Supplementary Material:

In vivo therapeutic effects of affinity-improved-TCR engineered T-cells on HBV-related hepatocellular carcinoma

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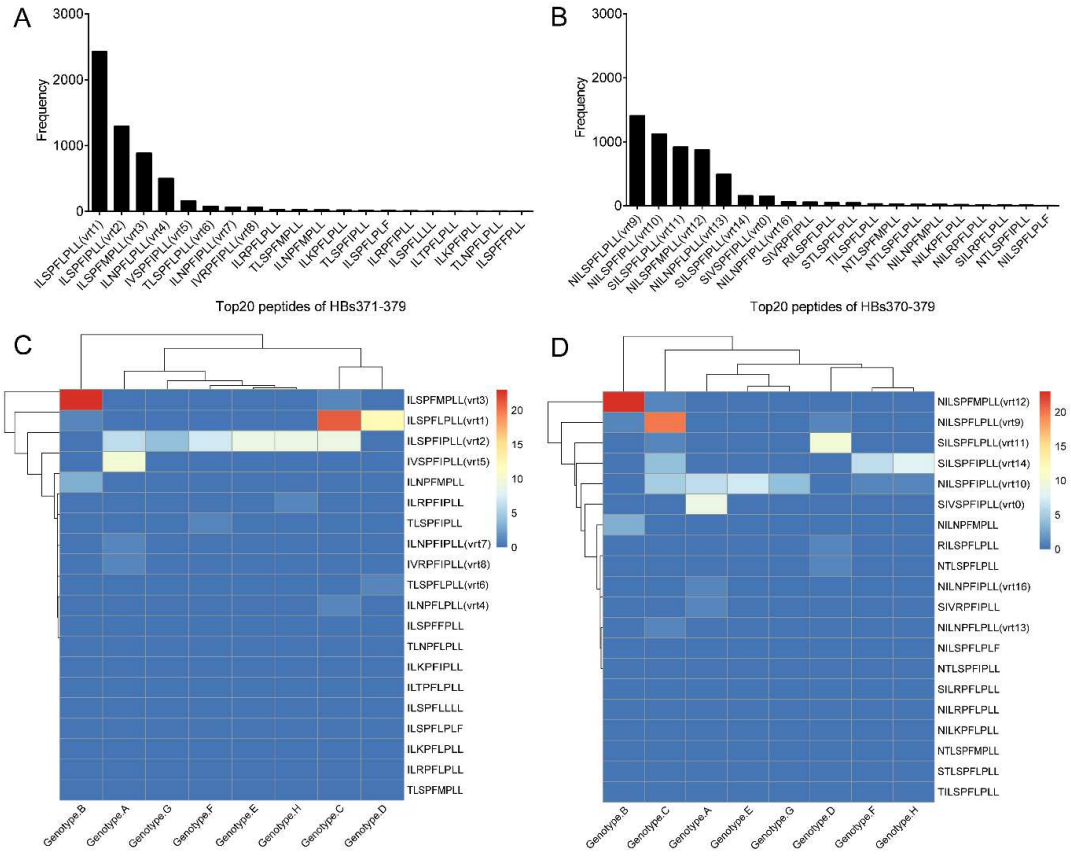
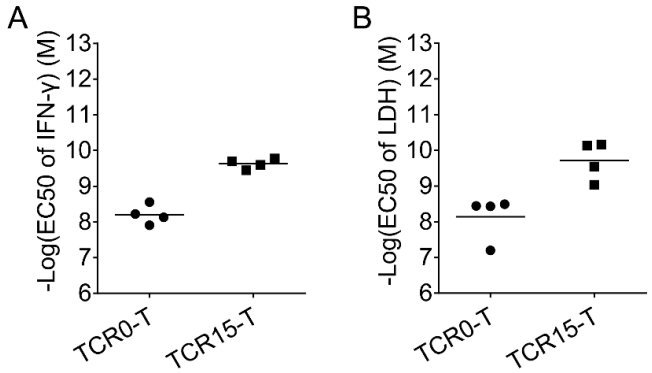
Supplementary Figures

