

SUPPLEMENTARY FILES

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Supplementary Fig. 1 Gating strategy for human ICS.

Supplementary Fig. 2 Frequencies expanded HLA-I-peptide-specific CD8+ T-cell populations.

Supplementary Fig. 3 *Ex vivo* characterisation of IBV-specific CD8+ T-cells across age groups.

Supplementary Fig. 4 IBV-specific CD8+ T-cells across human tissues.

Supplementary Fig. 5 Analysis of TCR repertoire.

Supplementary Fig. 6 Gibbs cluster analysis of IBV peptides.

Supplementary Table 1. Selected HLA-B*07:02, -B*08:01 and B*35:01 restricted IBV peptides.

Supplementary Table 2. Study donor demographics.

Supplementary Table 3. Immunogenic B7-I, B8-I and B35-I pools.

Supplementary Table 4. Data collection and refinement statistics.

Supplementary Table 5. Expanded clonotypes.

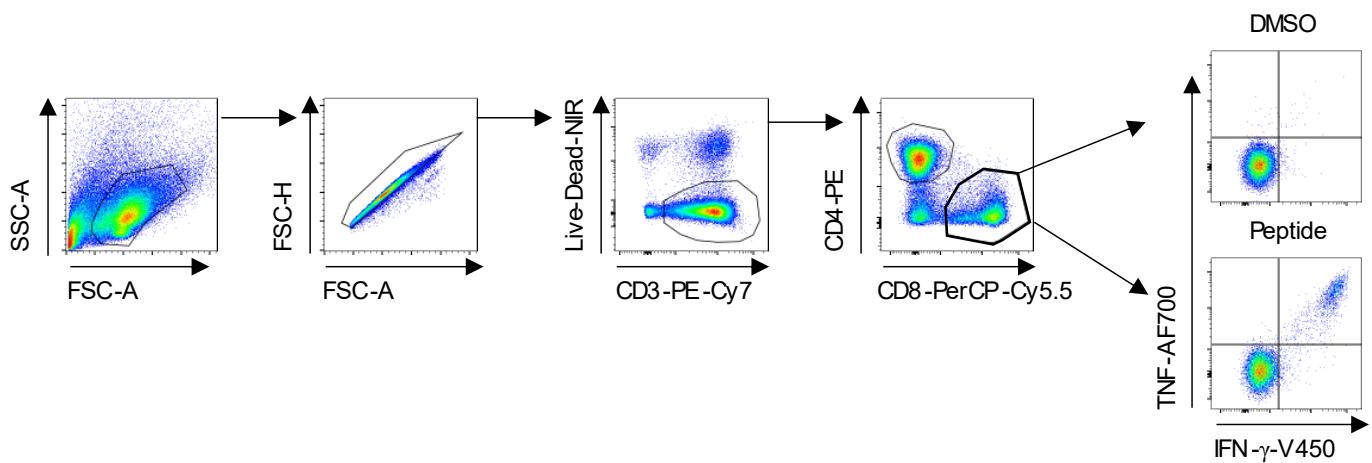
Supplementary Table 6. Clonotype counts of B7/NP₃₀₋₃₈.

Supplementary Table 7. Clonotype counts of B8/NP₃₀₋₃₈.

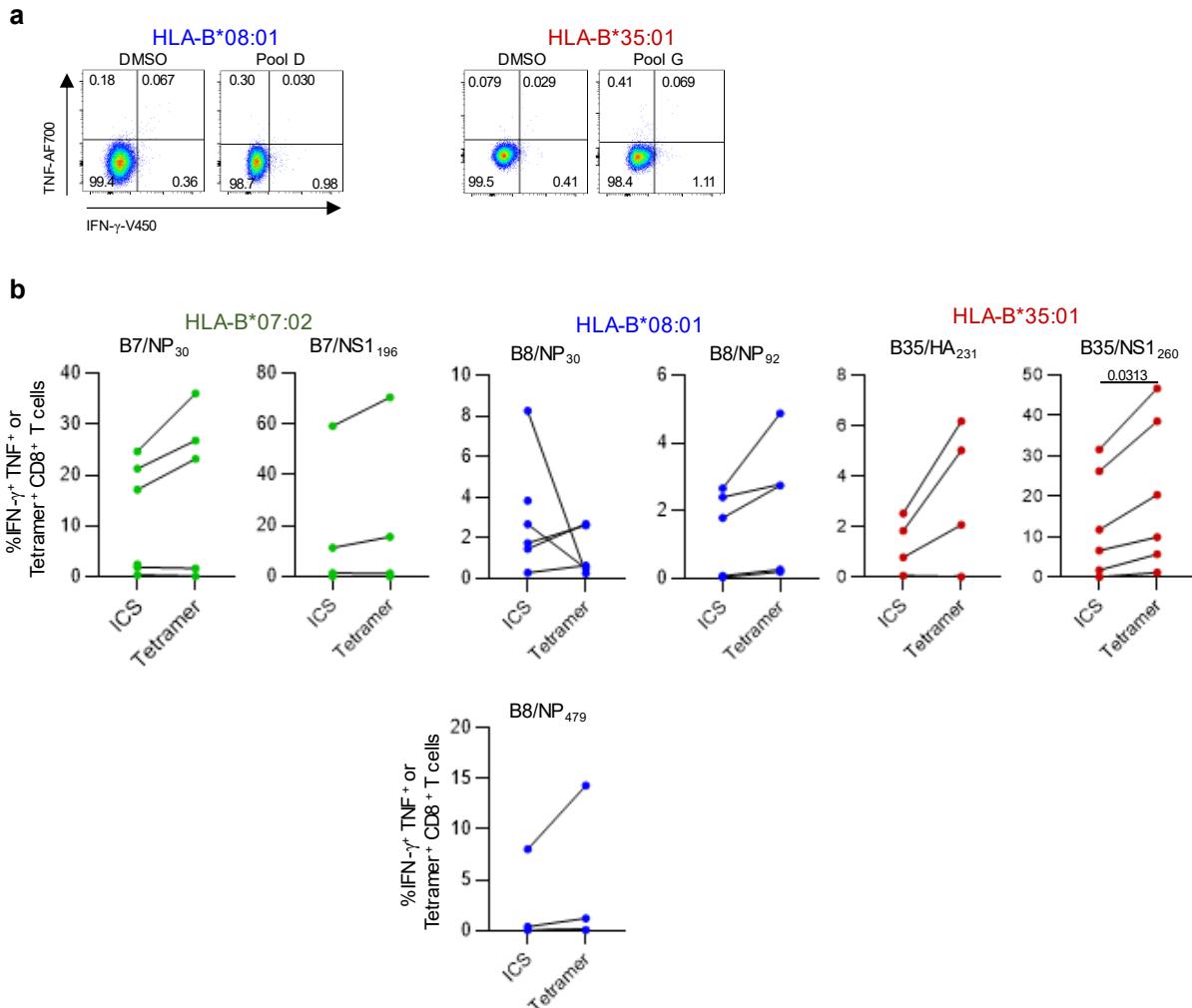
Supplementary Table 8. Clonotype counts of B7/NS1₁₉₆₋₂₀₆.

Supplementary Table 9. Clonotype counts of B8/NP₉₂₋₉₉.

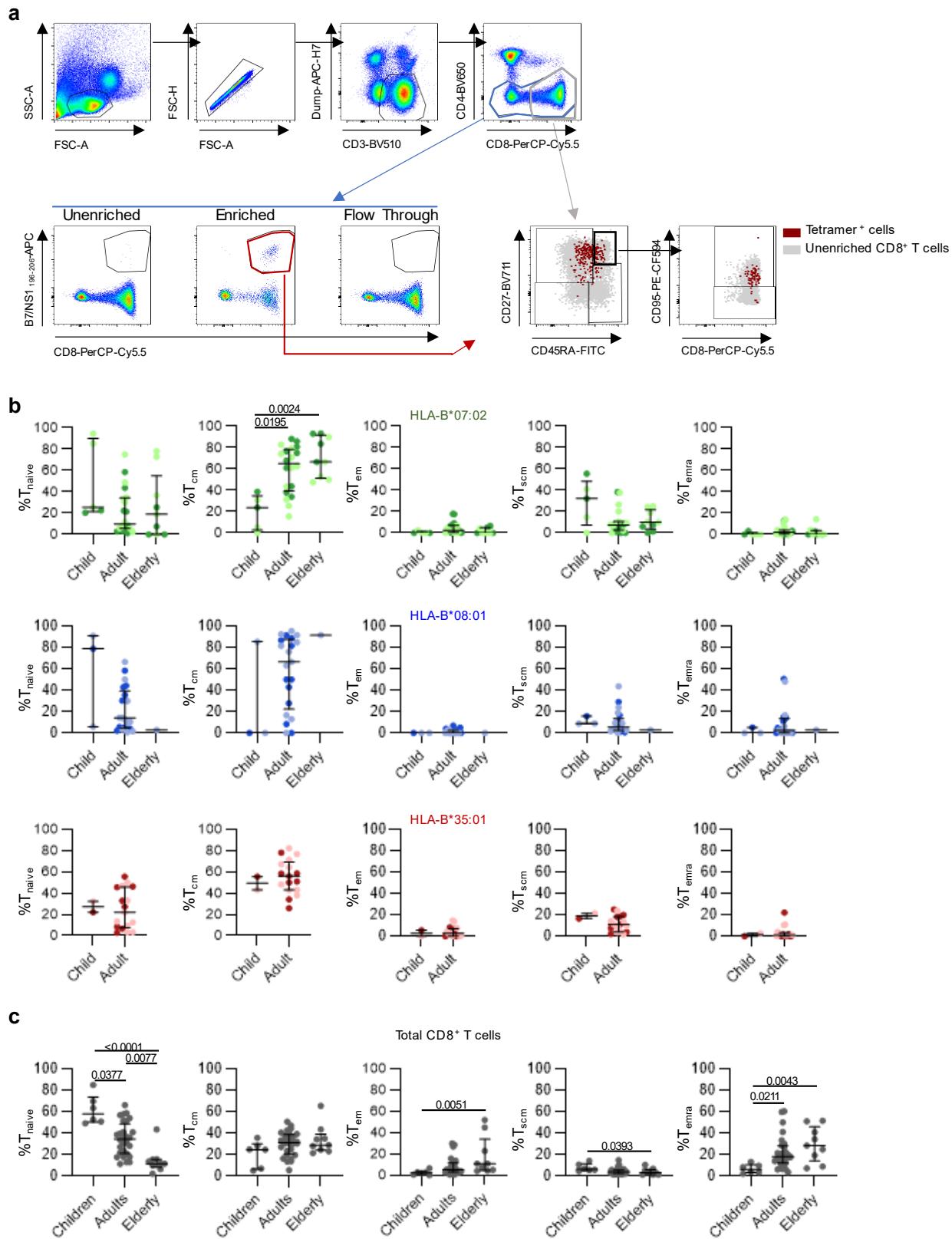
Supplementary Table 10. TCR sequencing primers



Supplementary Fig. 1. Gating strategy for human ICS. IFN- γ and TNF producing CD8 $^{+}$ T-cells were identified by first gating on CD3 $^{+}$ live lymphocytes.

