLV	A*02:01	0.80	27.3	43/95	0.01-0.10	
YFV_pp1397-1405	NS2B (43-51)	SVAGRVDGL	A*02:05	4.00	18.7	5/5	0.02-0.40	
YFV_pp1464-1472	NS2B (110-118)	HPFALLLV	B*35:01	0.30	5.9	22/23	0.05-0.90	(PMID: 11853408) ⁴ ; (PMID:19740333) ⁵
YFV_pp1464-1472	NS2B (110-118)	HPFALLLV	B*35:03	0.13	5.9	5/6	0.20-0.80	(PMID: 11853408) ⁴ ; (PMID:19740333) ⁵
YFV_pp1471-1479	NS2B (117-125)	VLAWLWFHV	A*02:01	0.01	27.7	75/86	0.01-0.50	(PMID: 22039500) ²
YFV_pp1488-1496	NS3 (4-12)	VLWDIPTPK	A*11:01	0.50	9.0	16/28	0.01-0.20	
YFV_pp1488-1496	NS3 (4-12)	VLWDIPTPK	A*03:01	0.18	6.2	31/40	0.01-0.40	(PMID:28386132) ¹
YFV_pp1508-1516	NS3 (24-32)	IYGIFQSTF	A*24:02	0.08	40.7	22/33	0.01-1.00	(PMID:28386132) ¹
YFV_pp1508-1516	NS3 (24-32)	IYGIFQSTF	A*23:01	0.13	40.6	4/5	0.01-0.20	
YFV_pp1557-1565	NS3 (73-81)	SVKEDLVAY	B*15:01	0.80	14.5	28/30	0.03-1.10	(PMID:28386132) ¹
YFV_pp1557-1565	NS3 (73-81)	SVKEDLVAY	B*35:01	1.50	3.2	13/23	0.01-0.10	(PMID:28386132) ¹
YFV_pp1608-1615	NS3 (124-131)	GEIGAVAL	B*40:01	0.01	3.2	5/17	0.02-0.10	