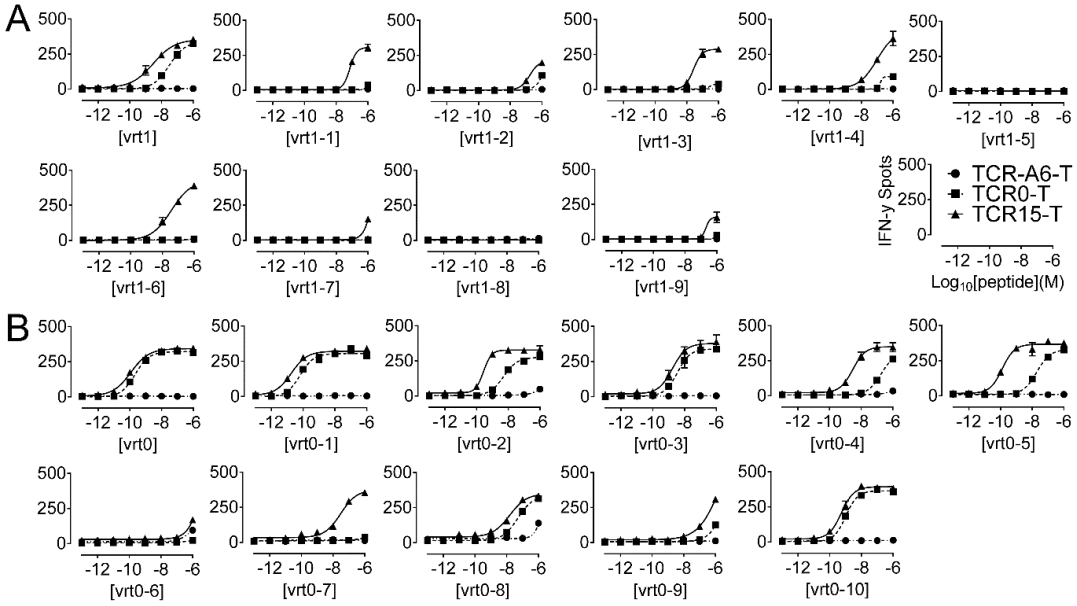


Supplementary Fig. S1. Analysis of HBs peptides and HBV genotypes. HBs371-379 epitope sequences (Supplementary Table S1.1**)** and HBs370-379 epitope sequences (Supplementary Table S1.2**)** were retrieved from 5855 unique full-length HBs polyproteins. The most common peptides of HBs371 and HBs370 from full-length HBs polyprotein sequences were statistically analyzed with Strawberry Perl 5.26.1.1 and R 3.6.1 according to HBV genotype classified in UniProt. The most common 20 peptides frequency of (A) HBs371-379 and (B) HBs370-379 were retrieved from 5657 (97% of 5855) and 5528 (94% of 5855) full-length HBs polyproteins. (C) The corresponding HBV genotypes of the most common 8 HBs371-379 peptides (vrt1 to vrt8). (D) The corresponding HBV genotypes of the most

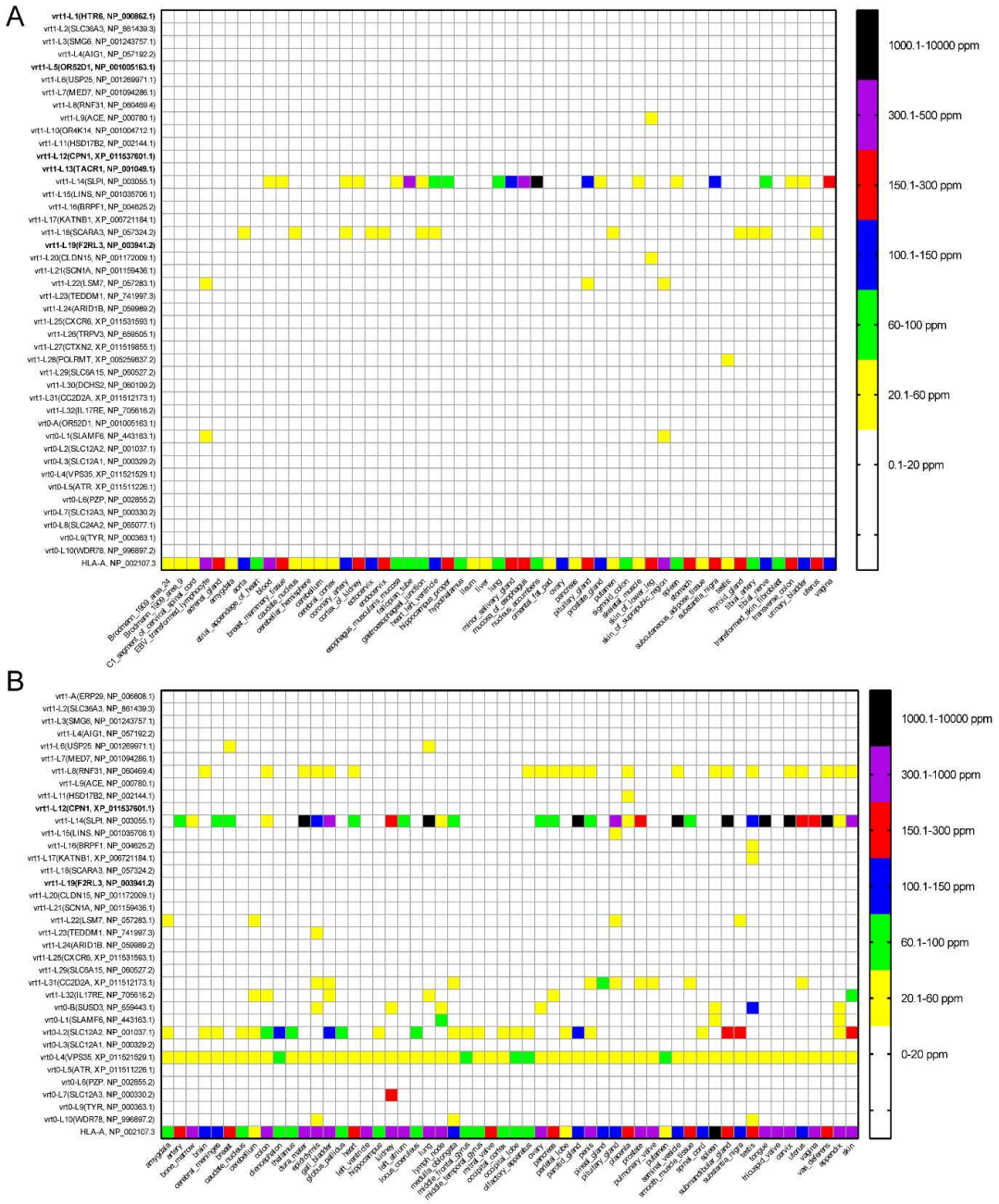
common 8 HBs370-379 peptides (vrt0, vrt9 to vrt16).