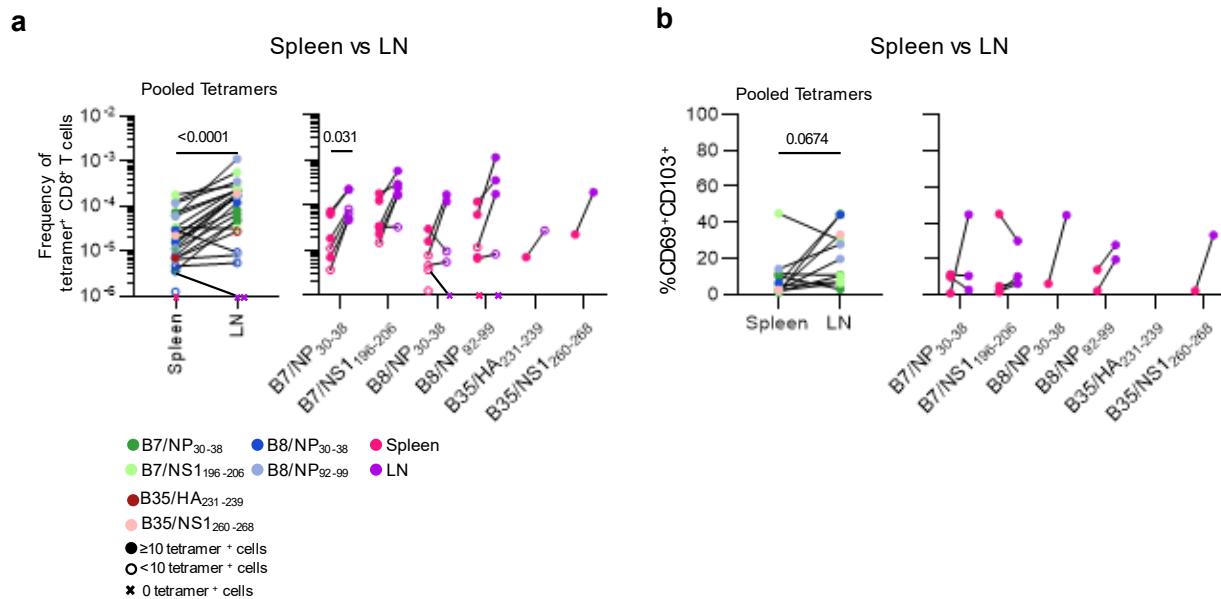


Supplementary Fig. 2. Frequencies expanded HLA-I-peptide-specific CD8⁺ T-cell populations. **(a)** Representative FACS plots of IFN- γ +TNF⁺ CD8⁺ T-cells restimulated with peptide pools D or G on day 10. **(b)** Comparison of IFN- γ +TNF⁺ and tetramer⁺ frequencies in IBV-specific CD8⁺ T-cells within day 12 expanded pool-specific CD8⁺ T-cells (n=4-6 donors). Statistical significance was determined with the Wilcoxon matched-pairs signed rank test. Source data are provided as a Source Data file.

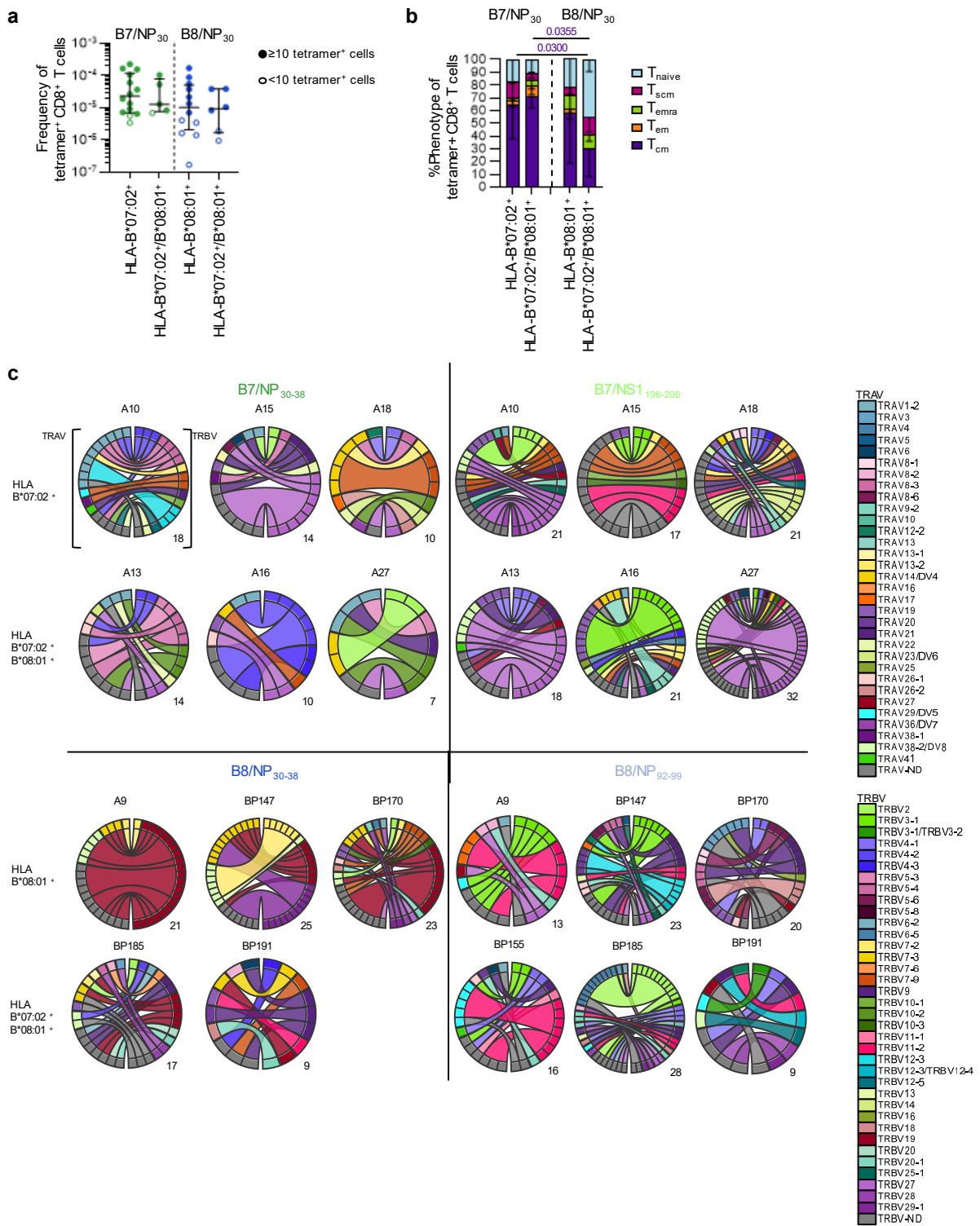


Supplementary Fig. 3. Ex vivo characterisation of IBV-specific CD8⁺ T-cells across age groups. (a) Representative FACS gating strategy used to characterize the total CD8⁺ T-cell population and IBV-specific CD8⁺ T-cells. The second line indicates unenriched, enriched and flowthrough fractions of the TAME assay. The unenriched fraction was used to characterize the frequency and phenotype of the total

CD8⁺ T-cell population (grey gate and cell populations), whereas the IBV-specific CD8⁺ T-cells of the enriched fraction were used to characterize the frequency and phenotype of the IBV-specific CD8⁺ T-cells (red gate and cell populations). Naïve/memory T-cell subsets were identified as T_{cm} (CD27⁺CD45RA⁻) cells, T_{eff} (CD27⁻CD45RA⁻), T_{emra} (CD27⁻CD45RA⁺), T_{naïve} (CD27⁺CD45RA⁺CD95⁻) and T_{scm} (CD27⁺CD45RA⁺CD95⁺) cells. **(b)** IBV/HLA-B*07:02 tetramers (n=18 donors), IBV/HLA-B*08:01 tetramers (n=14 donors) and IBV/HLA-B*35:01 tetramers (n=10 donors). **(c)** Proportions of memory phenotypes of total CD8⁺ T-cells in children (n=6), adults (n=28) and elderly donors (n=9). **(b-c)** Statistical significance was determined using a two tailed Kruskal-Wallis with Dunn's test for multiple comparisons (HLA-B*07:02, HLA-B*08:01 and Total CD8⁺ T cells) or **(b)** Mann-Whitney U test (HLA-B*35:01). Source data are provided as a Source Data file.

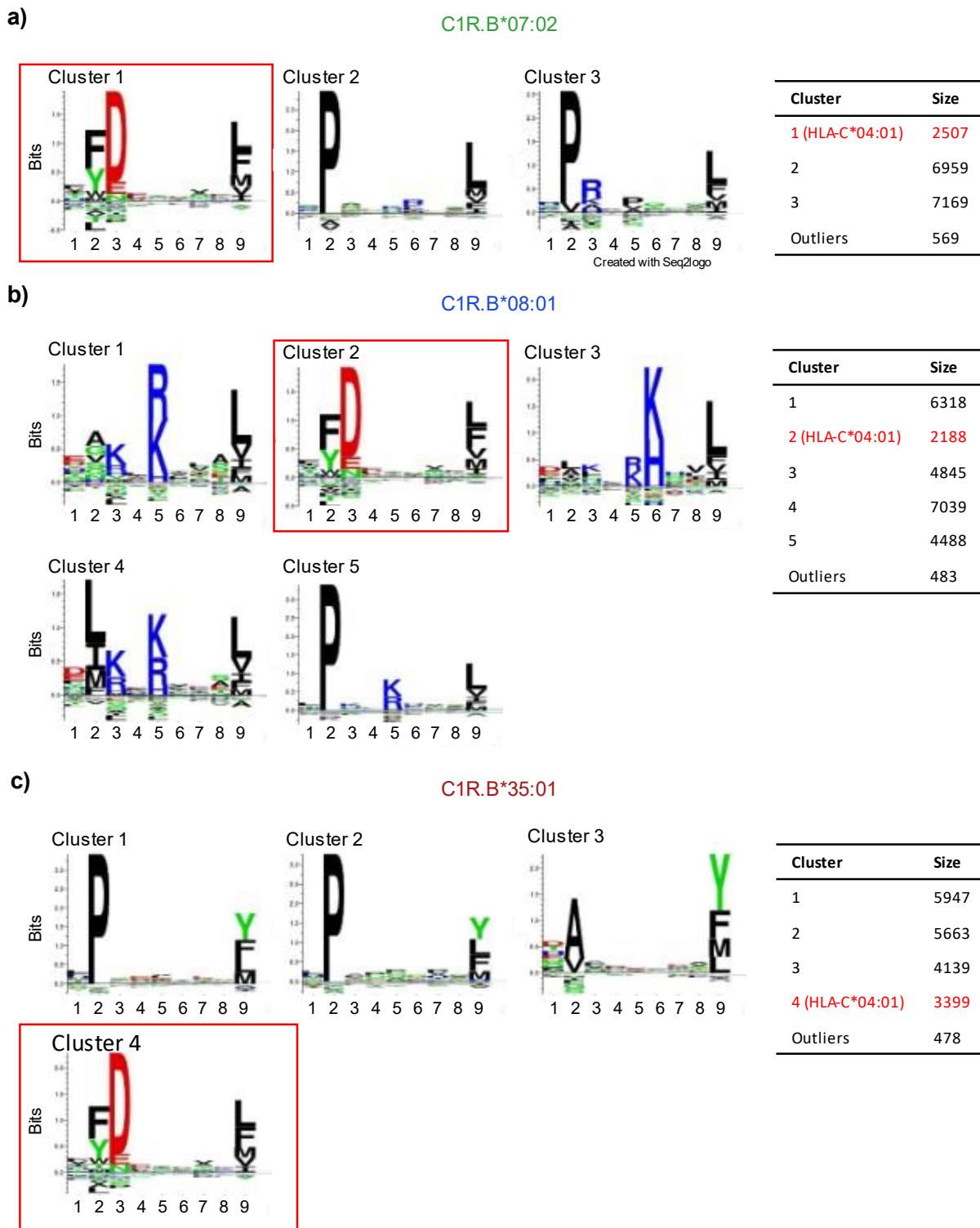


Supplementary Fig. 4. IBV-specific CD8⁺ T-cells across human tissues. **(a)** Frequency of IBV-specific CD8⁺ T-cells in paired spleen and LN samples with tetramers collated (n=26 donors; spleen and n=24 donors; LN) or separate (n=1-6 donors). Donors which had 0 tetramer⁺ cells counted are represented as “x”, and were included in statistics as 0. Open symbols represent <10 tetramer⁺ cells counted. **(b)** Proportion of IBV-specific CD8⁺ T_{rm} in paired spleen and LN with tetramers collated (n=11 donors each) or separate (n=1-3 donors). Statistical significance was determined using a two tailed Wilcoxon matched-pairs signed rank test. Source data are provided as a Source Data file.