YFV_pp1632-1641	NS3 (148-157)	EVIGLYGNGI	A*68:02	0.50	2.9	1/2	0.04-0.04	
YFV_pp1635-1643	NS3 (151-159)	GLYGNGLV	A*02:01	1.50	20.1	27/80	0.01-0.20	(PMID: 22039500) ²
YFV_pp1690-1697	NS3 (206-213)	RRFLPQIL	C*06:02	0.15	1.4	6/28	0.10-2.78	
YFV_pp1689-1697	NS3 (205-213)	TRRFLPQIL	C*06:02	8.00	17.7	27/28	0.02-1.90	
YFV_pp1702-1710	NS3 (218-226)	RRRLRTLVL	B*14:02	0.15	0.9	4/4	0.05-0.40	(PMID: 18762226) ⁶
YFV_pp1718-1727	NS3 (234-243)	SEMKEAFHGL	B*40:01	0.05	1.3	16/29	0.01-0.40	
YFV_pp1728-1736	NS3 (244-252)	DVKFHTQAF	A*25:01	0.15	3.2	10/11	0.02-0.30	(PMID: 18762226) ⁶
YFV_pp1770-1778	NS3 (286-294)	IIMDEAHFL	A*02:05	0.20	20.7	5/5	0.10-0.70	
YFV_pp1770-1778	NS3 (286-294)	IIMDEAHFL	A*02:01	0.50	9.2	43/93	0.01-0.10	(PMID: 22039500) ²
YFV_pp1777-1785	NS3 (293-301)	FLDPASIAA	A*02:01	0.40	9.9	56/84	0.01-0.70	
YFV_pp1831-1839	NS3 (347-355)	EPWNTGHDW	B*53:01	0.10	NA	2/3	0.10-0.10	
YFV_pp1910-1918	NS3 (426-434)	RVLDCRTAF	A*32:01	0.80	31.1	4/19	0.05-0.10	
YFV_pp1991-1999	NS3 (507-515)	GMVAPLYGV	A*02:01	0.10	9.4	37/96	0.01-0.20	
YFV_pp2030-2039	NS3 (546-555)	LPVWLSWQVA	B*56:01	0.05	2.3	3/3	0.10-0.10	
YFV_pp2060-2068	NS3 (576-584)	ILNDSGETV	A*02:01	1.50	12.2	42/92	0.01-0.40	
YFV_pp2128-2136	NS4A (21-29)	GEAMDTISV	B*40:01	0.40	1.3	7/32	0.01-0.20	
YFV_pp2129-2137	NS4A (22-30)	EAMDTISVF	B*35:01	0.10	3.7	3/21	0.01-0.03	
YFV_pp2130-2138	NS4A (23-31)	AMDTISVFL	A*02:01	0.80	11.0	5/95	0.01-0.03	(PMID:27017899)
YFV_pp2152-2160	NS4A (45-53)	SMMPEAMTI	B*52:01	0.10	9.1	3/3	0.01-0.03	
YFV_pp2154-2163	NS4A (47-56)	MPEAMTIVML	B*35:03	0.05	3.9	5/6	0.10-0.80	
YFV_pp2154-2163	NS4A (47-56)	MPEAMTIVML	B*35:01	0.30	3.8	21/25	0.03-1.00	
YFV_pp2154-2163	NS4A (47-56)	MPEAMTIVML	B*53:01	0.15	2.9	2/3	0.10-0.10	
YFV_pp2155-2163	NS4A (48-56)	PEAMTIVML	B*40:01	1.00	ND	13/17	0.10-0.80	
YFV_pp2180-2189	NS4A (73-82)	SPKGISRMMSM	B*07:02	0.10	8.6	29/43	0.01-0.10	
YFV_pp2389-2397	NS4B (133-141)	KLAQRRVFH	A*03:01	1.00	8.6	26/32	0.01-1.40	
YFV_pp2421-2429	NS4B (165-173)	ALYEKKLAL	A*02:01	2.00	19.2	3/85	0.01-0.50	
YFV_pp2421-2429	NS4B (165-173)	ALYEKKLAL	B*08:01	0.25	0.4	28/41	0.01-0.20	
YFV_pp2423-2431	NS4B (167-175)	YEKKLALYL	B*40:02	0.40	24.4	7/7	0.04-0.60	
YFV_pp2423-2431	NS4B (167-175)	YEKKLALYL	B*40:01	0.30	1.1	4/28	0.03-0.30	
YFV_pp2470-2478	NS4B (214-222)	LLWNGPMAV	A*02:01	0.13	38.2	98/98	0.03-11.50	(PMID 19933869)
YFV_pp2494-2502	NS4B (238-246)	VMYNLWKMK	A*03:01	0.05	0.8	17/38	0.01-2.40	
YFV_pp2524-2533	NSS (18-27)	LLDKRFELY	A*01:01	0.05	11.7	32/52	0.01-0.20	
YFV_pp2571-2579	NSS (65-73)	FHERGYVKL	B*38:01	0.10	5.2	7/7	0.10-0.60	
YFV_pp2571-2579	NSS (65-73)	FHERGYVKL	B*39:01	0.15	0.6	5/6	0.10-1.00	
YFV_pp2669-2677	NSS (163-171)	RVLDTVEKW	A*32:01	0.80	101.6	11/19	0.01-0.10	
YFV_pp2669-2677	NSS (163-171)	RVLDTVEKW	B*58:01	0.13	32.9	2/3	0.10-0.40	
YFV_pp2669-2677	NSS (163-171)	RVLDTVEKW	B*57:01	0.15	16.2	13/15	0.01-0.20	
YFV_pp2706-2714	NSS (200-208)	RRFGGTVIR	B*27:05	0.05	22.9	6/12	0.02-0.10	
YFV_pp2711-2719	NSS (205-213)	TVIRNPLSR	A*68:01	0.50	11.9	11/19	0.03-0.70	
YFV_pp2723-2731	NSS (217-225)	HEMYVYVSGA	B*50:01	0.08	NA	3/3	0.04-0.10	
YFV_pp2762-2770	NSS (256-264)	DVILPIGTR	A*68:01	0.50	37.4	20/20	0.01-0.90	
YFV_pp2792-2801	NSS (286-295)	KSEYMTSWFY	A*01:01	0.08	44.2	50/52	0.01-4.60	(PMID:28386132) ¹
YFV_pp2854-2862	NSS (348-356)	TPFGQQRVF	B*35:01	0.40	3.6	8/22	0.01-0.10	
YFV_pp2879-2887	NSS (373-381)	KIMKVNNRW	B*58:01	0.18	19.2	1/3	0.01-0.01	
YFV_pp2882-2890	NSS (376-384)	KVVNRWLFR	A*03:01	0.40	6.5	2/38	0.02-0.03	
YFV_pp2974-2982	NSS (468-476)	KAKGSRAIW	B*57:01	0.13	11.2	10/15	0.01-0.10	
YFV_pp2977-2985	NSS (471-479)	GSRAIWMW	B*57:01	0.08	9.1	5/15	0.01-0.02	
YFV_pp2981-2990	NSS (475-484)	IWYMWLGARY	A*29:02	0.10	0.6	2/8	0.10-0.20	
YFV_pp2982-2990	NSS (476-484)	WYMWLGARY	A*29:02	0.25	24.7	8/9	0.10-0.50	(PMID:28386132) ¹
YFV_pp2983-2990	NSS (477-484)	YMWLGARY	A*29:02	0.03	3.0	3/9	0.03-0.30	
YFV_pp2983-2990	NSS (477-484)	YMWLGARY	A*01:01	1.50	67.3	47/52	0.01-0.80	
YFV_pp3024-3032	NSS (518-526)	YVIRDLAAM	B*35:01	0.13	5.9	16/20	0.01-0.10	
YFV_pp3063-3071	NSS (557-565)	YMSPHHKKL	A*02:05	1.50	16.9	4/5	0.10-0.20	
YFV_pp3178-3186	NSS (672-680)	RPIDDRFGL	B*07:02	0.15	6.3	45/45	0.01-0.80	(PMID: 23338234) ³ ; (PMID: 28386132) ¹
YFV_pp3178-3187	NSS (672-681)	RPIDDRFGLA	B*07:02	0.80	3.1	8/46	0.01-0.50	
YFV_pp3178-3188	NSS (672-682)	RPIDDRFGLAL	B*07:02	0.03	2.5	41/47	0.01-0.60	
YFV_pp3178-3188	NSS (672-682)	RPIDDRFGLAL	B*35:03	0.25	3.5	3/6	0.01-0.10	
YFV_pp3389-3399	NSS (883-893)	YTDYLTVMDDRY	A*01:01	0.01	42.0	48/53	0.06-0.70	

Table S1. A complete list of the 120 peptide-specific, HLA-I-restricted CD8⁺ T cell epitopes identified by the HFRI approach.

The HFRI-based CD8⁺ T cell epitope discovery process detailed for donor YF1067 was extended to 50 randomly selected, primary YFV-vaccinated donors. Ninety-two different epitopes restricted by 40 HLA-I allotypes were discovered. The peptide-HLA-I affinity was predicted by NetMHCpan 2.4 (given in %Rank; the lower, the better); the stability was measured (given as half-life at 37°C in hours; the longer, the better). Productively interaction peptide-HLA-I combinations were used to design peptide-HLA-I tetramers. The resulting tetramers were used to stain and ex vivo analyze CD8⁺ T cells by flow cytometry gating on CD3⁺ CD8⁺ T cells. The prevalence of these responses is given as "the number of positive donors/the number of donors tested". The magnitudes are given as the range of frequencies (in %) of ex vivo tetramer-stained CD8⁺ T cells. Note, that for the prevalence and magnitude measurements, the specific responses identified in 50 vaccinees was extended to additional donors within our cohort of primary vaccinee, who expressed the relevant HLA-I allotype. PubMed ID (PMID) references are given in the event that an epitope had been reported before this study.