Supplementary Fig. S2. Analysis of TCR-T activation and detection of cytotoxicity of TCR-T cells. The EC_{50} values are shown for (A) IFN-γ ELISPOT and (B) LDH cytotoxicity obtained by titrating exogenous vrt1-HBs371 (ILSPFLPLL) peptide to HLA-A*02:01-T2 as the antigen-presenting cells. Black lines represent averages of the four batches of TCR-T cells prepared from different PBMC donors.

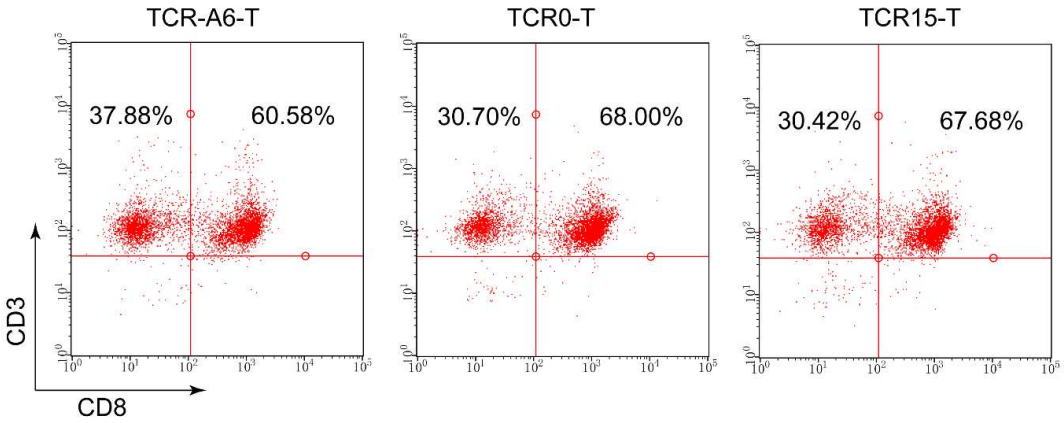


Supplementary Fig. S3. Determination of the critical residues in vrt1 and vrt0 for TCR recognition by alanine scanning. After coculturing TCR-T cells and peptide-pulsed T2 cells in triplicate overnight at an E:T ratio of 1:10, IFN-γ release was detected. The vrt1 **(A)** and vrt0 **(B)** peptides produced by alanine scanning (10^{-6} to 10^{-13} M) were analysed.



Supplementary Fig. S4. Expression profiling of human antigens containing 45 potential cross-reactive peptides related to vrt1 (ILSPFLPLL) and vrt0 (SIVSPFIPLL) from (Supplementary Table S3.2). Two gene expression database *E-MTAB-5214* and *E-MTAB-3358* containing highest number of tissues (53 and 56, respectively) were selected and combined to cover

potential cross-reactive peptides from all 45 polyproteins having expression information. There were 43 peptides presented in *E-MTAB-5214*, and 35 in *E-MTAB-3358*. The expression levels of HLA-A (NP002107.3) from these two database were also extracted to serve as an internal reference normalization. The values are in ppm (ppm - parts per million, so that the sums of all entries in the database for a tissue is equal to 1 million). The heat map was generated with GraphPad Prism version 7. (A) Expression heatmap of potential cross-reactive peptides in *E-MTAB-5214*. (B) Expression heatmap of potential cross-reactive peptides in *E-MTAB-3358*.



Supplementary Fig. S5. The CD8$^+$ cell rates of the human T cells used for the xenograft models prior injecting the mice.

Supplementary Tables

Supplementary Table S1.1 134 unique HBs371-379 peptides from 5855 unique full-length HBs protein. And the corresponding frequency.