Supplementary Fig. 5. Analysis of TCR repertoire. (a) Frequency of B7/NP₃₀⁺CD8⁺ and B8/NP₃₀⁺CD8⁺ T-cells across HLA-B*07:02⁺ (n=14 donors), HLA-B*08:01⁺ (n=12) and HLA-B*07:02⁺/B*08:01⁺ donors (n=7 donors). Open symbols represent <10 tetramer⁺ cells counted, excluded from phenotypic analysis. Statistical significance was determined with Mann-Whitney U test for frequency. Bars represent median and IQR. (b) Phenotype of B7/NP₃₀⁺CD8⁺ and B8/NP₃₀⁺CD8⁺ T-cells across HLA-B*07:02⁺ (n=12 donors), HLA-B*08:01⁺ (n=6) and HLA-B*07:02⁺/B*08:01⁺ donors (n=7 donors). Statistical significance was determined by two-way ANOVA with Sidak's

test for multiple comparisons for phenotype. Bars represent mean and SD **(c)** Circos plots of TRAV and TRBV gene usage per donor. Left arch segment colours indicate TRAV usage, right outer arch colours depict TRBV usage. Connecting lines indicated TRAV-TRBV gene pairing and are coloured based on their TRBV usage and segmented based on their CRD3 α and CDR3 β sequence, the thickness is proportional to the number of TCR clones with the respective pair. The number of sequences considered for each circos plot is shown at the right bottom. Source data are provided as a Source Data file.



Supplementary Fig. 6. Gibbs cluster analysis of IBV peptides. Peptide motifs for peptide sequence clusters generated via Gibbs cluster analysis of unfiltered 8-13 amino acid **(a)** C1R.B*07:02, **(b)** C1R.B*08:01 and **(c)** C1R.B*35:01 human peptide sequences identified at 1% FDR. Peptides from Cluster 1, aligning with the binding motif for HLA-C*04:01, were filtered from motif analyses for C1R-B*07:02, while Cluster 2 peptides were filtered from motif analyses for C1R.B*08:01 and Cluster 4 peptides were filtered from motif analyses for C1R.B*35:01.

Supplementary Table 1. Selected HLA-B*07:02, -B*08:01 and B*35:01 restricted IBV peptides.

HLA	Pool	Peptide Name	Sequence	Length
HLA-B*07:02	A	PB1+280-89	YPKIMSRVPM	10
		HA+3 ₂₁₁₋₂₂₀	RPNYRLGVPL	10
		PB1 ₇₀₆₋₇₁₄	KPVGQHSM	9
		HA ₂₂₄₋₂₃₂	KPQKFTSSA	9
		NS1 ₁₂₁₋₁₂₉	YPSTPGRCL	9
		HA ₂₅₅₋₂₆₃	<u>LPQSGRIVV</u>	9
		NP ₄₇₂₋₄₈₁	RPIALSKQAV	10
		HA ₉₁₋₉₉	IPSARVSIL	9
		NP ₂₃₃₋₂₄₄	<u>LPRRSGATGVAI</u>	12
		HA ₂₇₋₃₅	SPHVVKTAT	9
		NP+2 ₁₈₀₋₁₈₈	MIKPSTSAL	9
		NP ₃₀₋₃₈	RPIIRPATL	9
		NS1 ₆₆₋₇₄	EPESKRMSL	9
HLA-B*08:01	B	HA+3 ₈₂₋₉₂	MPQLHRSGRGL	11
		PB1 ₃₉₃₋₄₀₄	KPFFNEEGTASL	12
		NS1 ₂₅₃₋₂₆₅	KPIRAAETAVGVL	13
		NS1 ₁₉₆₋₂₀₆	<u>HPNGYKSLSTL</u>	11
		NA ₄₅₈₋₄₆₆	TVTGVNMAL	9
		NP ₅₃₆₋₅₄₆	IPIKQTIPNFF	11
		NS2 ₆₂₋₇₀	<u>TIRLVTEEL</u>	9
		HA ₁₁₀₋₁₁₉	FPIMHDRTKI	10
HLA-B*08:01	C	PA ₄₅₃₋₄₆₀	TVMMKYVL	8
		NS1 ₆₆₋₇₄	EPESKRMSL	9
		NS2 ₁₁₋₁₉	EWRMKKMAI	9
		NA ₂₀₁₋₂₀₉	LLKIKYGEA	9
		NP ₃₀₋₃₈	<u>RPIIRPATL</u>	9
		PB1 ₁₈₆₋₁₉₃	NIKKKLPA	8
		NP ₄₀₇₋₄₁₄	EFKPRSL	8
		NP ₅₀₀₋₅₀₈	LLKMMNDSM	9
		NP ₄₆₈₋₄₇₆	<u>FAVERPIAL</u>	9
		NP ₁₇₃₋₁₈₁	FLKEEVKTM	9
		PB2 ₅₆₀₋₅₆₇	TLKAQFLL	8
		PB2 ₂₀₇₋₂₁₅	YMLERELVA	9
		NA ₁₅₀₋₁₅₉	RNKLRHHLISV	10
		NA ₁₃₀₋₁₃₇	FALTHYAA	8
		NP ₄₇₉₋₄₈₇	<u>QAVRRMLSM</u>	9
		NP ₉₂₋₉₉	<u>QMMVKAGL</u>	8
		PA ₄₅₈₋₄₆₅	YVLFHTSL	8
		PB2 ₁₈₇₋₁₉₅	LIKEKREKL	9
		NP ₅₁₇₋₅₂₅	FIGKKMFQI	9
HLA-B*35:01	D	HA ₄₈₁₋₄₈₈	ERKLKKML	8
		NA ₁₅₀₋₁₅₇	RNKLRHLI	8
		PA ₁₃₂₋₁₃₉	FWKKKEKL	8
		HA ₁₁₀₋₁₁₉	FPIMHDRTKI	10
		PB1 ₂₁₆₋₂₂₄	EYIKRALSL	9
		NS1 ₁₆₈₋₁₇₅	EGKFRLTI	8
		NS2 ₁₁₅₋₁₂₂	EVYSRQCL	8
		PB2 ₂₀₇₋₂₁₄	YMLERELV	8
		M1 ₁₇₀₋₁₇₇	VPGVRREM	8
		NP ₇₄₋₈₂	EIKKSVYNM	9
		NA ₄₁₄₋₄₂₂	EIKDKKCDV	9
		NP ₃₉₆₋₄₀₃	DLRVLSAL	8
		PB2 ₅₉₄₋₆₀₁	SGFARAVL	8
		PB2 ₄₉₇₋₅₀₅	VSITKNLSL	9
		PA ₁₃₁₋₁₃₉	YFWKKKEKL	9
		NP ₂₆₃₋₂₇₁	ADRGLLRDI	9
		NP ₃₇₇₋₃₈₅	DAKDKSQLF	9

HLA-B*35:01	E	PB1 ₂₂₋₃₀	FPYTGVPPY	9
		PB2 ₆₆₋₇₄	MANRIPLEY	9
		NP ₄₆₈₋₄₇₆	FAVERPIAL	9
		NA ₃₈₆₋₃₉₄	DPWADSDAL	9
		NS2 ₄₇₋₅₆	YPNLVKSTDY	10
		PB2 ₄₃₁₋₄₃₉	SPMYQLQRY	9
		M1 ₁₃₂₋₁₄₀	YLNPGNYSM	9
		NA ₃₇₅₋₃₈₃	MGMGLYVKY	9
		NP ₈₂₋₉₀	MVVKLGEFY	9
		NP ₁₅₇₋₁₆₅	MVRDDKTIY	9
		NP ₅₃₆₋₅₄₅	IPIKQTIPNF	10
		PA ₃₉₉₋₄₀₇	VAAWVQTEM	9
		HA ₂₃₁₋₂₃₉	<u>SANGVTTHY</u>	9
		NA ₁₆₄₋₁₇₂	IPTVENSIF	9
		HA ₃₃₆₋₃₄₄	CPIWVKTPL	9
		NP ₅₃₆₋₅₄₄	IPIKQTIPN	9
		NA ₄₀₋₅₀	FPSTEITAPTM	11
	F	NS1 ₂₆₀₋₂₆₈	TAVGVLSQF	9
		HA ₁₁₀₋₁₁₈	FPIMHDRTK	9
		NA ₃₈₆₋₃₉₆	DPWADSDALAF	11
		NA ₁₁₁₋₁₁₉	APLIIREPF	9
		NP ₇₁₋₈₀	TPTEIKKSVY	10
		NP ₅₃₆₋₅₄₆	IPIKQTIPNFF	11
		NP ₁₆₅₋₁₇₃	<u>YFSPIRVTF</u>	9
		PB2 ₂₇₇₋₂₈₅	NPLELAVEI	9
		HA ₂₅₅₋₂₆₅	LPQSGRIVVDY	11
		HA ₂₅₅₋₂₆₃	LPQSGRIVV	9
		HA ₉₁₋₉₉	IPSARVSIL	9
		PB2 ₁₅₆₋₁₆₆	MPPDEASNIVM	11
		HA ₃₀₇₋₃₁₅	EADCLHEKY	9
		PA ₂₁₆₋₂₂₉	VPAGFSNFEGMRSY	14
		HA ₁₆₃₋₁₇₁	NGNGFFATM	9
		PB1 ₁₄₈₆₋₄₉₄	TGMFEFTSM	9
		NP ₁₅₇₋₁₆₆	MVRDDKTIYF	10
		HA ₂₄₆₋₂₅₅	FPNQTEDGGL	10
		PB1 ₆₀₄₋₆₁₂	HIPEIVLVKY	9
		HA ₅₅₆₋₅₆₄	AASSLAVTL	9
		NA ₄₅₈₋₄₆₆	TVTGVNMAL	9
	G	HA ₁₁₀₋₁₂₂	FPIMHDRTKIRQL	13
		HA ₂₅₅₋₂₆₆	LPQSGRIVVDYM	12
		PA ₄₅₀₋₄₅₈	KASTVMMKY	9
		NA ₄₄₀₋₄₄₈	SAATAIYCL	9
		PB1 ₁₅₇₋₆₅	ISDVTGCTM	9
		HA ₁₁₀₋₁₁₉	FPIMHDRTKI	10
		HA+2 ₁₇₂₋₁₈₂	LPMETDFSQQW	11
		NA ₂₋₁₂	LPSTIQTLLF	11
		NA ₃₈₆₋₃₉₅	DPWADSDALA	10
		NP ₂₅₃₋₂₆₂	EAIRFIGRAM	10
		NP ₃₀₋₃₈	RPIIRPATL	9
		NA ₃₈₇₋₃₉₄	PWADSDAL	8
		HA ₃₉₂₋₄₀₀	HGVAVAADL	9
		NA ₅₆₋₆₄	NASNVQAVN	9
		PA ₂₆₃₋₂₇₀	RPIGPHIY	8
		NP ₁₇₃₋₁₈₁	FLKEEVKTM	9
		PB1 ₂₂₋₃₈	FPYTGVPPYSHGTGTGY	17

Bold indicates overlapping between peptides. Underline indicates immunogenic peptides.