Proteome position	Protein position	Sequence	HLA restriction	Predicted affinity (%RANK)	Stability (t _{1/2} ; h)	Responders per donors tested	Tetramer validated (%CD8 ⁺ T cells)
YFV_pp438-446	EnvE (153-161)	NTDIKTLKF	A*01:01	0.15	1.70	46/51	0.02-0.90
YFV_pp511-519	EnvE (226-234)	REMHHLVEF	B*40:02	0.03	17.7	3/7	0.01-0.02
YFV_pp1131-1140	NS2A (1-10)	GEIHAVPFGL	B*40:02	0.05	11.8	5/7	0.03-0.10
YFV_pp1504-1512	NS3 (20-28)	LEDGIYGIF	B*40:01	0.4	2.30	6/27	0.01-0.10
YFV_pp2762-2770	NS5 (256-264)	DVILPIGTR	A*33:01	0.18	NA	2/2	0.01-0.10
YFV_pp3024-3032	NS5 (518-526)	YVIRDLAAM	A*26:01	0.01	10.6	7/10	0.01-0.30
YFV_pp3089-3098	NS5 (583-592)	RPAPGGKAYM	B*07:02	0.03	8.5	22/44	0.01-0.20
YFV_pp3116-3124	NS5 (610-618)	ALNTITNLK	A*03:01	0.10	14.8	12/33	0.01-0.10
YFV_pp3268-3276	NS5 (762-770)	YANMWSLMY	B*35:01	0.30	8.6	7/22	0.01-0.10

Supplementary Table SII. CD8⁺ T cell epitopes derived from past epitope discovery efforts.

A panel of 533 YFV-derived peptides obtained from past epitope discovery efforts were evaluated by NetMHCpan 2.4 in an effort to discover additional CD8⁺ T cell epitopes. The stability of predicted peptide-HLA-I binders were verified experimentally. An additional 90 peptide-HLA-I tetramers could be generated and tested in appropriate primary YFV-vaccinated donors. Additionally 9 epitopes and their restriction elements were identified. The prevalence and response magnitude of the corresponding CD8⁺ T cell responses were evaluated as described in Supplementary Table SI.

Protein Position	Sequence	Predicted	Measured	T cell analysis	
		%Rank	Stability (T½, h)	Responders /donor tested	Suggested by HFRI
NS2A (97-104)	SPRERLVL	0.01	4.1	4/44	Yes ¹
NS1 (243-251)	MPRSIGGPV	0.03	4.6	0/18	
NS2A (97-106)	SPRERLVLTL	0.03	1.8	40/44	Yes ¹
NS5 (672-682)	RPIDDRFGLAL	0.03	2.5	41/47	Yes
NS1 (336-345)	RPRKTHESHL	0.03	4.8	19/44	Yes
NS5 (583-592)	RPAPGGKAYM	0.03	8.5	22/44	No
NS4B (163-173)	MPALYEKKLAL	0.05	2.0	0/16	
CapsidC (15-23)	MVRRGVRSLS	0.05	3.3	0/16	
NS5 (112-119)	KPMNVQSL	0.05	3.4	0/18	
NS5 (246-253)	RPTGKVTL	0.08	6.5	0/18	
NS1 (336-346)	RPRKTHESHLV	0.10	3.0	12/44	Yes
NS4A (73-82)	SPKGISRMSM	0.10	8.6	29/43	Yes ²
NS4A (47-55)	MPEAMTIVM	0.10	0.8	0/17	Yes ³
NS4B (218-228)	GPMVAVSMTGVM	0.10	14.4	0/16	
NS3 (133-142)	YPSGTSGSPI	0.10	2.5	0/17	
prM (128-136)	NPFFAVTAL	0.12	2.3	0/18	
NS3 (367-376)	LPSIRAAVM	0.12	5.7	0/18	
NS4B (107-117)	MPLLCGIGCAM	0.12	3.5	0/18	
NS1 (102-111)	HPFSRIRDGL	0.12	3.0	0/16	
NS5 (672-680)	RPIDDRFGL	0.15	6.3	45/45	Yes
NS5 (559-569)	SPHHKKLAQAV	0.15	1.4	0/18	
NS5 (259-266)	LPIGTRSV	0.17	0.7	0/18	Yes
NS3 (199-209)	HPGAGKTRRFL	0.20	1.6	0/17	
NS2B (110-118)	HPFALLLVL	0.20	NF	ND	
NS5 (710-720)	VPFCSHHFHEL	0.25	3.9	0/18	
NS4A (100-108)	KPTHISYVM	0.25	6.5	0/18	
NS1 (266-273)	GPWMQVPL	0.25	0.4	0/18	
NS5 (185-192)	APYMPDVL	0.25	6.4	0/18	
NS3 (361-370)	RPTAWFLPSI	0.25	1.7	0/17	
NS1 (226-236)	WPLTHTIGTSV	0.25	2.6	0/18	
NS5 (583-590)	RPAPGGKA	0.25	NA	ND	
EnvE (52-59)	RPAEVRKV	0.25	NA	ND	
NS4A (47-56)	MPEAMTIVML	0.30	NA	0/18	Yes ³
NS3 (588-596)	APGGAKKPL	0.30	13.5	0/18	
NS3 (308-318)	RARANESATIL	0.30	3.7	0/18	
NS5 (209-219)	NPLSRNSTHEM	0.30	2.6	0/18	
NS4B (84-93)	IPFMKMNISV	0.30	NA	ND	
NS4B (84-94)	IPFMKMNISVI	0.30	NA	ND	
NS2A (6-13)	VPFGLVSM	0.30	0.4	0/16	
CapsidC (37-44)	RPGPSRGV	0.30	NA	ND	
EnvE (38-45)	KPSLDISL	0.40	NA	ND	
NS4A (73-80)	SPKGISRM	0.40	1.4	0/18	Yes ²
NS1 (125-133)	SPGRKNGSF	0.40	2.7	0/18	
NS3 (227-236)	APTRVVLSEM	0.40	5.3	0/18	
NS1 (143-153)	CPFSNRVWNSF	0.40	1.0	0/16	
NS4B (51-58)	SPMLHHWI	0.40	NA	ND	
NS1 (243-252)	MPRSIGGPVS	0.40	NA	ND	
NS5 (583-591)	RPAPGGKAY	0.40	6.2	0/18	
CapsidC 37-47)	RPGPSRGVQGF	0.40	NA	ND	
NS2B (71-78)	SARYDVAL	0.40	NA	ND	
PrM (83-89))	RSRRSRAI	0.40	NA	ND	
NS2B (92-102)	VPWDQVMTSL	0.40	NA	ND	
NS4B (205-214)	GPLIEGNTSL	0.40	1.7	0/17	
EnvE ((52-60)	RPAEVRKVC	0.40	NA	ND	
NS5 672-681)	RPIDDRFGLA	0.80	3.1	8/46	Yes
EnvE (284-292)	RVKLSALTL	1.50	4.8	5/41	Yes

Table SIII. "hybrid forward-reverse immunology" vs "reverse immunology" approaches to HLA-B*07:02-restricted T cell epitope discovery.