HBs371-Peptides	Frequency	HBs371-Peptides	Frequency	HBs371-Peptides	Frequency
ILSPFLPLL(vrt1)	2426	TLTPFIPLL	3	ILSPFLPLV	1
ILSPFIPLL(vrt2)	1292	TLSPFLLLL	2	ILSPFLPTL	1

ILSPFMPLL(vrt3)	887	ILSPFIPLS	2	ILSPFLQLL	1
ILNPFLPLL(vrt4)	501	ILNLFLPLL	2	NLSPFLPLL	1
IVSPFIPLL(vrt5)	160	NLSPFIPLL	2	ILSSFLPLL	1
TLSPFLPLL(vrt6)	78	ILSHFLPLL	2	ILNPFTPLL	1
ILNPFIPLL(vrt7)	66	TLSPYLPLF	2	IMNPFMPLL	1
IVRPFIPLL(vrt8)	62	ILSPLLPLL	2	TLRPFIPLL	1
ILRPFLPLL	30	ILTPFMPLL	1	IVRPFMPLL	1
TLSPFMPLL	28	IVNPFIPLL	1	ILTLFIPLL	1
ILNPFMPLL	24	ILNLFIPLL	1	FLSPFLPLL	1
ILKPFLPLL	21	IGSPFIPLL	1	ILNSFLPLL	1
TLSPFIPLL	17	ILSPFMPVL	1	IWSPLLPLL	1
ILSPFLPLF	13	TLRPFLQLL	1	TLSPFILLF	1
ILRPFIPLL	12	TVSPFIPLL	1	ILNTFLPLL	1
ILSPFLLLL	10	TLSPFLPLS	1	NLNPFLPLL	1
ILTPFLPLL	8	ILSPFLALL	1	ILSHFLPLF	1
ILKPFIPLL	8	ILRPFTPLL	1	TLSPFLTLL	1
TLNPFLPLL	8	ILSPFISLL	1	ILSPFITLL	1
ILSPFFPLL	6	ILSPFMPLS	1	TVKPFIPLL	1
ILSLFIPLL	6	ILNPLIPLL	1	ISRPFIPLL	1
ILSPFTPLL	6	IASPFLPLL	1	TVSPFILLL	1
IVSPFLPLL	6	IFSPFIPLL	1	ILSPFIPLY	1
ISSPFLPLL	5	TLTPFLPLL	1	TLKPFIPLL	1
ILSRFLPLL	5	ILSPYILLL	1	ILSPFLPML	1
IVNPFLPLL	5	ILSPFMQLL	1	IWNPFLHLS	1
ILSPFLPLS	5	ILSRFIPLL	1	ILSPCMPLL	1
ILGPFLPLL	5	ILKHFMPLL	1	ILSPFTLLL	1
ILSHFIPLL	4	ILSPFLPPL	1	IWSPFMPLL	1
ILSPYLPLL	4	IFSPFLPLL	1	TLTPFMPLL	1
IWSPFLPLL	4	ILSPFIQLL	1	TVSPFLPLL	1
ILSPFSPLL	4	ILIPFLPLL	1	TLSPFTPLL	1
TLKPFLPLL	4	ILSLFMPLL	1	ILSPFIPLI	1
IVKPFIPLL	4	IWSRFIPLL	1	ILMPFLPLL	1
ILSPFILLL	3	ILNPFMPPL	1	IMSPVVPLL	1
IVRPFLPLL	3	IVRHFIPLL	1	ILSPCTPLL	1
ILSPFMSLL	3	IMSPFLPLL	1	ILSPYMPLL	1
TLSPFLLLF	3	ILSPFMPLF	1	ILSPSLPLL	1
ISSPFIPLL	3	ILSPFLTLL	1	ILSSFMPLL	1
ILTPFIPLL	3	ILSPLMPLL	1	ILSPFLPRL	1
ILNPFLPLF	3	ILNPFFPLL	1	ILNPYIQLL	1
TLRPFLPLL	3	IWSPFIPLL	1	TLNPFIPLL	1
ILSPFIPLF	3	ILNPFLPQL	1	ILNHFLPLL	1
ILRPFMPLL	3	ILSPFIPVL	1	TLSPFIQLL	1
IVKPFLPLL	3	ILSPFMLLL	1		

Supplementary Table S1.2 190 unique HBs370-379 peptides from 5855 unique full-length HBs protein. And the corresponding frequency.