Supplementary Table 2. Study donor demographics.

Cohort	ID	Age group	Tissue	HLA-A	HLA-A	HLA-B	HLA-B	HLA-C	HLA-C	Peptide screen	HLA confirmation	Tetramer testing	TAME	Ex vivo TCR	Tetramer staining
Adult	A1	Adult	PBMC	01:01	03:01	35:01	57:01						Yes		
Median 39 yrs	A2	Adult	PBMC	02:01	03:01	35:01	57:01	04:01	06:02				Yes		
Range 25-59 yrs	A3	Adult	PBMC	02:01	24:02	27:05	35:01	01:02	04:01				Yes		
42% F	A4	Adult	PBMC	24:02		07:02		07:02		Yes	Yes	Yes	Yes	Yes	
2 Unk sex	A5	Adult	PBMC	01:01	24:02	35:01	57:01	04:01	06:02	Yes	Yes	Yes	Yes	Yes	
	A6	Adult	PBMC	01:01	31:01	07:02	08:01	07:01	07:02	Yes	Yes	Yes	Yes	Yes	
	A7	Adult	PBMC	01:01	32:01	08:01	40:01	03:04	07:01	Yes	Yes	Yes	Yes	Yes	
	A8	Adult	PBMC	01:01	03:01	18:01	35:01	04:01	07:01	Yes	Yes	Yes	Yes	Yes	
	A9	Adult	PBMC	26:01	32:01	08:01	35:03	04:01	07:02		Yes		Yes	Yes	
	A10	Adult	PBMC	01:01	24:02	07:02	57:01	06:02	07:02				Yes	Yes	
	A11	Adult	PBMC	01:01	30:02	08:01	51:01	07:18	14:02	Yes	Yes	Yes	Yes	Yes	
	A12	Adult	PBMC	26:01	30:01	35:01	50:01	04:01	06:02	Yes	Yes	Yes	Yes	Yes	
	A13	Adult	PBMC	01:01	03:01	07:02	08:01	07:01	07:02	Yes	Yes	Yes	Yes	Yes	
	A14	Adult	PBMC	01:01	23:01	08:01	15:01	03:03	07:01	Yes	Yes	Yes	Yes	Yes	
	A15	Adult	PBMC	03:01	24:02	07:02	35:08	04:01	07:02	Yes	Yes	Yes	Yes	Yes	
	A16	Adult	PBMC	01:01	03:01	07:02	08:01	07:01	07:02	Yes	Yes	Yes	Yes	Yes	
	A17	Adult	PBMC	02:01	24:02	35:01	44:02	04:01	05:01	Yes	Yes	Yes	Yes	Yes	
	A18	Adult	PBMC	03:01	24:02	07:02	40:02	02:02	07:02	Yes	Yes	Yes	Yes	Yes	
	A19	Adult	PBMC	02:01	11:01	35:01	40:01	03:04	04:01	Yes	Yes	Yes	Yes	Yes	
	A20	Adult	PBMC	01:01		07:02	08:01	07:01	07:02	Yes	Yes	Yes	Yes	Yes	
	A21	Adult	PBMC	02:01	11:01	18:01	35:01	04:01	07:01	Yes	Yes	Yes	Yes	Yes	
	A22	Adult	PBMC	01:01	29:02	08:01	44:03	07:01	16:01		Yes		Yes		
	A23	Adult	PBMC	01:01	23:01	08:01	45:01	06:02	07:01		Yes		Yes		
	A24	Adult	PBMC	03:01	26:01	07:02	15:01				Yes		Yes		
	A25	Adult	PBMC	03:01	31:01	07:02		03:04	07:02		Yes		Yes		
	A26	Adult	PBMC	01:01	02:01	07:02	44:03	07:02	16:01		Yes		Yes		
	A27	Adult	PBMC	01:01	03:01	07:02	08:01	07:01	07:02		Yes		Yes	Yes	
	A28	Adult	PBMC	01:01		07:02	08:01	07:01	07:02				Yes		
Elderly	E1	Elderly	PBMC	02:01	32:01	07:02	44:03						Yes		
Median 73 yrs	E2	Elderly	PBMC	01:01		07:02	08:01	07:01	07:02				Yes		
Range 65-87 yrs	E3	Elderly	PBMC	02:01	03:01	07:02	44:03	07:02	16:01				Yes		
57% F	E4	Elderly	PBMC	01:01	03:01	08:01	35:01						Yes		
2 Unk sex	E5	Elderly	PBMC	01:01	02:01	07:02	15:01	03:04	07:02				Yes		
	E6	Elderly	PBMC	02:01	25:01	07:02	44:02	05:01	07:02				Yes		
	E7	Elderly	PBMC	01:01	24:02	08:01	57:01	07:01				Yes			
	E8	Elderly	PBMC	01:01	29:02	08:01	44:03	07:01	16:01				Yes		
	E9	Elderly	PBMC	01:01	03:01	08:01	40:02	02:02	07:01				Yes		
Child	C1	Child	PBMC	01:01	25:01	08:01	18:01	07:01	07:01				Yes		
Median 9 yrs	C2	Child	PBMC	24:02	33:01	07:02	15:01	03:03	07:02				Yes		
Range 1-16 yrs	C3	Child	PBMC	03:01		07:02	44:03	07:02	16:01				Yes		
50% F	C4	Child	PBMC	01:01	32:01	08:01	14:01	07:01	08:02				Yes		
	C5	Child	PBMC	03:01	30:02	07:02	18:01	05:01	07:02				Yes		
	C6	Child	PBMC	11:01	31:01	07:02	35:01	04:01	07:02				Yes		
Spleen	S1	Adult	Spleen	02:01	11:01	15:01	35:01	1	4				Yes		
Median 51 yrs	S2	Adult	Spleen	03:01	11:01	08:01	38:01	7	12				Yes		

Range 35-64 yrs 27% F	S3	Adult	Spleen	02:01	24:02	27:05	35:01	2	4		Yes
	S4	Adult	Spleen	02:01	24:02	27:05	35:01	2	4		Yes
	S5	Adult	Spleen	01:01	31:01	08:01		7			Yes
	S6	Adult	Spleen	1	2	8	13	6	7		Yes
	S7	Adult	Spleen	1	68	7	18	7			Yes
	S8	Adult	Spleen	2	3	7	57	6	7		Yes
	S9	Adult	Spleen	24	31	7	14:02	7	8		Yes
	S10	Adult	Spleen	2	25	7	8	7			Yes
	S11	Adult	Spleen	01:01	24:02	08:01	13:01	03:04	07:01		Yes
	S12	Adult	Spleen	01:01		08:01		07:01			Yes
	S13	Adult	Spleen	2	11	7	44	05	07		Yes
	S14	Elderly	Spleen	3	24	35	39	04	07		Yes
	S15	Adult	Spleen	03	25	07	07				Yes
Lymph nodes	N1	Adult	Lymph node	03:01	11:01	08:01	38:01	7	12		Yes
Median 49 yrs	N2	Adult	Lymph node	01:01	31:01	08:01		7			Yes
Range 35-64 yrs 27% F	N3	Adult	Lymph node	1	2	8	13	6	7		Yes
	N4	Adult	Lymph node	1	68	7	18	7			Yes
	N5	Adult	Lymph node	2	3	7	57	6	7		Yes
	N6	Adult	Lymph node	24	31	7	14:02	7	8		Yes
	N7	Adult	Lymph node	2	25	7	8	7			Yes
	N8	Adult	Lymph node	01:01		08:01		07:01			Yes
	N9	Adult	Lymph node	2	11	7	44	05	07		Yes
	N10	Elderly	Lymph node	3	24	35	39	04	07		Yes
	N11	Adult	Lymph node	03	25	07	07				Yes
Tonsil	T1	Child	Tonsil	01:01	25:01	08:01	18:01	07:01	07:01		Yes
Median 10 yrs	T2	Child	Tonsil	01:01	25:01	07:02	08:01	07:01	07:02		Yes
Range 6-34 yrs 53% F	T3	Child	Tonsil	03:01	32:01	07:02	08:01	07:01	07:02		Yes
	T4	Child	Tonsil	24:02	33:01	07:02	15:01	03:03	07:02		Yes
	T5	Child	Tonsil	02:01		08:01	44:02	05:01	07:01		Yes
	T6	Child	Tonsil	03:01		07:02	44:03	07:02	16:01		Yes
	T7	Child	Tonsil	01:01	32:01	08:01	14:01	07:01	08:02		Yes
	T7	Child	Tonsil	02:01	23:01	35:01	49:01	04:01	07:01		Yes
	T8	Adult	Tonsil	01:01	24:02	07:02	40:01	03:04	07:02		Yes
	T9	Child	Tonsil	03:01	30:02	07:02	18:01	05:01	07:02		Yes
	T10	Child	Tonsil	11:01	31:01	07:02	35:01	04:01	07:02		Yes
	T11	Adult	Tonsil	01:01	02:01	08:01	51:01	07:01	14:02		Yes
	T12	Adult	Tonsil	01:01	25:01	07:02	18:01	07:02	12:03		Yes
	T13	Child	Tonsil	01:01	03:01	07:02	08:01	07:01	07:02		Yes
	T14	Adult	Tonsil	02:01	03:01	07:02	40:01	03:04	07:02		Yes
Lung	L1	Adult	Lung	2	32	7	8	7	7		Yes
Median 26 yrs	L2	Adult	Lung	1	3	8	35	4	7		Yes
Range 22-41 yrs 33% F	L3	Adult	Lung	7	8	7	8	7			Yes
3 Unk age/sex	L4	Unknown	Lung	2	31	7	44	5	7		Yes
	L5	Unknown	Lung	1	25	8	58	7	7		Yes
	L6	Unknown	Lung	1	3	35	55	3	4		Yes

F, female; Unk, unknown.

Supplementary Table 3. Immunogenic B7-I, B8-I and B35-I pools.

Pool H	Pool I	Pool J
HA ₂₅₅₋₂₆₃	NP ₃₀₋₃₈	HA ₂₃₁₋₂₃₉
NP ₃₀₋₃₈	NP ₉₂₋₉₉	NP ₁₆₅₋₁₇₃
NP ₂₃₃₋₂₄₄	NP ₄₆₈₋₄₇₇	NP ₄₆₈₋₄₇₆
NS1 ₁₉₆₋₂₀₆	NP ₄₇₉₋₄₈₇	NS1 ₂₆₀₋₂₆₈
NS2 ₆₂₋₇₀		PB2 ₆₆₋₇₀

Supplementary Table 4. Data collection and refinement statistics.