NetMHCpan 2.4 was used to identify YFV-derived peptides predicted to bind with a high affinity to HLA-B*07:02 (threshold <0.5% Rank), and a selection of these were tested experimentally for their stability of HLA-B*07:02 binding, their ability to support peptide-HLA-B*07:02 tetramer generation, and their ability to stain CD8+ T cells obtained *ex vivo* from YFV vaccinees.

Note: HFRI suffix means that the peptides with the same suffix (1, 2 or 3) were found within the same 15mer peptide

Proteom position	Protein position	Sequence	Positive donors of 50 tested
YFV_pp9-23	Capsid C (9-23)	KTLGVNMVRRGVRSLS	3
YFV_pp13-27	Capsid C (13-27)	VNMVRRGVRSLSNKI	9
YFV_pp17-31	Capsid C (17-31)	RRGVRSLSNKIKQKT	14
YFV_pp49-63	Capsid C (49-63)	FFFLFNILTGKKITA	11
YFV_pp53-67	Capsid C (53-67)	FNILTGKKITAHLLKR	9
YFV_pp57-71	Capsid C (57-71)	TGKKITAHLLKRLWKM	3
YFV_pp61-75	Capsid C (61-75)	ITAHLLKRLWKMLDPR	4
YFV_pp65-79	Capsid C (65-79)	LKRLWKMLDPRQGLA	6
YFV_pp73-87	Capsid C (73-87)	DPRQGLAVLRKVVRV	4
YFV_pp77-91	Capsid C (77-91)	GLAVLRKVVRVVASL	4
YFV_pp81-95	Capsid C (81-95)	LRKVVRVVASLMRGL	10
YFV_pp85-99	Capsid C (85-99)	KRVVVASLMRGLSSRK	2
YFV_pp121-135	prM (1-14)	GVTLVRKNRWLLLN	1
YFV_pp125-139	prM (4-18)	VRKNRWLLLNVTSED	1
YFV_pp133-147	prM (12-26)	LNVTSEDLGKTFVSG	1
YFV_pp201-215	prM (80-94)	SAGRSRRSRRRAIDL	1
YFV_pp205-219	prM (84-98)	SRRSRRRAIDLPTHE	2
YFV_pp213-227	prM (92-106)	DLPTHEHGLKTRQE	1
YFV_pp217-231	prM (96-110)	HENHGLKTRQEKWMT	1
YFV_pp221-235	prM (100-114)	GLKTRQEKWMTGRMG	1
YFV_pp237-251	prM (116-130)	RQLQKIERWFVRNPF	2
YFV_pp245-259	prM (124-138)	WFVRNPFVAVTALTI	1
YFV_pp249-263	prM (128-142KK)	NPFVAVTALTIAYLK	3
YFV_pp253-267	prM (132-146K)	AVTALTIAYLVGSNMK	4
YFV_pp257-271	prM (136-150KK)	KKLTIAYLVGSNMTQ	1
YFV_pp265-279	prM (144-158KK)	SNMTQRVVIALLVLA	1
YFV_pp285-299	EnvE (1-13)	SAHCIGITDRDFIEG	1
YFV_pp301-315	EnvE (16-30)	HGGTWVSAATLEQDK	2
YFV_pp329-343	EnvE (44-58)	SLETVAIDRPAEVRK	22
YFV_pp333-347	EnvE (48-62)	VAIDRPAEVRKVCYN	5
YFV_pp341-355	EnvE (56-70)	VRKVCYNVAVLTHVK	6
YFV_pp345-359	EnvE (60-74)	CYNVAVLTHVKINDK	4
YFV_pp409-423	EnvE (124-138)	SMSLFEVDQTKIQYV	4
YFV_pp413-427	EnvE (128-142)	FEVDQTKIQYVIRAQ	6
YFV_pp417-431	EnvE (132-146)	QTKIQYVIRAQLHVG	4
YFV_pp421-435	EnvE (136-150)	QYVIRAQLHVGAKQE	9
YFV_pp489-503	EnvE (204-218)	IVDRQWAQDLTLPWQ	2
YFV_pp493-507	EnvE (208-222)	QWAQDLTLPWQSGSG	1
YFV_pp505-519	EnvE (220-234)	GSGGVWREMHHLVEF	2
YFV_pp509-523	EnvE (224-238)	VWREMHHLVEFEPH	3
YFV_pp525-539	EnvE (240-254)	ATIRVLALGNQEGSL	3
YFV_pp537-551	EnvE (252-266)	GSLKTALTGAMRVTK	1
YFV_pp553-567	EnvE (268-282)	TNDNNLYKLHGGHVS	1
YFV_pp557-571	EnvE (272-286)	NLYKLHGGHVSCRVK	9
YFV_pp573-587	EnvE (288-302)	SALTLKGTSYKICTD	2
YFV_pp589-603	EnvE (304-318)	MFFVKNPDTDTGHGT	4