HBs370-Peptides	Frequency	HBs370-Peptides	Frequency	HBs370-Peptides	Frequency
NILSPFLPLL(vrt9)	1410	NTLSPFLLLF	2	NILSPLMPLL	1
NILSPFIPLL(vrt10)	1125	NILNLFLPLL	2	NILNPFFPLL	1
SILSPFLPLL(vrt11)	921	NILTPFIPLL	2	SIWSPFIPLL	1
NILSPFMPLL(vrt12)	874	SIVRPFLPLL	2	SIVKPFLPLL	1
NILNPFLPLL(vrt13)	491	SNLSPFIPLL	2	NILNPFLPQL	1
SILSPFIPLL(vrt14)	158	STLSPYLPLF	2	HILNPFLPLL	1
SIVSPFIPLL(vrt0)	151	NILSPFIPLF	2	SILSPFIPVL	1
NILNPFIPLL(vrt16)	63	NIVSPFLPLL	2	TTLSPFIPLL	1
SIVRPFIPLL	59	SILSPLLPLL	2	NILSPFMLLL	1
RILSPFLPLL	51	IILSPFLPLL	2	NTLRPFLPLL	1
STLSPFLPLL	48	DILSPFMPLL	2	NILSPFLPLV	1
TILSPFLPLL	32	RTLSPFLPLL	2	NILSPFLPTL	1
NTLSPFMPLL	28	SILSHFIPLL	2	NILSPFLQLL	1
NTLSPFLPLL	24	SILSPFSPLL	2	SNLSPFLPLL	1
NILNPFMPLL	24	NIVKPFLPLL	2	SIVKPFIPLL	1
NILKPFLPLL	20	NILTPFMPLL	1	NILSSFLPLL	1
NILRPFLPLL	16	SIVNPFIPLL	1	NILNPFTPLL	1
SILRPFLPLL	13	NIVRPFLPLL	1	NIMNPFMPLL	1
NTLSPFIPLL	12	NILNLFIPLL	1	RILSPFSPLL	1
NILSPFLPLF	8	SIGSPFIPLL	1	STLRPFIPLL	1
NILKPFIPLL	8	RISSPFLPLL	1	NIVRPFMPLL	1
TILSPFMPLL	8	TILNPFLPLL	1	NILTLFIPLL	1
NTLNPFLPLL	8	RIVSPFIPLL	1	RFLSPFLPLL	1
SILNPFLPLL	7	NILSPFMPVL	1	NILNSFLPLL	1
NIVSPFIPLL	7	NTLRPFLQLL	1	SILTPFIPLL	1
NILSPFFPLL	6	STVSPFIPLL	1	TIWSPLLPLL	1
NILRPFIPLL	6	STLSPFLPLS	1	RTLSPFILLF	1
NILSPFTPLL	6	NILSPFSPLL	1	NILNTFLPLL	1
SILRPFIPLL	6	SILSPFLALL	1	NNLNPFLPLL	1
SILSPFLLLL	5	HTLSPFLPLL	1	DILSPFLPLL	1
SILSPFLPLF	5	SILSLFIPLL	1	NILSHFLPLF	1
RILSPFIPLL	5	TILKPFLPLL	1	STLSPFLTLL	1
NILSLFIPLL	5	NILRPFTPLL	1	NILSPFITLL	1
RILSPFLLLL	5	RILRPFLPLL	1	TILSPYLPLL	1
NIVNPFLPLL	5	NILSPFISLL	1	STVKPFIPLL	1

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NILTPFLPLL	5	NILSPFMPLS	1	SISRPFIPLL	1
NILSPFLPLS	5	NILSHFLPLL	1	STVSPFILLL	1
NILGPFLPLL	5	SILSPFILLL	1	NILSPFIPLY	1
PILSPFLPLL	4	TIVSPFIPLL	1	NTLKPFIPLL	1
HILSPFLPLL	4	NILNPLIPLL	1	SILSPFLPML	1
TILSPFIPLL	4	NIASPFLPLL	1	NIWNPFLHLS	1
SIVSPFLPLL	4	NIFSPFIPLL	1	NILSPCMPLL	1
STLSPFIPLL	4	STLTPFLPLL	1	NILSPFTLLL	1
NISSPFLPLL	4	SILSPYILLL	1	NIWSPFMPLL	1
SILSPFMPLL	3	STLRPFLPLL	1	NTLTPFMPLL	1
SILTPFLPLL	3	NILSPFMQLL	1	STVSPFLPLL	1
NILSPFMSLL	3	NILSRFIPLL	1	RTLSPFLLLF	1
SILSPYLPLL	3	NILKHFMPLL	1	TTLSPFTPLL	1
NIWSPFLPLL	3	SILSHFLPLL	1	CILSPFLPLL	1
NISSPFIPLL	3	NILSPFLPPL	1	NILSPFIPLI	1
SILNPFIPLL	3	HIFSPFLPLL	1	SIWSPFLPLL	1
NILNPFLPLF	3	NILSPFIQLL	1	SILMPFLPLL	1
SILSRFLPLL	3	NILIPFLPLL	1	SIMSPVVPLL	1
NIVRPFIPLL	3	TTLRPFLPLL	1	HILSPCTPLL	1
NILRPFMPLL	3	NILSLFMPLL	1	NILSPYMPLL	1
TTLSPFLPLL	3	NIWSRFIPLL	1	NILSPSLPLL	1
NIVKPFIPLL	3	DILNPFLPLL	1	NILSSFMPLL	1
NTLKPFLPLL	3	NILNPFMPPL	1	NILSPFLPRL	1
NTLTPFIPLL	3	SIVRHFIPLL	1	NILNPYIQLL	1
NILSHFIPLL	2	NIMSPFLPLL	1	NTLNPFIPLL	1
STLSPFLLLL	2	NILSPFMPLF	1	SILNHFLPLL	1
NILSPFILLL	2	SILSPFIPLF	1	NTLSPFIQLL	1
NILSRFLPLL	2	TTLKPFLPLL	1		
NILSPFIPLS	2	SILSPFLTLL	1		