	B*07:02/NS1₁₉₆₋₂₀₆ (8TUB)	B*07:02/NP₃₀₋₃₈ (8TUH)
Wavelength	0.95366	0.95366
Resolution range	43.36 - 2.4 (2.486 - 2.4)	48.03 - 2.2 (2.27 - 2.2)
Space group	P 1	P 61 2 2
Unit cell (a, b, c)	49.2 90.7 104.6	57.2 57.2 396.4
(α , β , γ)	97.5 93.8 90.2	90 90 120
Total reflections	186122 (18249)	442482 (33657)
Unique reflections	66085 (6521)	21009 (1718)
Multiplicity	2.8 (2.8)	21.1 (19.6)
Completeness (%)	94.46 (93.12)	100 (100)
Mean I/sigma(I)	6.49 (1.10)	7.9 (2.4)
R-pim	0.13 (0.34)	0.064 (0.30)
CC1/2	0.953 (0.706)	0.993 (0.885)
R-work	0.197	0.178
R-free	0.237	0.241
Number of non-hydrogen atoms	13217	3320
macromolecules	12627	3203
ligands	77	28
solvent	559	89
RMS(bonds)	0.021	0.007
RMS(angles)	1.35	0.88
Ramachandran favoured (%)	97.36	97.7
Ramachandran allowed (%)	2.64	2.3
Ramachandran outliers (%)	0	0
Rotamer outliers (%)	0.45	2.6
B factor	37.77	43.3

Supplementary Table 5. Expanded clonotypes

B7/NP ₃₀															
Clone ID	TRAV	TRAJ	CDR3 α	CDR3 α length	TRBV	TRBJ	CDR3 β	CDR3 β length	BP146	BP155	BP184	BP185	BP189	KK102	
A	TRAV1-2	TRAJ33	CAVNDGSNYQLIW	8	TRBV12-3	TRBJ2-1	CASSSPPSGGGYEQFF	11	3 (17%)						
Q					TRBV10-2	TRBJ1-5	CASSEETGNQPQHF	9		2 (14%)					
R	TRAV26-1	TRAJ42	CIVRLRTNYGGSQGNLIF	13	TRBV5-4	TRBJ1-3	CASSFDRGTGNTIYF	10		2 (14%)					
S					TRBV5-3	TRBJ1-3	CASFDRGTGNTIYF	10		2 (14%)					
T					TRBV5-4	TRBJ1-3	CASFDRGTGNTIYF	10		2 (14%)					
AA					TRBV27	TRBJ1-3	CASSPYGGPGNTIYF	10		5 (36%)					
AK					TRBV4-2	TRBJ1-1	CASSQSSGGGRSEAFF	11			3 (30%)				
AL	TRAV1-2	TRAJ28	CAVRDAGAGSYQLTF	10	TRBV4-2	TRBJ1-1	CASQSSGGGRSEAFF	11			2 (20%)				
AM					TRBV4-3	TRBJ2-3	CASQPSPQGGRLEQYF	11			2 (20%)				
AQ	TRAV14/DV4	TRAJ44	CAMREVGGTAKLTF	10	TRBV7-9	TRBJ1-6	CASIYPGQLYNNSPLHF	12				3 (30%)			
AY	TRAV14/DV4	TRAJ18	CAITIEGSTLGRLYF	10	TRBV2	TRBJ1-4	CAGRGRPNEKLFF	8					2 (29%)		
									Other singletons	15 (83%)	6 (43%)	9 (64%)	3 (30%)	7 (70%)	5 (71%)
									Total	18	14	14	10	10	7

B8/NP ₃₀														
Clone ID	TRAV	TRAJ	CDR3 α	CDR3 α length	TRBV	TRBJ	CDR3 β	CDR3 β length	BP140	BP147	BP170	BP185	BP191	
A					TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10	5 (24%)		7 (30%)			
B	TRAV38-2/DV8	TRAJ42	CAPNYGGSQGNLIF	9	TRBV19	TRBJ2-2	CASGRIAGELFF	7	4 (19%)					
C					TRBV19	TRBJ1-1	CASSMVPDMNTEAFF	10	3 (14%)					
D					TRBV19	TRBJ2-7	CASSLVGGEQYF	7	2 (10%)					

L					TRBV29-1	TRBJ1-2	CSVVQGAECTF	6	6 (24%)					
M	TRAV38-2/DV8	TRAJ40	CAPS GTYKYIF	6	TRBV7-2	TRBJ2-7	CASS LVGGEQYF	7	6 (24%)					
N	TRAV14/DV4	TRAJ12	CAM SQGMDSYYKLIF	11	TRBV29-1	TRBJ1-2	CSVVQGAECTF	6	5 (20%)					
O	TRAV14/DV4	TRAJ53	CAM RGGGSNYKLT F	9	TRBV19	TRBJ1-1	CASS SIPDFNTEAFF	10	2 (8%)					
V	TRAV14/DV4	TRAJ33	CAM REGGSNYQLIW	9	TRBV19	TRBJ1-1	CAS SMIPDMNTEAFF	10		2 (9%)				
								Other singletons	7 (33%)	6 (24%)	14 (61%)	17 (100%)	9 (100%)	
								Total	21	25	23	17	9	
B7/NS1₁₉₆														
Clone ID	TRAV	TRAJ	CDR3 α	CDR3 α length	TRBV	TRBJ	CDR3 β	CDR3 β length	KK102	BP146	BP155	BP184	BP185	BP189
A	TRAV38-2/DV8	TRAJ33	CAY RSAVGYQLIW	8	TRBV27	TRBJ1-5	CAS SQYSNQPQHF	8	8 (25%)					
B					TRBV27	TRBJ1-5	CAS SQYSNQPQHF	8	5 (16%)					
C					TRBV27	TRBJ1-1	CAS SLMGNTAEAFF	8	2 (6%)	1 (5%)				
D	TRAV38-2/DV8	TRAJ43	CAY RSAVTYDMRF	8	TRBV27	TRBJ1-5	CAS SLYGNQPQHF	8	2 (6%)					
E					TRBV28	TRBJ1-1	CAS SLSRGWTEAFF	9	2 (6%)					
S	TRAV19	TRAJ4	CAL TRPGGGYNKLIF	10	TRBV2	TRBJ2-1	CAS RGLQGRIDYNEQFF	12		4 (19%)				
T					TRBV27	TRBJ2-7	CAS RIYAGSPYEQYF	10		2 (10%)				
AI					TRBV27	TRBJ2-1	CAS SPHPGTSGGASYNEQFF	15			3 (17%)			
AJ	TRAV38-2/DV8	TRAJ30	CAY RSAIQDKIIF	8	TRBV27	TRBJ2-1	CAS SPHPGTSGGASYNEQFF	15			2 (11%)			
AK	TRAV38-2/DV8	TRAJ41	CAY RSATGYALNF	8	TRBV27	TRBJ2-1	CAS SLYGSVQNEQFF	10			2 (11%)			
AL	TRAV3	TRAJ27	CAV RDIGTNAKGSTF	10	TRBV27	TRBJ2-2	CAS SYRGLSGELFF	9			2 (11%)			

AM	TRAV19	TRAJ13	CAL SEYSGGYQKV TF	10	TRBV9	TRBJ2-1	CAS SVATSGGSQQFF	10		2 (11%)				
AU					TRBV7-9	TRBJ1-1	CAS NGQGDTEAFF	8		2 (12%)				
AV	TRAV3	TRAJ28	CAV RAPGAGSYQL TF	10						2 (12%)				
AW	TRAV3	TRAJ28	CAV RDPGAGSYQL TF	10						2 (12%)				
AX					TRBV11-2	TRBJ1-1	CAS SPGSTEAFF	7		2 (12%)				
AY					TRBV11-2	TRBJ2-2	CAS SLGVEELFF	7		2 (12%)				
BG	TRAV19	TRAJ4	CAL LLFSGGYNKLIF	10	TRBV3-1	TRBJ2-5	CAS SPREGGETQYF	9		7 (33%)				
BH	TRAV14/DV4	TRAJ10	CAM REGPELTGGGNKLT TF	13	TRBV20-1	TRBJ1-2	CAS KRNRAYHYGY TF	10		3 (14%)				
BT					TRBV14	TRBJ2-7	CAS ATSGTYYEQYF	9		2 (10%)				
Other singletions								13 (41%)	14 (67%)	7 (39%)	7 (41%)	11 (52%)	19 (90%)	
Total								32	21	18	17	21	21	
B8/NP₉₂														
Clone ID	TRAV	TRAJ	CDR3 α	CDR3 α length	TRBV	TRBJ	CDR3 β	CDR3 β length	BP140	BP147	BP155	BP170	BP185	BP191
A	TRAV17	TRAJ31	CAT DESNARLMF	7	TRBV11-2	TRBJ2-7	CAS SLIRTWDEQYF	9	3 (23%)					
B					TRBV11-2	TRBJ2-7	CAS SLIRTWDEQYF	9	2 (15%)					
K					TRBV3-1	TRBJ2-5	CAS SQWGRPQETQYF	10		3 (13%)				
L	TRAV20	TRAJ45	CAV RTYSGGADGL TF	11	TRBV12-3	TRBJ2-3	CAS APRRDRGTDQYF	11		3 (13%)				
M					TRBV9	TRBJ2-3	CAS SPSELAGGRDLTQYF	13		2 (9%)				
N	TRAV8-3	TRAJ20	CAC GDYKL SF	5	TRBV9	TRBJ2-3	CAS SPSELAGGRDLTQYF	13		2 (9%)				
O	TRAV8-6	TRAJ32	CAV TNGGATNKL IF	9	TRBV3-1	TRBJ2-5	CAS SQWGRPQETQYF	10		2 (9%)				

AA	TRAV29/DV5	TRAJ49	CAA NTGNQFYF	6	TRBV11-2	TRBJ2-2	CAS SWRTGNSGELFF	10	4 (25%)
AB					TRBV11-2	TRBJ2-2	CAS SWRTGNSGELFF	10	3 (19%)
AL	TRAV3	TRAJ5	CAV AMDTGRRALTF	9					3 (15%)
AM	TRAV3	TRAJ5	CAV AMDTGRRALTF	9	TRBV9	TRBJ2-3	CAS SNYPGGARTDTQYF	12	3 (15%)
AN	TRAV8-6	TRAJ52	CAV SLNAGGTSYGKLTF	12	TRBV18	TRBJ2-7	CAS SPPRNMEPSYEQYF	12	3 (15%)
AO	TRAV19	TRAJ48	CAL SEAPSNFGNEKLTF	12	TRBV4-1	TRBJ2-6	CAS SHRDGRGISGANVLTF	13	2 (10%)
AP	TRAV8-1	TRAJ13	CAV NMALGGGYQKVTF	11	TRBV5-6	TRBJ2-7	CAS SPPARDRDHEQYF	11	2 (10%)
AQ	TRAV8-3	TRAJ20	CAV GDYKLSF	5	TRBV9	TRBJ2-3	CAS SPSQTSGGRTDTQYF	13	2 (10%)
AW	TRAV4	TRAJ39	CLV GDSGNAGNMLTF	10	TRBV2	TRBJ1-4	CAS RMTGGKTNEKLFF	11	8 (29%)
AX					TRBV2	TRBJ1-4	CAS RMTGGKTNEKLFF	11	2 (7%)
AY	TRAV4	TRAJ45	CLV MDSGGGADGLTF	10					2 (7%)
Other singletons								8 (62%)	11 (48%)
Total								13	23
								16	20
								28	9
								16	9
								(57%)	(100%)

Supplementary Table 7. Clonotype counts of B8/NP₃₀₋₃₈.