YFV_pp601-615	EnvE (316-330)	GTVVMQVKVSKGAPC	4
YFV_pp613-627	EnvE (328-342)	APCRIPVIVADDLTA	1
YFV_pp625-639	EnvE (340-354)	LTAAINKGILVTVNP	3
YFV_pp629-643	EnvE (344-358)	INKGILVTVNPIAST	1
YFV_pp669-683	EnvE (384-398)	RLTYQWHKEGSSIGK	2
YFV_pp673-687	EnvE (388-402)	QWHKEGSSIGKLFTQ	6
YFV_pp681-695	EnvE (396-410)	IGKLFTQTMKGVERL	4
YFV_pp733-747	EnvE (KK448-462)	KKGLNWITKVIMGAVLI	1
YFV_pp745-759	EnvE (460-474K)	VLIWVGINTRNMTMSK	3
YFV_pp809-823	NS1 (31-45)	KYSYYPEDPVKLASI	3
YFV_pp841-855	NS1 (63-77)	LEHEMWRRADEINA	3
YFV_pp845-859	NS1 (67-81)	MWRRADEINAIFEE	4
YFV_pp849-863	NS1 (71-85)	RADEINAIFEENEVD	4
YFV_pp865-879	NS1 (87-101)	SVVVQDPKNVYQRGT	7
YFV_pp889-903	NS1 (111-125)	LQYGWKTWGKNLVFS	4
YFV_pp893-907	NS1 (115-129)	WKTWGKNLVFSPGRK	2
YFV_pp905-919	NS1 (127-140)	GRKNGSFIIDGKSRK	2
YFV_pp909-923	NS1 (131-144)	GSFIIDGKSRKECPF	4
YFV_pp921-935	NS1 (143-157)	CPFSNRVWNSFQIEE	1
YFV_pp945-959	NS1 (167-181)	VYMDAVFEYTIDCDG	2
YFV_pp953-967	NS1 (175-189)	YTIDCDGSILGAAVND	2
YFV_pp985-999	NS1 (207-221)	VNGTWMIHTLEALDY	5
YFV_pp989-1003	NS1 (211-225)	WMIHTLEALDYKECE	3
YFV_pp1001-1015	NS1 (223-237)	ECEWPLTHTIGTSVE	2
YFV_pp1005-1019	NS1 (227-241)	PLTHTIGTSVEESEM	1
YFV_pp1085-1099	NS1 (307-321)	VIPEWCCRSCMPPV	1
YFV_pp1105-1119	NS1 (327-341)	DGCWYPMEIRPRKTH	4
YFV_pp1129-1143	NS2A (1-13)	TAGEIHAVPFGLVSM	1
YFV_pp1133-1147	NS2A (3-17KK)	IHAVPFGLVSMMIAMKK	1
YFV_pp1141-1155	NS2A (11-25)	VSMMIAMEVVLRKRQ	1
YFV_pp1177-1191	NS2A (47-61KK)	KKTLDDLKLTVAVGLH	4
YFV_pp1181-1195	NS2A (51-65)	LLKLTVAVGLHFHEM	1
YFV_pp1197-1211	NS2A (KK67-80)	KKNGGDAMYMALIAAFS	1
YFV_pp1217-1231	NS2A (87-101)	LIGFGLRTLWSPRER	3
YFV_pp1229-1243	NS2A (99-113)	RERLVLTGAAMVEI	1
YFV_pp1233-1247	NS2A (103-117KK)	VLTGAAMVEIALGGKK	1
YFV_pp1245-1259	NS2A (115-129)	LGGVMGGLWKYLNVA	1
YFV_pp1249-1263	NS2A (119-133)	MGGLWKYLNVAVSLCI	7
YFV_pp1253-1267	NS2A (123-137KK)	KKWKYLNVAVSLCILTIN	4
YFV_pp1337-1351	NS2A (207-221)	QPFLGLCAFLATRIFK	1
YFV_pp1373-1387	NS2B (19-33)	GLAFQEMENFLGPIA	1
YFV_pp1377-1391	NS2B (23-37)	QEMENFLGPIAVGGL	1
YFV_pp1385-1399	NS2B (31-45KK)	KKPIAVGGLMMLVSVVA	1
YFV_pp1485-1499	NS3 (1-15)	SGDVLWDIPTPKIIE	2
YFV_pp1489-1503	NS3 (5-19)	LWDIPTPKIIEECEH	1
YFV_pp1505-1519	NS3 (21-35)	EDGIYGIFQSTFLGA	2
YFV_pp1529-1543	NS3 (45-59)	GGVFHTMWHVTRGAF	1
YFV_pp1533-1547	NS3 (49-63)	HTMWHVTRGAFLVRN	11
YFV_pp1537-1551	NS3 (53-67)	HVTRGAFLVRNGKKL	1