Supplementary Table S2. pHLA used for testing the specificity of TCR0 (WT) and TCR15[a]

HLA	Peptide	Derived from	TCR0 binding	TCR15 binding
A0201	ILSPFLPLL	HBs	3.4μM	0.46μM
A0201	SLLMWITQC	NY-ESO-1	NB	NB
A0201	VLDFAPPGA	WT1	NB	NB
A0201	LLMPLLSVI	MAGE-B4	NB	NB
A0201	AASDNVFSTV	SAGE1	NB	NB
A0201	LLMPLLGVI	MAGE-B2	NB	NB
A0201	GIYDGILHSI	MAGEB6	NB	NB
A0201	FIWRAISI	CX048	NB	NB
A0201	RLTEVIASII	TERT	NB	NB

A0201	LMSVYVVEL	TERT	NB	NB
A0201	SVYDFFVWL	TYRP2	NB	NB
A0201	GLYDGMEHL	MAGEA10	NB	NB
A0201	KVTDLVQFL	MAGEA10	NB	NB
A0201	LMSVYVVELL	TERT	NB	NB
A0201	YTWDFGDSSGTL	PMEL	NB	NB
A0201	ILTIRLTAA	CTG1B	NB	NB
A0201	ALLPSLSHC	K9MRS9	NB	NB
A0201	FLNGTGGQTHL	TYRP1	NB	NB
A1101	SVFGEPWKLITK	MAGE-B2	NB	NB
A2401	LYATVTQNV	SAGE1	NB	NB

a. Shown are the biochemical affinities, as determined by ProteOn analysis. NB, none binding.

Supplementary Table S3.1 vrt1（ILSPFLPLL）and vrt0 (SIVSPFIPLL) alanine scanning peptides

vrt1	**ILSPFLPLL**	**vrt0**	**SIVSPFIPLL**
		vrt0-1	**A**IVSPFIPLL
vrt1-1	**A**LSPFLPLL	vrt0-2	S**A**VSPFIPLL
vrt1-2	I**A**SPFLPLL	vrt0-3	SI**A**SPFIPLL
vrt1-3	IL**A**PFLPLL	vrt0-4	SIV**A**PFIPLL
vrt1-4	ILS**A**FLPLL	vrt0-5	SIVS**A**FIPLL
vrt1-5	ILSP**A**LPLL	vrt0-6	SIVSP**A**IPLL
vrt1-6	ILSPF**A**PLL	vrt0-7	SIVSPF**A**PLL
vrt1-7	ILSPFL**A**LL	vrt0-8	SIVSPFI**A**LL
vrt1-8	ILSPFLP**A**L	vrt0-9	SIVSPFIP**A**L
vrt1-9	ILSPFLPL**A**	vrt0-10	SIVSPFIPL**A**

Supplementary Table S3.2 vrt1（ILSPFLPLL）and vrt0 (SIVSPFIPLL) potential cross-reactive human peptides

vrt1: ILSPFLPLL				**vrt0: SIVSPFIPLL**	
2 mismatch aa		*3 mismatch aa fix F5 & L8*		*2 mismatch and 3 mismatch aa*	
vrt1-A	**F**LSP**L**LPLL	vrt1-L16	**Q**L**T**PFL**I**LL	vrt0-A	**A**IVSPFI**F**LL
3 mismatch aa fix F5 & L8		vrt1-L17	IL**QR**FLPL**I**	vrt0-B	SIVS**CA**I**I**LL
vrt1-L1	**A**L**AS**FLPLL	vrt1-L18	IL**YL**FL**A**LL	*4 mismatch aa & fix F6 & L9*	
vrt1-L2	I**IL**PFL**I**LL	vrt1-L19	**LGC**FLPLL	vrt0-L1	**C**IV**FG**FI**I**LL
vrt1-L3	**L**LS**G**FVPLL	vrt1-L20	IL**LG**FL**G**LL	vrt0-L2	S**M**VS**G**F**T**PL**I**