Clone ID	TRAV	TRAJ	CDR3α	CDR3α length	TRBV	TRBJ	CDR3β	CDR3β length	BP140	BP147	BP170	BP185	BP191	
A														
B	TRAV38-2/DV8	TRAJ42	CAPNYGGSQGNLIF	9	TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10	5			7		
C					TRBV19	TRBJ2-2	CASGRIAGELFF	7	4					
D					TRBV19	TRBJ1-1	CASSMVPDMNTEAFF	10	3					
E	TRAV14/DV4	TRAJ53	CAMRGGGSNYKLT	9	TRBV19	TRBJ2-7	CASSLVGGEQYF	7	2					
F					TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10	1					
G	TRAV14/DV4	TRAJ28	CAMREGDTSNSGAGSYQLTF	15	TRBV19	TRBJ1-1	CASSMVPDMNTEAFF	10	1					
H					TRBV19	TRBJ1-1	CASSVIPDMNTEAFF	10	1					
I	TRAV13-2	TRAJ13	CAEISGGYQKVTF	8	TRBV7-2	TRBJ1-1	CASSLVGATAFF	7	1					
J	TRAV14/DV4	TRAJ16	CAMREGGQKL	7	TRBV19	TRBJ1-6	CATSTVDPYNsplHF	10	1					
K	TRAV38-2/DV8	TRAJ53	CAPYSGGSNYKLT	9	TRBV19	TRBJ2-1	CASSLIGNEQFF	7	1					
L					TRBV29-1	TRBJ1-2	CSVVQGAECTF	6		6				
M	TRAV38-2/DV8	TRAJ40	CAPS GT KY IF	6	TRBV7-2	TRBJ2-7	CASSLVGGEQYF	7		6				
N	TRAV14/DV4	TRAJ12	CAMS RQ GMD NS KLI	11	TRBV29-1	TRBJ1-2	CS V QGA ECTF	6		5				
O	TRAV14/DV4	TRAJ53	CAMRGGGSNYKLT	9	TRBV19	TRBJ1-1	CASS S I P D F N T E A F F	10		2				
P	TRAV14/DV4	TRAJ53	CAMREDSGGSNYKLT	11	TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10		1				
Q	TRAV14/DV4	TRAJ53	CAMRGGGSNYKLT	11	TRBV19	TRBJ1-1	CASSIIPDMNTEAFF	10		1				
R	TRAV14/DV4	TRAJ6	CAMRESASGGSYIPTF	11	TRBV19	TRBJ1-1	CASSIIPDMNTEAFF	10		1				
S					TRBV19	TRBJ1-1	CASSNIPDMNTEAFF	10		1				
T	TRAV14/DV4	TRAJ53	CAMRDGGSNYKLT	10	TRBV19	TRBJ1-1	CASSNVPDMMTEAFF	10		1				
U	TRAV38-2/DV8	TRAJ43	CAYRAPYNNNDMR	9	TRBV13	TRBJ1-2	CAS SQARDRGN RGYTF	10		1				
V	TRAV14/DV4	TRAJ33	CAMREGGSNYQLI	9	TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10		2				
W	TRAV14/DV4	TRAJ53	CAMREGGGGSNYKLT	11	TRBV19	TRBJ1-1	CASSIIPDMNTEAFF	10		1				
X					TRBV27	TRBJ2-1	CASPSGTGANEQFF	10		1				
Y					TRBV7-9	TRBJ1-2	CASSLEGQQHGYTF	9		1				
Z					TRBV7-9	TRBJ2-1	CASSSSGSSYNEOFF	10		1				
AA	TRAV1-2	TRAJ33	CA VR DSD NY QL I W	8	TRBV28	TRBJ1-5	CASTAQGF SNQ PQ HF	10		1				
AB	TRAV14/DV4	TRAJ5	CAMSLHDTGRRALTF	10	TRBV7-2	TRBJ1-5	CASSLNFV GLN QP Q HF	11		1				
AC	TRAV19	TRAJ34	C ALSE A Y N TD K L I F	9	TRBV10-3	TRBJ1-5	CA I A NR GTE AFF	7		1				
AD	TRAV19	TRAJ5	CAL SD PY GG R RA LT F	10	TRBV29-1	TRBJ2-7	CSA V GL AG V RS Y EQ YF	11		1				
AE	TRAV26-1	TRAJ48	CIV RR QS NF G NE K LT F	11	TRBV7-9	TRBJ1-6	CASS L A RE Y S PL H F	9		1				
AF	TRAV26-2	TRAJ34	CIL RDAY NT DK L I F	9	TRBV20-1	TRBJ1-1	CSA RR S DR VN TE AFF	10		1				
AG	TRAV38-2/DV8	TRAJ12	CAYR SAP D S S Y K L I F	10	TRBV2	TRBJ2-2	CAS RGLS NT GEL FF	9		1				
AH	TRAV38-2/DV8	TRAJ33	CAYRS AM DS NY QL I W	10	TRBV19	TRBJ2-2	CAS STI G PY GEL FF	9		1				
AI	TRAV4	TRAJ30	CLL R DDK I F	5	TRBV7-9	TRBJ1-1	CSA SPH QEV TE AFF	9		1				
AJ	TRAV9-2	TRAJ43	CAL SEID M RF	5	TRBV29-1	TRBJ1-1	CSA GT GS ANTE AFF	9		1				
AK					TRBV19	TRBJ1-1	CASSMIPDMNTEAFF	10		1				
AL					TRBV19	TRBJ2-1	CAS NP SAG TLY NEQ FF	11		1				
AM					TRBV20-1	TRBJ2-2	CSA RP R SAGE L FF	9		1				
AN					TRBV20	TRBJ2-2	CSA EG LAGG K NT GEL FF	12		1				
AO					TRBV6-2	TRBJ1-6	CASS Y SKMT A YN SPL HF	12		1				
AP					TRBV9	TRBJ1-6	CASS VGGI SPL HF	8		1				
AQ					TRBV9	TRBJ2-7	CAS PPGQV Y EQ YF	9		1				
AR	TRAV13-1	TRAJ41	CA AS QRM MN S G Y AL NF	10	TRBV19	TRBJ1-5	CAS SL GTL QP Q HF	8		1				
AS	TRAV13-2	TRAJ26	CA E KS Y Y Q N F V F	8	TRBV2	TRBJ1-1	CAS SG RT G N T E A F F	9		1				
AT	TRAV14/DV4	TRAJ23	CAMREF YN QGG K L I F	10	TRBV19	TRBJ2-2	CAS SV SR DR N G E L FF	10		1				
AU	TRAV14/DV4	TRAJ26	CAM RG GY Q Q N F V F	8										1
AV	TRAV19	TRAJ15	C AL SE AT RD Q AG T AL I F	12										1
AW	TRAV3	TRAJ31	CA VR N AR L MF	5	TRBV28	TRBJ2-3	CAS SQ GQ GI ADT Q YF	10		1				
AX	TRAV38-2/DV8	TRAJ39	CAY RSV VY N N A G M N L TF	12	TRBV4-2	TRBJ2-1	CAS SQ NS V G SY NE OFF	11		1				
AY	TRAV38-2/DV8	TRAJ56	C A Y PT G A N S K L T F	8										1
AZ	TRAV8-2	TRAJ27	CA VR VNT NAG K S T F	9	TRBV7-6	TRBJ2-7	CAS SSS Y E Q Y F	6		1				
BA	TRAV8-3	TRAJ29	CA VA PL NS G N T PL V F	10	TRBV28	TRBJ2-3	CAS SF A RT R W E Q Y F	9		1				
BB					TRBV4-3	TRBJ1-6	CAS SQ AR D P Q Q G I L HF	10		1				
BC					TRBV7-9	TRBJ2-1	CAS S S A G V E Q F F	7		1				
BD					TRBV9	TRBJ1-2	CAS S PGG V V G Y T F	8		1				
BE	TRAV14/DV4	TRAJ48	CAI WT FG GE K L T F	8	TRBV19	TRBJ2-3	CAS S RSL T D T Q Y F	8		1				
BF	TRAV19	TRAJ22	CAL TP SGS AR Q L T F	10	TRBV11-2	TRBJ1-2	CAS SFF GA Q Q V D G Y TF	11		1				
BG	TRAV20	TRAJ34	CA A K G Y N TD K L I F	8	TRBV9	TRBJ2-2	CAS KR NT G EL FF	7		1				
BH	TRAV26-2	TRAJ12	C IL RD D S S Y K L I F	9	TRBV20-1	TRBJ2-5	CAS RD PAPE ET Q Y F	9		1				
BI	TRAV6	TRAJ42	CA LE NY G GS Q G N L I F	10	TRBV9	TRBJ2-7	CAS SAS A E F SS Y E Q Y F	11		1				

BJ	TRAV8-2	TRAJ42	CVVSEEGIIRIGSQGNLIF	14	TRBV7-3	TRBJ2-1	CASSPPTSGSVYEQFF	10	Grand total	21	25	23	17	1	9
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Red denotes truncated CDR3 regions.

Supplementary Table 8. Clonotype counts of B7/NS1₁₉₆₋₂₀₆.