YFV_pp1541-1555	NS3 (57-71)	GAFIVRNGKKLIPSW	1
YFV_pp1581-1595	NS3 (97-111)	VQLIAAVPGKNVVNV	1
YFV_pp1629-1643	NS3 (145-159)	RNGEVIGLYGNGILV	2
YFV_pp1633-1647	NS3 (149-163)	VIGLYGNGILVGDNS	6
YFV_pp1641-1655	NS3 (157-171)	ILVGDNSFVSAISQT	1
YFV_pp1685-1699	NS3 (201-215)	GAGKTRRFLPQILAE	4
YFV_pp1689-1703	NS3 (205-219)	TRRFLPQILAECAARR	5
YFV_pp1693-1707	NS3 (209-223)	LPQILAECAARRRLRT	8
YFV_pp1697-1711	NS3 (213-227)	LAECAARRRLRTLVA	1
YFV_pp1701-1715	NS3 (217-231)	ARRRLRTLVLAPTRV	1
YFV_pp1713-1727	NS3 (229-243)	TRVVLSEMKEAFHGL	1
YFV_pp1737-1751	NS3 (253-267)	SAHGSGREVIDAMCH	1
YFV_pp1753-1767	NS3 (269-283)	TLTYRMLEPTRVVNW	4
YFV_pp1765-1779	NS3 (281-295)	VNWEVIIMDEAHFLD	15
YFV_pp1769-1783	NS3 (285-299)	VIIMDEAHFLDPASI	10
YFV_pp1773-1787	NS3 (289-303)	DEAHFLDPASIAARG	1
YFV_pp1777-1791	NS3 (293-307)	FLDPASIAARGWAAH	1
YFV_pp1797-1811	NS3 (313-327)	ESATILMTATPPGTS	1
YFV_pp1821-1835	NS3 (337-351)	IEDVQTDIPSEPWNT	3
YFV_pp1833-1847	NS3 (349-363)	WNTGHDWILADKRPT	3
YFV_pp1837-1851	NS3 (353-367)	HDWILADKRPTAWFL	16
YFV_pp1841-1855	NS3 (357-371)	LADKRPTAWFLPSIR	2
YFV_pp1845-1859	NS3 (361-375)	RPTAWFLPSIRAANV	2
YFV_pp1849-1863	NS3 (365-379)	WFLPSIRAANVMAAS	10
YFV_pp1853-1867	NS3 (369-383)	SIRAANVMAASLRKA	8
YFV_pp1861-1875	NS3 (377-391)	AASLRKAGKSVVVLNK	1
YFV_pp1869-1883	NS3 (385-399)	KSVVVLNRKTFEREY	4
YFV_pp1877-1891	NS3 (393-407)	KTFEREYPTIKQKKP	4
YFV_pp1897-1911	NS3 (413-427)	TDIAEMGANLCVERV	1
YFV_pp1929-1943	NS3 (445-459)	VAIKGPLRISASSAA	1
YFV_pp1933-1947	NS3 (449-463)	GPLRISASSAAQRRG	3
YFV_pp1941-1955	NS3 (457-471)	SAAQRRGRIGRPNR	2
YFV_pp1945-1959	NS3 (461-475)	RRGRIGRPNRNDGDS	2
YFV_pp1957-1971	NS3 (473-487)	GDSYYYSEPTSENNA	4
YFV_pp1961-1975	NS3 (477-491)	YYSEPTSENNAHHVC	2
YFV_pp1969-1983	NS3 (485-499)	NNAHHVCWLEASMLL	2
YFV_pp1973-1987	NS3 (489-503)	HVCWLEASMLLDNME	1
YFV_pp1989-2003	NS3 (505-519)	RGGMVAPLYGVEGTK	1
YFV_pp2021-2035	NS3 (537-551)	FRELVRNCDLPVWLS	1
YFV_pp2029-2043	NS3 (545-559)	DLPVWLSWQVAKAGL	2
YFV_pp2033-2047	NS3 (549-563)	WLSWQVAKAGLKTND	1
YFV_pp2185-2199	NS4A (78-92)	SRMSMAMGTMAGCGY	1
YFV_pp2189-2203	NS4A (82-96K)	MAMGTMAGCGYLMFLK	2
YFV_pp2285-2299	NS4B (29-43)	WPDLDLKPGAAWTVY	1
YFV_pp2289-2303	NS4B (33-47)	DLKPGAAWTVYVGIV	3
YFV_pp2293-2307	NS4B (37-51K)	GAAWTVYVGIVTMLSK	1
YFV_pp2297-2311	NS4B (41-55K)	TVYVGIVTMLSPMLHK	5
YFV_pp2329-2343	NS4B (73-87)	SASVLSFMDKGIPFM	1
YFV_pp2337-2351	NS4B (81-95K)	DKGIPFMKMNISVIMK	4

YFV_pp2341-2355	NS4B (85-99KK)	KKPFMKMNISVIMLLVS	1
YFV_pp2353-2367	NS4B (97-111)	LVSGWNSITVMPLLC	4
YFV_pp2357-2371	NS4B (101-115KK)	KKWNSITVMPLLCGIGC	1
YFV_pp2381-2395	NS4B (125-139)	PGIKAQQSKLAQRRV	2
YFV_pp2385-2399	NS4B (129-143)	AQQSKLAQRRVFHGV	1
YFV_pp2389-2403	NS4B (133-147 (E->K))	KLAQRRVFHGVAKNP	5
YFV_pp2393-2407	NS4B (137-151 (E->K))	RRVFHGVAKNPVVDG	4
YFV_pp2397-2411	NS4B (141-155 (E->K))	HGVAKNPVVDGNPTV	1
YFV_pp2401-2415	NS4B (146-159)	KNPVVDGNPTVDIEE	2
YFV_pp2405-2419	NS4B (149-163)	VDGNPTVDIEEAPEM	1
YFV_pp2425-2439	NS4B (KK169-183)	KKKKLALYLLLALSAS	1
YFV_pp2437-2451	NS4B (181-195)	LASVAMCRTPFSLAE	6
YFV_pp2481-2495	NS4B (225-239)	TGVMRGNHYAFVGV	1
YFV_pp2485-2499	NS4B (229-241)	RGNHYAFVGVMYNLW	1
YFV_pp2489-2503	NS4B (233-247K)	YAFVGVMYNLWKMKTK	10
YFV_pp2513-2527	NS5 (7-21)	TLGEVWKRELNLLDK	2
YFV_pp2517-2531	NS5 (11-25)	VWKRELNLLDKRQFE	1
YFV_pp2529-2543	NS5 (23-37)	QFELYKRTDIVEVDR	4
YFV_pp2565-2579	NS5 (59-73)	TAKLRWFHERGYVKL	2
YFV_pp2569-2583	NS5 (63-77)	RWFHERGYVKLEGRV	1
YFV_pp2573-2587	NS5 (67-81)	ERGYVKLEGRVIDLG	2
YFV_pp2677-2691	NS5 (171-185K)	WLACGVDNFCVKVLAK	3
YFV_pp2833-2847	NS5 (327-341)	KILTYPWDRIEEVTR	1
YFV_pp2877-2891	NS5 (371-385)	TRKIMKVVNRWLFRRH	11
YFV_pp2881-2895	NS5 (375-389)	MKVVRWLFRRHLARE	3
YFV_pp2885-2899	NS5 (379-393)	NRWLFRRHLAREKNPR	3
YFV_pp2905-2919	NS5 (399-413)	EFIAKVRSHAAIGAY	1
YFV_pp2957-2971	NS5 (451-465)	CVYNNMMGKREKKLSE	1
YFV_pp2977-2991	NS5 (471-485)	GSRAIWYMWLGARYL	10
YFV_pp2981-2995	NS5 (475-489(KK))	IWYMWLGARYLEFEAKK	8
YFV_pp2989-3003	NS5 (483-497)	RYLEFEALGFLNEDH	1
YFV_pp3057-3071	NS5 (551-565)	EQEILNYMSPHHKKL	5
YFV_pp3061-3075	NS5 (555-569)	LNYSMPHHKKLAQAV	2
YFV_pp3069-3083	NS5 (563-577)	KKLAQAVMEMTYKNK	1
YFV_pp3073-3087	NS5 (567-581)	QAVMEMTYKNKVVKV	2
YFV_pp3077-3091	NS5 (571-585)	EMTYKNKVVKVLRPA	2
YFV_pp3117-3131	NS5 (611-625)	LNTITNLKVQLIRMA	3
YFV_pp3145-3159	NS5 (639-653(KK))	KKCDESVLTRLA WLTE	1
YFV_pp3205-3219	NS5 (699-713)	QPSKGWNDWENVPC	1
YFV_pp3213-3227	NS5 (707-727)	WENVPCSHHFHELQ	1
YFV_pp3277-3291	NS5 (771-785)	FHKRDMRLLSLAVSS	3
YFV_pp3281-3295	NS5 (775-789)	DMRLLSLAVSSAVPT	4
YFV_pp3313-3327	NS5 (807-821)	WMTTEDMLEVWNRVW	1
YFV_pp3369-3383	NS5 (863-877)	WASHIHLVIHRIRTL	2
YFV_pp3373-3387	NS5 (867-881)	IHLVIHRIRTLIGQE	13
YFV_pp3377-3391	NS5 (871-885)	IHRIRTLIGQEKYTD	9