vrt1-L4	IL**MN**FL**Y**LL	vrt1-L21	IL**T**PF**N**PL**R**	vrt0-L3	S**M**VS**G**F**G**PL**I**
vrt1-L5	I**V**SPF**IF**LL	vrt1-L22	IL**KG**F**D**PLL	vrt0-L4	S**L**V**GR**FI**H**LL
vrt1-L6	**FIV**PFLPLL	vrt1-L23	IL**VV**FL**L**LL	vrt0-L5	S**C**VS**G**F**FI**LL
vrt1-L7	IL**IN**FL**D**LL	vrt1-L24	**Q**LS**G**FL**E**LL	vrt0-L6	**KM**VS**G**FIPL**K**
vrt1-L8	**Q**LS**E**F**D**PLL	vrt1-L25	**T**L**GF**FLPLL	vrt0-L7	S**M**VS**G**F**A**PL**I**
vrt1-L9	**M**LS**Y**F**K**PLL	vrt1-L26	ILS**V**FL**Y**L**F**	vrt0-L8	**A**IV**LL**FI**M**LL
vrt1-L10	**S**LS**C**FL**L**LL	vrt1-L27	IL**CI**FL**G**LL	vrt0-L9	S**YMV**PFIPL**Y**
vrt1-L11	ILSPF**WG**L**I**	vrt1-L28	**S**L**Y**PFL**C**LL	vrt0-L10	**R**I**R**S**I**FI**W**LL
vrt1-L12	**L**LS**V**FL**H**LL	vrt1-L29	**M**L**E**PFL**I**LL		
vrt1-L13	**V**L**IY**FLPLL	vrt1-L30	**S**L**EM**FLPLL		
vrt1-L14	G**L**F**F**FL**V**LL	vrt1-L31	**T**L**RH**FLPLL		
vrt1-L15	IL**MC**FL**D**LL	vrt1-L32	**M**L**A**PFL**L**LL		

The mismatches are in bold.

Supplementary Table S4. The HLA genotyping information of PBMC from health donors.

No.	HLA-A genotype	No.	HLA-A genotype
#1	HLA-A*11:01:01 / A*33:03:01:01	#16	HLA-A*02:06 / A*24:02:01G
#2	HLA-A*11:01:01 / A*11:01:01	#17	HLA-A*2:01:01 / A*32:01:01:01
#3	HLA-A*2:01:01 / A*02:05:01:01	#18	HLA-A*02:06:01 / A*33:03:01:01
#4	HLA-A*02:01:00 / A*68:02:00	#19	HLA-A*02:01:01 / A*02:07:01
#5	HLA-A*11:01:01 / A*33:03:01:01	#20	HLA-A*11:01:01 / A*33:03:01:01
#6	HLA-A*02:01:01 / A*32:01:01:01	#21	HLA-A*11:01:01 / A*24:02:01G
#7	HLA-A*02:07:01 / A*02:07:01	#22	HLA-A*02:01:01 / A*30:01:01:01
#8	HLA-A*11:01:01 / A*11:263	#23	HLA-A*11:01:01 / A*24:02:01G
#9	HLA-A*02:03:01 / A*68:01:02	#24	HLA-A*11:01:01 / A*24:02:01G
#10	HLA-A*01:01:01:01 / A*11:01:01	#25	HLA-A*02:07:01 / A*11:01:01
#11	HLA-A*24:02:01G / A*33:03:01:01	#26	HLA-A*02:03:01 / A*02:07:01
#12	HLA-A*02:03:01 / A*24:02:01G	#27	HLA-A*11:01:01 / A*24:02:01G
#13	HLA-A*11:01:01 / A*11:263	#28	HLA-A*02:01 / A*24:02:01G
#14	HLA-A*01:01:01:01 / A*24:03:01:01	#29	HLA-A*24:21:01G / A*31:01:02:01
#15	HLA-A*02:07:01 / A*03:01:01:01	#30	HLA-A*02:01:01 / A*02:07:01

Supplementary Table S5. Human normal primary cells (Sciencell) used for verifying the specificity of TCR15-T.

Cell line	Abbreviation	Culture Medium	HLA-A genotype

Human Bronchial Smooth Muscle Cells	HBSMC	SMCM (Smooth Muscle Cell Medium)	HBSMC-A	A*11:01:01:01 A*30:01:01
			HBSMC-B	A*11:01:01:01 A*30:01:01
Human Aortic Smooth Muscle Cells	HASMC	SMCM (Smooth Muscle Cell Medium)	HASMC-A	A*11:01:01:01 A*24:02:01:01
			HASMC-B	A*02:01:01:01 A*03:01:01:01
Human Meningeal Cells	HMC	MCM (Meningeal Cell Medium)	HMC-A	A*02:01:01:01 A*02:01:01:01
			HMC-B	ND
Human Renal Mesangial Cells	HRMC	MCM (Meningeal Cell Medium)	HRMC-A	A*02:01:01:01 A*30:01:01:01
			HRMC-B	A*01:01:01:01 A*11:01:01:01
Human Gastric Smooth Muscle Cells	HGSMC	SMCM (Smooth Muscle Cell Medium)	HGSMC-A	A*23:01:01 A*80:01:01:01
			HGSMC-B	A*02:01:01:01 A*32:01:01
Human Renal Epithelial Cells	HREpiC	EpiCM (Epithelial Cell Medium)	HREpiC-A	A*02:01:01:01 A*32:01:01
			HREpiC-B	A*01:01:01:01 A*29:02:01:01

ND, none detected.