Clone ID	TRAV	TRAJ	CDR3α	CDR3α length	TRBV	TRBJ	CDR3β	CDR3 β length	KK102	BP146	BP155	BP184	BP185	BP189	
A	TRAV38-2/DV8	TRAJ33	CAYRSAVGYQLIW	8	TRBV27	TRBJ1-5	CASSQYSNQPQHF	8	8						
B					TRBV27	TRBJ1-5	CASSQYSNQPQHF	8	5						
C					TRBV27	TRBJ1-1	CASSLMGNTEAFF	8	2	1					
D	TRAV38-2/DV8	TRAJ43	CAYRSAVTYDMRF	8	TRBV27	TRBJ1-5	CASSLYGNQPQHF	8	2						
E					TRBV28	TRBJ1-1	CASSLSRGWTEAFF	9	2						
F	TRAV6	TRAJ11	CAPLYSTLTTF	5	TRBV27	TRBJ1-1	CASSLMGNTEAFF	8	1						
G	TRAV6	TRAJ29	CAPRNTPLVF	5	TRBV27	TRBJ1-5	CASSLYGGQPQHF	8	1						
H					TRBV27	TRBJ1-5	CASSLYGPGGVGQQPQHF	12	1						
I	TRAV38-2/DV8	TRAJ33	CAYRSANNYQLIW	8	TRBV27	TRBJ2-1	CASSLYGSSYNEQFF	10	1						
J	TRAV3	TRAJ28	CAVRDPGAGSYQLTF	10	TRBV10-3	TRBJ2-7	CAISESTGFEQYF	9	1						
K					TRBV11-2	TRBJ2-3	CASSLLTDQTQYF	7	1						
L					TRBV14	TRBJ2-5	CASSQDFGRTOYF	8	1						
M	TRAV27	TRAJ34	CAGPPRPSYNTDKLIF	11	TRBV28	TRBJ1-2	CASTPRGRGLVGYTF	11	1						
N	TRAV19	TRAJ13	CALSSSTSGGYQKVTF	10	TRBV3-1	TRBJ1-1	CASSQERKAGGPTEAFF	12	1						
O	TRAV19	TRAJ4	CALGSFSGGYQKVLF	10	TRBV4-1	TRBJ2-5	CASSQLEQGGETQYF	10	1						
P	TRAV3	TRAJ6	CAVRDPGAGSYIPTF	10	TRBV5-8	TRBJ2-1	CASPPGSSGRLGEOQFF	11	1						
Q	TRAV3	TRAJ28	CAVNSPGAGSYQLTF	10	TRBV7-3	TRBJ2-2	CASSSQGAQELFF	9	1						
R	TRAV38-2/DV8	TRAJ44	CAYMSGTASKLTF	8				1							
S	TRAV19	TRAJ4	CALTRPGGGYQNLIF	10	TRBV2	TRBJ2-1	CASRGLQGRIDYNEQFF	12		4					
T					TRBV27	TRBJ2-7	CASRIYAGSPYEQYF	10		2					
U	TRAV38-2/DV8	TRAJ33	CAYRSAASNQYLW	8	TRBV27	TRBJ1-1	CASSLYPGANTEAFF	10		1					
V	TRAV38-2/DV8	TRAJ39	CAYRSAASNAGNMLTF	10	TRBV27	TRBJ1-5	CASSLYRGSNQPQHF	10		1					
W					TRBV27	TRBJ1-6	CASSLYGAGNSPLHF	10		1					
X	TRAV38-2/DV8	TRAJ43	CAYRSSYNNNDMRF	9	TRBV27	TRBJ2-7	CASRIYAGSPYEQYF	10		1					
Y					TRBV27	TRBJ2-7	CASRLMPGSTYEQYF	10		1					
Z	TRAV10	TRAJ40	CVVSGTSGTYKYYIF	9	TRBV19	TRBJ2-1	CASRARVLDEQFF	8		1					
AA	TRAV3	TRAJ8	CAVRDIMNTGFQKLVF	11	TRBV20-1	TRBJ2-1	CSARDSGLSHGEOFQFF	10		1					
AB					TRBV25-1	TRBJ2-2	CASSESGAGELF	8		1					
AC					TRBV28	TRBJ1-2	CASNPAGGAGLGYGYTF	12		1					
AD	TRAV3	TRAJ23	CAVRDIRKIYNQQGKLF	13	TRBV7-2	TRBJ2-5	CASSL GALGETQYF	9		1					
AE					TRBV7-9	TRBJ1-3	CASSLDSSSGNTIYF	10		1					
AF					TRBV7-9	TRBJ2-1	CASSLAGAGNEQFF	9		1					
AG	TRAV1-2	TRAJ28	CAVRLYSGAGSYQLTF	11	TRBV7-9	TRBJ2-7	CASSLDSSGGNEQYF	10		1					
AH					TRBV9	TRBJ1-5	CASSVGGAQPOHF	8		1					
AI					TRBV27	TRBJ2-1	CASSPHPGTSGGASNEQFF	15		3					
AJ	TRAV38-2/DV8	TRAJ30	CAYRSAIQDKIIF	8	TRBV27	TRBJ2-1	CASSPHPGTSGGASNEQFF	15		2					
AK	TRAV38-2/DV8	TRAJ41	CAYRSATGYALNF	8	TRBV27	TRBJ2-1	CASSLYGSVQNEQFF	10		2					
AL	TRAV3	TRAJ27	CAVRDIGTNAGKSTF	10	TRBV27	TRBJ2-2	CASSYRGLSGELFF	9		2					
AM	TRAV19	TRAJ13	CALSEYSGGYQKVTF	10	TRBV9	TRBJ2-1	CASSVATGGSSQFFF	10		2					
AN	TRAV38-2/DV8	TRAJ53	CAYRSAGSGGSNYKLT	12	TRBV27	TRBJ1-5	CASSLMTNQPF	8		1					
AO	TRAV41	TRAJ26	CAVDNYQQNFVF	7	TRBV27	TRBJ2-3	CASSLYGADTQYF	8		1					
AP					TRBV4-1	TRBJ2-5	CAS SQEVETQYF	7		1					
AQ	TRAV19	TRAJ13	CALRSDSGGYQKVTF	10	TRBV4-1	TRBJ2-5	CAS SQEVETQYF	7		1					
AR					TRBV19	TRBJ2-4	CASSIVRGORETKNIQYF	13		1					
AS	TRAV19	TRAJ4	CALGLFSGGYQNLIF	10	TRBV4-1	TRBJ2-5	CASSHRTGGETQYF	9		1					
AT					TRBV5-6	TRBJ2-6	CASSTILGPGANVLTF	11		1					
AU					TRBV7-9	TRBJ1-1	CASNGQGDTEAFF	8		2					
AV	TRAV3	TRAJ28	CAVRAPGAGSYQLTF	10						2					
AW	TRAV3	TRAJ28	CAVRDPGAGSYQLTF	10						2					
AX					TRBV11-2	TRBJ1-1	CASPGSTEAFF	7		2					
AY					TRBV11-2	TRBJ2-2	CASLGVEELFF	7		2					
AZ	TRAV3	TRAJ28	CAVRAPGAGSYQLTF	10	TRBV10-3	TRBJ2-7	CAISGGQASYEQYF	9		1					
BA	TRAV3	TRAJ28	CAVSGWGAGSYQLTF	10	TRBV7-9	TRBJ1-1	CASNGQGDTEAFF	8		1					

R	S	TRAV12-2	TRAJ40	CAVNPGBTYKYIF	7	TRBV9	TRBJ2-5	CASSVDPGGGRQETQYF	13	1		
T	TRAV17	TRAJ54	CATDGRGGAQKLVF	9	TRBV12-3	TRBJ2-3	CASAPRRDRGTDQYF	11	1			
U	TRAV20	TRAJ45	CAVRTYSGGGADGLTF	11	TRBV3-1	TRBJ1-4	CASSSIAGRGEKLFF	10	1			
V	TRAV22	TRAJ22	CAVEFPSSGSARQLTF	11	TRBV12-3/TRBV12-4	TRBJ2-3	CASAPRRDRGTDQYF	11	1			
W	TRAV26-1	TRAJ26	CIVRVAPSDDYQQNFVF	12	TRBV11-2	TRBJ2-3	CASSSPRVAQRPDQTQYF	12	1			
X	TRAV26-1	TRAJ30	CIVRVAVSVSYRDKLF	12	TRBV20-1	TRBJ1-1	CASARGDRGLNTEAFF	10	1			
Y	TRAV5	TRAJ37	CAETPIGSSNTGKLIF	11	TRBV25-1	TRBJ2-7	CASSVRYEQYF	6	1			
Z	TRAV8-3	TRAJ47	CAVGADGNKLVF	7	TRBV27	TRBJ2-7	CASSIGQGKSSYEQYF	11	1			
AA	TRAV29/DV5	TRAJ49	CAA NTGNQFYF	6	TRBV11-2	TRBJ2-2	CASSWRTGNGSELFF	10	4			
AB					TRBV11-2	TRBJ2-2	CASSWRTGNGSELFF	10	3			
AC					TRBV11-1	TRBJ2-3	CASSLASGHRPTDTQYF	12	1			
AD					TRBV3-1	TRBJ2-3	CASSSPRREQGDTQYF	10	1			
AE					TRBV4-1	TRBJ1-1	CASSLPPRNTEAFF	9	1			
AF	TRAV1-2	TRAJ11	CAVRPSGYSTLTF	8					1			
AG	TRAV20	TRAJ6	CAVRGSYIPTF	6	TRBV20-1	TRBJ1-1	CSAREGVNTEAFF	8	1			
AH	TRAV26-1	TRAJ26	CIVRVGPADNYGQNVF	12	TRBV3-1	TRBJ2-3	CASSPRREQGDTQYF	10	1			
AI	TRAV29/DV5	TRAJ49	CAANTGNQFYF	6					1			
AJ	TRAV41	TRAJ49	CAVENTGNQFYF	7	TRBV4-1	TRBJ1-4	CASRAWGREGEKLFF	10	1			
AK	TRAV6	TRAJ38	CALPSNAGNNRKLW	10	TRBV9	TRBJ2-2	CASSVERGRNTGELFF	11	1			
AL	TRAV3	TRAJ5	CAVAMDTGRRALTF	9					3			
AM	TRAV3	TRAJ5	CAVAMDTGRRALTF	9	TRBV9	TRBJ2-3	CASNYPGGARTDTQYF	12	3			
AN	TRAV8-6	TRAJ52	CAVSINAGGTSYGKLTF	12	TRBV18	TRBJ2-7	CASSPPRNMEPSYEQYF	12	3			
AO	TRAV19	TRAJ48	CALSEAPSNFGNEKLT	12	TRBV4-1	TRBJ2-6	CASSHSDRDRGISGANVLT	13	2			
AP	TRAV8-1	TRAJ13	CAVNMALGGGYQKVTF	11	TRBV5-6	TRBJ2-7	CASSPARDRHDHEQYF	11	2			
AQ	TRAV8-3	TRAJ20	CAVGDYKLSF	5	TRBV9	TRBJ2-3	CASSPSQSTSGGRTDTQYF	13	2			
AR					TRBV5-6	TRBJ1-2	CASSLGDRGRGYGYTF	11	1			
AS	TRAV19	TRAJ48	CALSEAPSNFGNEKLT	12					1			
AT	TRAV26-1	TRAJ41	CIVRVAAVSNSNGYALNF	13	TRBV19	TRBJ1-1	CASSSSRDRGLGTEAFF	11	1			
AU	TRAV3	TRAJ13	CAVRDLDGGYQKVTF	11	TRBV16	TRBJ2-7	CASSHLDRGKKDYEQYF	12	1			
AV	TRAV8-3	TRAJ20	CAVGDYKLSF	5					1			
AW	TRAV4	TRAJ39	CLVGDSGNAGNM	10	TRBV2	TRBJ1-4	CASRMTGGKTNEKLFF	11	8			
AX					TRBV2	TRBJ1-4	CASRMTGGKTNEKLFF	11	2			
AY	TRAV4	TRAJ45	CLVMDSGGGADGLTF	10					2			
AZ					TRBV27	TRBJ2-7	CASSWGQGKSSYEQYF	11	1			
BA					TRBV27	TRBJ2-7	CASSLGGQGKSSYEQYF	11	1			
BB					TRBV3-1	TRBJ2-7	CASSPSRVLYEQYF	9	1			
BC					TRBV4-1	TRBJ2-1	CASSQDSGRGELFF	9	1			
BD					TRBV6-2	TRBJ1-1	CASTEPRGTEAFF	8	1			
BE	TRAV1-2	TRAJ15	CAVDQAGTALIF	7	TRBV18	TRBJ1-1	CASSPRSEAFF	7	1			
BF	TRAV13	TRAJ26	CAASGNYGGQNFVF	8	TRBV4-1	TRBJ1-4	CASSQDPGPRLGKLF	11	1			
BG	TRAV20	TRAJ33	CAVRGMDSNYQLIW	10	TRBV28	TRBJ2-7	CASSFLFRDGTYEQYF	11	1			
BH	TRAV22	TRAJ45	CAVSWYSGGGADGLTF	12	TRBV9	TRBJ2-1	CASSPGDRGKTNEQFF	11	1			
BI	TRAV26-2	TRAJ49	CILRDVMNTGNQFYF	10	TRBV4-1	TRBJ2-7	CASSPRDRARGDEQYF	11	1			
BJ	TRAV29/DV5	TRAJ47	CAA MEYGNKLVF	7	TRBV9	TRBJ2-1	CASSVEIAGRYNEQFF	11	1			
BK	TRAV3	TRAJ28	CAVRQTA YSAGGSQY QLTF	13	TRBV2	TRBJ2-3	CASSSSPRGDTQYF	9	1			
BL	TRAV36/DV7	TRAJ40	CAVSLPQEPTNTS	8	TRBV11-2	TRBJ2-1	CASTSRAGFNEQFF	9	1			
BM	TRAV8-2	TRAJ29	CVVSDPFGNTPLVF	9	TRBV29-1	TRBJ2-5	CSVVVGREQETQYF	9	1			
BN	TRAV9-2	TRAJ37	CAPLKGLKLIF	5	TRBV11-2	TRBJ2-5	CASSLEGRREGETQYF	11	1			
BO	TRAV9-2	TRAJ39	CAQNAGNM	6	TRBV20-1	TRBJ2-7	CSANPEGPYEQYF	8	1			
BP					TRBV28	TRBJ2-1	CASSLRLVAGRSYNEQFF	13	1			
BQ					TRBV29-1	TRBJ2-3	CSV EGLGR AVRTQYF	9	1			
BR					TRBV4-1	TRBJ2-2	CASSQAGQAGELFF	9	1			
BS					TRBV9	TRBJ1-1	CASSSTRRNTEAFF	8	1			
BT	TRAV12-2	TRAJ4	CAVNSGFSGGYQNKLF	11	TRBV11-2	TRBJ1-1	CASSFRQGEAFF	7	1			
BU	TRAV21	TRAJ49	CAVLNTGNQFYF	7	TRBV12-3/TRBV12-4	TRBJ1-2	CASTVNRCSEGTYF	9	1			
BV	TRAV27	TRAJ31	CAGEGDNNARLMF	8					1			
BW	TRAV29/DV5	TRAJ26	CAARCHGQNFVF	7	TRBV3-1/TRBV3-2	TRBJ2-7	CASSYRSSYEQYF	8	1			
BX	TRAV38-2/DV8	TRAJ33	CAYRSAARDSNYQLIW	11	TRBV12-5	TRBJ2-1	CASGLLTSGSINEQFF	11	1			
						Grand total	13	23	16	20	28	9