Supplementary Table IV: List of 192 CD4⁺ T cell stimulatory 15mer epitopes

Proteome position	Protein position	Sequence	TMR validated HLA-II restriction	Predicted affinity (%RANK)	Measured affinity (nM)	Responders /donors tested
YFV_pp17-31	Capsid C (17-31)	RRGVRSLSNKIKQKT	DRB5*01:01	0.50	4	6/6
YFV_pp49-63	Capsid C (49-63)	FFFLFNILTGKKITTA	DRB1*01:01	0.70	27	8/8
YFV_pp53-67	Capsid C (53-67)	<u>FNILTGKKITTA</u> HLKR	DRB1*01:01	6.50	7	8/8
YFV_pp65-79	Capsid C (65-79)	LKRLWRMLDPPRQGLA	DRB1*01:01	4.50	15	5/5
YFV_pp73-87	Capsid C (73-87)	DPRQGLAVLRKVKRV	DRB1*13:01	0.12	4	1/1
YFV_pp73-87	Capsid C (73-87)	DPRQGLAVLRKVKRV	DRB1*13:02	32.00	5	5/5
YFV_pp77-91	Capsid C (77-91)	GLAVLRKVKRVVASL	DRB1*14:54	0.17	6	1/1
YFV_pp81-95	Capsid C (81-95)	LRKVKRVVASLMRGL	DRB1*07:01	0.70	7	5/5
YFV_pp81-95	Capsid C (81-95)	LRKVKRVVASLMRGL	DRB1*11:01	0.25	4	2/2
YFV_pp85-99	Capsid C (85-99)	<u>KRVVASLMRGLSSRK</u>	DRB1*11:01	0.12	5	1/1
YFV_pp237-251	prM (116-130)	RQLQKIERWFFVNF	DRB1*14:54	3.50	8	1/1
YFV_pp329-343	EnvE (44-58)	SLETVAIDRPAEVRK	DRB1*03:01	0.40	21	14/15
YFV_pp329-343	EnvE (44-58)	<u>SLETVAIDRPAEVRK</u>	DRB3*03:01	9.00	21	11/11
YFV_pp333-347	EnvE (48-62)	<u>VAIDRPAEVRKVCYN</u>	DRB3*03:01	32.00	12	5/7
YFV_pp333-347	EnvE (48-62)	VAIDRPAEVRKVCYN	DRB1*03:01	11.00	15	4/5
YFV_pp341-355	EnvE (56-70)	VRKVCYNAVLTHVKI	DRB5*01:01	1.30	4	6/6
YFV_pp345-359	EnvE (60-74)	<u>CYNAVLTHVKI</u> INDRC	DRB5*01:01	7.00	9	5/5
YFV_pp417-431	EnvE (132-146)	QTKIQYVIRAOQLHVG	DRB1*14:54	1.90	23	1/1
YFV_pp525-539	EnvE (240-254)	ATIRVLALGNQEGSL	DRB1*04:04	4.50	22	2/2
YFV_pp557-571	EnvE (272-286)	NLYKLHGHHVSCRVK	DRB1*13:02	44.00	9	7/7
YFV_pp673-687	EnvE (288-402)	QWHKEGSSIGKLFYQ	DRB1*04:01	43.00	567	2/2
YFV_pp601-615	EnvE (316-330)	GTVMQVQVKSQKAPC	DRB1*04:04	13.00	16	1/1
YFV_pp625-639	EnvE (340-354)	LTAAINGKILLVWNP	DRB3*03:01	1.50	2	5/5
YFV_pp865-879	NS1 (87-101)	SVVQDPKPNVYQRG	DRB1*03:01	0.80	10	5/5
YFV_pp889-903	NS1 (111-125)	LQYGWKTWGNLVS	DRB1*13:01	6.50	6	1/1
YFV_pp889-903	NS1 (111-125)	<u>LQYGWKTWGNLVS</u>	DRB1*13:02	30.00	9	4/4
YFV_pp893-907	NS1 (115-129)	<u>WKTWGNLVS</u> SPGRK	DRB1*13:02	34.00	5	3/3
YFV_pp1105-1119	NS1 (327-341)	DGCWYPMELRFRKTH	DRB5*01:01	1.50	2	8/8
YFV_pp1373-1387	NS2B (19-33)	GLAFQEMENFLGPIA	DRB1*15:01	16.00	42	1/1
YFV_pp1533-1547	NS3 (49-63)	HTMWHVTRGAFVLRN	DRB1*07:01	0.01	3	8/8
YFV_pp1541-1555	NS3 (57-71)	GAPLVRNGKKLIPSW	DRB1*13:01	0.06	2	1/1
YFV_pp1541-1555	NS3 (57-71)	GAPLVRNGKKLIPSW	DRB1*13:02	1.70	3	1/1
YFV_pp1541-1555	NS3 (57-71)	GAPLVRNGKKLIPSW	DRB1*14:54	2.50	6	1/1
YFV_pp1633-1647	NS3 (149-163)	VIGLYGNGLVGDNS	DRB1*15:01	18.00	14	4/4
YFV_pp1765-1779	NS3 (281-295)	<u>VNWEVIIMDEAHFLD</u>	DRB1*03:01	0.07	43	5/5
YFV_pp1769-1783	NS3 (285-299)	<u>VIIMDEAHFLDPASI</u>	DRB1*03:01	0.10	13	6/6
YFV_pp1765-1779	NS3 (281-295)	<u>VNWEVIIMDEAHFLD</u>	DRB3*01:01	0.02	3	8/10
YFV_pp1769-1783	NS3 (285-299)	<u>VIIMDEAHFLDPASI</u>	DRB3*01:01	0.08	8	1/1
YFV_pp1765-1779	NS3 (281-295)	<u>VNWEVIIMDEAHFLD</u>	DRB3*03:01	4.00	15	4/4