Supplementary Table S6. The EC_{50} of the IFN-γ release of vrt1-HBs371 pulsed T2 cells incubated with TCR-T.

TCR No.	EC_{50} of IFN-y release (M)	Fold TCR0-T EC_{50}
TCR0-T	6.0E-09	1.0
TCR14-T	1.6E-10	38.0
TCR15-T	2.5E-10	24.0
TCR17-T	8.2E-11	73.1
TCR19-T	1.1E-11	527.8

Supplementary Table S7. The EC_{50} of the IFN-γ release and LDH release of HBs370 or HBs371 variants pulsed T2 cells incubated with TCR-T.

EC_{50} of peptide pulsed T2	EC_{50} of IFN-y release (M)		EC_{50} of LDH release (M)	
	TCR0-T	TCR15-T	TCR0-T	TCR15-T
vrt1	7.4E-09	2.0E-10	3.7E-09	2.9E-10
vrt2	6.7E-10	9.7E-11	4.7E-11	4.4E-12
vrt3	9.3E-10	2.9E-10	2.0E-10	4.4E-11
vrt4	0	0	0	0
vrt5	1.2E-10	6.4E-11	4.8E-11	1.9E-11
vrt6	~8.0E-06	4.1E-09	-	1.3E-10
vrt7	0	0	0	0
vrt8	0	0	0	0
vrt9	1.1E-07	5.1E-09	4.6E-08	1.9E-09
vrt10	2.3E-09	3.6E-10	6.8E-10	5.6E-11
vrt11	1.3E-08	1.3E-09	8.6E-09	9.9E-11
vrt12	1.3E-08	2.0E-09	8.3E-10	5.7E-11
vrt13	0	0	0	0
vrt14	5.5E-10	8.3E-11	1.3E-10	1.5E-11
vrt0	7.8E-10	3.4E-10	4.3E-11	1.2E-11
vrt16	0	0	0	0

Supplementary Table S8. Percentage of CD3 and CD8 positive T-cells in all cells of the tumor.

All pictures were taken under 400×, scale bar, 90μm.

PBS

	CD3 of PBS						CD8 of PBS					
Piture	P1	P2	P3	P4	P5	P6	P1	P2	P3	P4	P5	P6
Positive cells	0	0	0	0	0	0	0	0	0	0	0	0
Total cells	1569	1760	1133	1351	1222	1478	1511	1691	1695	1372	1419	1689
Positive rate%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Average%	0.0						0.0					

TCR-A6-T (3.0×10^7)

	CD3 of TCR-A6-T (3.0×10^7)						CD8 of TCR-A6-T (3.0×10^7)					
Piture	P1	P2	P3	P4	P5	P6	P1	P2	P3	P4	P5	P6
Positive cells	21	26	14	15	23	15	0	0	0	0	0	0
Total cells	1944	2440	2511	2604	2464	2461	2608	1811	1740	2116	2372	2420
Positive rate%	1.1	1.1	0.6	0.6	0.9	0.6	0.0	0.0	0.0	0.0	0.0	0.0
Average%	0.8						0.0					

TCR0-T (3.0×10^7)

	CD3 of TCR0-T (3.0×10^7)						CD8 of TCR0-T (3.0×10^7)					
Piture	P1	P2	P3	P4	P5	P6	P1	P2	P3	P4	P5	P6
Positive cells	188	248	175	187	190	151	88	57	62	81	5	83
Total cells	1467	1694	1588	1483	1650	1546	1388	1686	1597	1428	1728	1576
Positive rate%	12.8	14.6	11.0	12.6	11.5	9.8	6.3	3.4	3.9	5.7	0.3	5.3
Average%	12.1						4.1					

TCR15-T (3.3×10^6)

	CD3 of TCR15-T (3.3×10^6)						CD8 of TCR15-T (3.3×10^6)					
Piture	P1	P2	P3	P4	P5	P6	P1	P2	P3	P4	P5	P6
Positive cells	449	528	606	352	582	271	264	274	393	425	280	112
Total cells	1704	1632	1841	1634	2089	1920	2057	2123	1449	1686	1802	1504
Positive rate%	26.3	32.4	32.9	21.5	27.9	14.1	12.8	12.9	27.1	25.2	15.5	7.4
Average%	25.9						16.8					

TCR15-T (1.0×10^7)

	CD3 of TCR15-T (1.0×10^7)						CD8 of TCR15-T(1.0×10^7)					
Piture	P1	P2	P3	P4	P5	P6	P1	P2	P3	P4	P5	P6
Positive cells	1561	1627	1158	761	1274	510	1192	1121	1055	800	675	823
Total cells	2278	2295	2222	1759	1742	1460	2570	2525	2462	2435	2526	2131
Positive rate%	68.5	70.9	52.1	43.3	73.1	34.9	46.4	44.4	42.9	32.9	26.7	38.6
Average%	57.1						38.6					