Red denotes truncated CDR3 regions.

Supplementary Table 10. TCR sequencing primers

Primer Name	Sequence
huTRAV1ext	AACTGCACGTACCAGACATC
huTRAV2ext	GATGTGCACCAAGACTCC
huTRAV3ext	AAGATCAGGTCAACGTTGC
huTRAV4ext	CTCCATGGACTCATATGAAGG
huTRAV5ext	CTTTTCCTGAGTGTCCGAG
huTRAV6ext	CACCCCTGACCTGCAACTATAC
huTRAV7ext	GCAAAATACAGGGATGGG
huTRAV8-1ext	CTCACTGGAGTTGGGATG
huTRAV8-3ext	CACTGTCTCTGAAGGAGCC
huTRAV8-2,4ext	GCCACCCCTGGTTAAAGG
huTRAV8-6ext	GAGCTGAGGTGCAACTACTC
huTRAV8-7ext	CTAACAGAGGCCACCCAG
huTRAV9-1_2ext	TGGTATGTCCAATATCCTGG
huTRAV10ext	CAAGTGGAGCAGAGTCCTC
huTRAV12-1_3ext	CARTGTTCCAGAGGGAGC
huTRAV13-1ext	CATCCTTCACCCCTGAGTG
huTRAV13-2ext	CAGCGCCTCAGACTACTTC
huTRAV14ext	AAGATAACTCAAACCCAACCAG
huTRAV16ext	AGTGGAGCTGAAGTGCAAC
huTRAV17ext	GGAGAAGAGGATCCTCAGG
huTRAV18ext	TCCAGTATCTAAACAAAGAGCC
huTRAV19ext	AGGTAACTCAAGCGCAGAC
huTRAV20ext	CACAGTCAGCGGTTAACAG
huTRAV21ext	TTCCTGCAGCTTGAGTG
huTRAV22ext	GTCCTCCAGACCTGATTCTC
huTRAV23ext	TGCTTATGAGAACACTGCG
huTRAV24ext	CTCAGTCACTGCATGTTAG
huTRAV25ext	GGACTTCACCACGTACTGC
huTRAV26-1ext	GCAAACCTGCCTTGTAAATC
huTRAV26-2ext	AGCCAAATTCAATGGAGAG
huTRAV27ext	TCAGTTCTAAGCATCCAAGAG
huTRAV29ext	GCAAGTTAACAAAATTCAAC
huTRAV30ext	CAACAACCAGTGCAGAGTC
huTRAV34ext	AGAACTGGAGCAGAGTCCTC
huTRAV35ext	GGTCAACAGCTGAATCAGAG
huTRAV36ext	GAAGACAAGGTGGTACAAAGC
huTRAV38ext	GCACATATGACACCAAGTGAG
huTRAV39ext	CTGTTCTGAGCATGCAG
huTRAV40ext	GCATCTGTGACTATGAACGTG
huTRAV41ext	AATGAAGTGGAGCAGAGTCC
huTRACext	GACCAGCTTGACATCACAG
huTRBV2ext	TCGATGATCAATTCTCAGTTG
huTRBV3ext	CAAAATACCTGGTCACACAG
huTRBV4ext	TCGCTTCTCACCTGAATG
huTRBV5-1_4ext	GATTCTCAGGKCKCCAGTTC
huTRBV5-5_8ext	GTACCAACAGGYCCTGGGT
huTRBV6-1_3,5_9ext	ACTCAGACCCAAAATTCC

huTRBV6-4ext	ACTGGCAAAGGAGAAGTCC
huTRBV7-1_3ext	TRTGATCCAATTCAGGTCA
huTRBV7-4_9ext	CGSWTCTYTGCAGARAGGC
huTRBV9ext	GATCACAGCAACTGGACAG
huTRBV10-1ext	CAGAGCCCAGACACAAG
huTRBV10-2ext	ACCTTGATGTGTCACCAGAC
huTRBV11ext	CGATTTCTGCAGAGACGC
huTRBV12ext	ARGTGACAGARATGGGACAA
huTRBV13ext	AGCGATAAAGGAAGCATCC
huTRBV14ext	CCAACAATCGATTCTTAGCTG
huTRBV15ext	AGTGACCCCTGAGTTGTTCTC
huTRBV16ext	GTCTTGATGAAACAGGTATGC
huTRBV17ext	CAGACCCCCAGACACAAG
huTRBV18ext	CATAGATGAGTCAGGAATGCC
huTRBV19ext	AGTTGTGAACAGAACATTGAACC
huTRBV20ext	AAGTTCTCATCAACCATGC
huTRBV23ext	GCGATTCTCATCTCAATGC
huTRBV24ext	CCTACGGTTGATCTATTACTCC
huTRBV25ext	ACTACACCTCATCCACTATTCC
huTRBV27,28ext	TGGTATCGACAAGACCCAG
huTRBV29ext	TTCTGGTACCGTCAGCAAC
huTRBV30ext	TCCAGCTGCTTTACTCC
huTRBCext	TAGAACTGGACTTGACAGCG
huTRAV1int	GCACCCACATTCTKTCTTAC
huTRAV2int	CACTCTGTGTCATGCTTAC
huTRAV3int	ATGCACCTATTCACTCTGG
huTRAV4int	ATTATATCACGTGGTACCAACAG
huTRAV5int	TACACAGACAGCTCCCTCCAC
huTRAV6int	TGGTACCGACAAGATCCAG
huTRAV7int	TATGAGAAGCAGAAAGGAAGAC
huTRAV8-1int	GTCAACACCTTCAGCTTCTC
huTRAV8-3int	TTTGAGGCTGAATTAAAGAGG
huTRAV8-2,4int	AGAGTGAAACCTCCTCCAC
huTRAV8-6int	AACCAAGGACTCCAGCTTC
huTRAV8-7int	ATCAGAGGTTTGAGGCTG
huTRAV9-1_2int	GAAACCACCTCTTCCACCTG
huTRAV10int	GAAAGAACTGCACCTTCAATG
huTRAV12-1_3int	AAGATGGAAGGTTACAGCAC
huTRAV13-1int	TCAGACAGTGCCTCAAATAC
huTRAV13-2int	CAGTGAAACATCTCTCTGC
huTRAV14int	AGGCTGTGACTCTGGACTG
huTRAV16int	GTCCAGTACTCCAGACAAACG
huTRAV17int	CCACCATGAACTGCAGTTAC
huTRAV18int	TGACAGTTCTTCCACCTG
huTRAV19int	TGTGACCTTGGACTGTGTG
huTRAV20int	TCTGGTATAGGCAAGATCCTG
huTRAV21int	AACTTGGTTCTCAACTGCAG
huTRAV22int	CTGACTCTGTGAACAATTGC

huTRAV23int	TGCATTATTGATAGCCATACG
huTRAV24int	TGCCTTACACTGGTACAGATG
huTRAV25int	TATAAGCAAAGGCCTGGTG
huTRAV26-1int	CGACAGATTCACTCCCAG
huTRAV26-2int	TTCACTTGCCTTGTAAACCAC
huTRAV27int	CTCACTGTGTACTGCAACTCC
huTRAV29int	CTGCTGAAGGT CCTACATT C
huTRAV30int	AGAAGCATGGTGAAGCAC
huTRAV34int	ATCTCACCATAAACTGCACG
huTRAV35int	ACCTGGCTATGGTACAAGC
huTRAV36int	ATCTCTGGTTGTCCACGAG
huTRAV38int	CAGCAGGCAGATGATTCTC
huTRAV39int	TCAACCAC TT CAGACAGACTG
huTRAV40int	GGAGGCGGAAATATTAAAGAC
huTRAV41int	TTGTTTATGCTGAGCTCAGG
huTRACint	TGTTGCTCTTGAAGTCCATAG
huTRBV2int	TTCACTCTGAAGATCCGGTC
huTRBV3int	AATCTTCACATCAATTCCCTG
huTRBV4int	CCTGCAGCCAGAACAGACTC
huTRBV5-1_4int	CTTGGAGCTGGRSGACTC
huTRBV5-5_8int	TCTGAGCTGAATGTGAACG
huTRBV6-1_3,5_9int	GTGTRCCCAGGATATGAACC
huTRBV6-4int	TGGTTATAGTGTCTCCAGAGC
huTRBV7-1_3int	TCYACTCTGAMGWTCCAGCG
huTRBV7-4_9int	TGRMGATYCAGCGCACA
huTRBV9int	GTACCAACAGAGCCTGGAC
huTRBV10-1int	TGGTATCGACAAGACCTGG
huTRBV10-3int	GGAACACCAAGTGA C T G A G
huTRBV11int	GA C T C C A C T C T C A A G A T C C A
huTRBV12int	CYACTCTGARGATCCAGCC
huTRBV13int	CATTCTGA ACT GA AC AT GAGC
huTRBV14int	ATTCTACTCTGAAGGTGCAGC
huTRBV15int	ATAACTTCCAATCCAGGAGG
huTRBV16int1	CTGTAGCCTTGAGATCCAGG
huTRBV17int	TGTTCACTGGTACCGACAG
huTRBV18int	CGATTTCTGCTGAATTCC
huTRBV19int	TTCCTCTCACTGTGACATCG
huTRBV20int	ACTCTGACAGTGACCAGTGC
huTRBV23int	GCAATCCTGTCCTCAGAAC
huTRBV24int	GATGGATACAGTGTCTCTGA
huTRBV25int	CAGAGAAGGGAGATCTTCC
huTRBV27,28int	TTCYCCCTGATYCTGGAGTC
huTRBV29int	TCTGACTGTGAGCAACATGAG
huTRBV30int	AGAATCTCTCAGCCTCCAGAC
huTRBCint	TTCTGATGGCTAAACACAG