YFV_pp1769-1783	NS3 (285-299)	<u>VIIMDEAHFLDPASI</u>	DRB3*03:01	6.00	11	4/4
YFV_pp1833-1847	NS3 (349-363)	<u>WNTGHDWILADKRPT</u>	DRB1*03:01	8.50	28	3/3
YFV_pp1837-1851	NS3 (353-367)	<u>HDWILADKRPTAWFL</u>	DRB1*03:01	0.01	2	12/12
YFV_pp1849-1863	NS3 (365-379)	<u>WFLPSIRAAVMAAS</u>	DRB1*04:04	0.08	4	1/1
YFV_pp1853-1867	NS3 (369-383)	<u>SIRAAVMAASLRKA</u>	DRB1*04:04	0.80	13	1/1
YFV_pp1877-1891	NS3 (393-407)	KTFEREYPTIKQKPK	DRB5*01:01	11.00	2	5/5
YFV_pp2021-2035	NS3 (537-551)	FRELVRNCDLPVWLS	DRB3*03:01	0.70	5	1/2
YFV_pp2337-2351	NS4B (81-95K)	DGIGIPMKRNISVIMK	DRB3*03:01	0.15	3	5/5
YFV_pp2401-2415	NS4B (146-159)	<u>KNPVVDGNPTVDIEE</u>	DRB3*03:01	44.00	7	5/5
YFV_pp2405-2419	NS4B (149-163)	<u>VDGNPTVDIEEAPEM</u>	DRB3*03:01	90.00	22	5/5
YFV_pp2437-2451	NS4B (181-195)	LASVAMCRTPFSLAE	DRB1*04:04	0.04	2	1/1
YFV_pp2489-2503	NS4B (233-247K)	<u>YAFVGVMYNLWKMRTK</u>	DPA1*01:03-DPB1*04:01	5.00	NA	4/4
YFV_pp2565-2579	NS5 (59-73)	TAKLRWFHERGVYKL	DRB1*13:01	12.00	7	1/1
YFV_pp2565-2579	NS5 (59-73)	TAKLRWFHERGVYKL	DRB1*13:02	47.00	10	1/2
YFV_pp2565-2579	NS5 (59-73)	TAKLRWFHERGVYKL	DRB5*01:01	3.00	4	4/4
YFV_pp2569-2583	NS5 (63-77)	<u>RWFHERGVYKLEGRV</u>	DRB5*01:01	5.50	5	1/1
YFV_pp2877-2891	NS5 (371-385)	TRKIMKVVNRWLFERH	DRB1*15:01	0.60	7	5/5
YFV_pp2905-2919	NS5 (399-413)	EPIAKVRSAAIGAY	DRB1*15:01	1.20	2	1/1
YFV_pp2977-2991	NS5 (471-485)	<u>GSRAIWYMWLGARYL</u>	DRB1*01:01	6.50	6	8/8
YFV_pp2981-2995	NS5 (475-489KK)	<u>IWYMWLGARYLEFEAKK</u>	DRB1*01:01	17.00	4	8/8
YFV_pp3057-3071	NS5 (551-565)	<u>EQEILNYMSPHHKKL</u>	DRB1*15:01	0.15	29	5/5
YFV_pp3057-3071	NS5 (551-565)	<u>EQEILNYMSPHHKKL</u>	DRB5*01:01	0.08	2	5/5
YFV_pp3061-3075	NS5 (555-569)	<u>LNYSMPHHKLAQAV</u>	DRB5*01:01	0.50	2	3/3
YFV_pp3373-3387	NS5 (867-881)	<u>IHLVIHRIRTLIGQE</u>	DRB1*04:04	0.10	14	2/2
YFV_pp3377-3391	NS5 (871-885)	<u>IHRIRTLIGQERYTD</u>	DRB1*04:04	1.80	27	2/2

Table SV. A complete list of the 50 CD4⁺ T cell epitopes identified by the HFRI approach.

The CD4⁺ T cell epitope discovery process detailed for donor YF1067 was extended to 50 randomly selected, primary YFV vaccinated donors. 50 different CD4⁺ T cell responses restricted by 14 HLA-II allotypes (13 HLA-DR-restricted and one HLA-DP-restricted) were discovered. The peptide-HLA-I affinities were predicted by NetMHCIIpan (given in %Rank) and the binding affinity was measured (given in nM) (the lower the prediction or measurement, the better the affinity). Productively interacting peptide-HLA-II combinations were used to design and generate peptide-HLA class II tetramers. The resulting tetramers were used to stain and analyze expanded CD4⁺ T cells by flow cytometry gating on CD3⁺ CD4⁺ T cells. The prevalence of these responses is given as "the number of responding donors/the number of donors tested". In the event that two overlapping peptides were identified, the overlapping sequence has been colored red. For solubilization purpose, lysines have in some cases been added to the N- or C-terminal of the peptide (indicated here by underlining these added lysines).