

Supplementary Methods

Peptide specificity profile using X-scan assay

To investigate TCR specificity using TCR T cells, a peptide library targeting the KRAS^{G12D} peptide sequence (VVVGADGVGK) was designed and synthesized by Genscript (Supplementary Table 4). Each library member (n = 200) was individually presented to HLA-A*11:01⁺ K562 cells at a final concentration of 10 μ M. These cells were then co-cultured with TCR-transduced T cells. Following overnight incubation, the level of IFN- γ secretion was quantified via ELISA. Background activation levels, as determined from DMSO-treated controls, were subtracted from all measured responses, which were then normalized with the DMSO group as 0% and the KRAS^{G12D} group as 100%. A threshold of 20% reactivity relative to the KRAS^{G12D} induced response was as a cutoff to define a TCR recognition motif, facilitating the identification of allowable amino acids at each position within the peptide sequence. This TCR recognition motif was subsequently utilized to scan the UniProtKB human proteome database using the ScanProsite tool, searching for homologous peptide sequences potentially cross-recognized by the TCR. NetMHCpan-4.1 was utilized to filter out peptides capable of binding to HLA, which were then utilized for validation in subsequent minigene experiments.

Each minigene encodes a 10mer homologous peptide, flanked by 10 native amino acids from the corresponding protein. A total of 10 such minigenes were strung to form a minigene-cluster (MC), which was then fused with NGFR gene (Uniprot ID P08138, residues 29-275) through the P2A linker to generate a bicistronic MC-NGFR construct. The codon-optimized MC-NGFR constructs were cloned into the pWPXL vector for production of lentiviral particles. HLA-A*11:01⁺ K562 cells were transduced with these lentiviral particles to express the minigene-cluster, with the NGFR protein serving as a marker for quality control of viral transduction efficiency. Co-culturing TCR T cells with these engineered K562 cells, the expression of the CD137 was analyzed via flow cytometry after 24 hours. A P64 minigene, encoding an HLA-A*11:01-restricted epitope from the COVID-19 N protein (KTFPPTEPK) and known to activate P64 TCR, was included in each minigene-cluster as a positive control. This setup ensures the proper intracellular processing and presentation of minigenes.

To evaluate TCR specificity using TCR Jurkat cells, each library component was individually applied to HLA-A*11:01⁺ K562 cells at a 10 μ M concentration, followed by co-culturing with

TCR Jurkat cells. After 6 hours, Cells were stained with APC-anti-human CD69 antibody for 10 minutes at 4°C in the dark. After washing twice with PBS, flow cytometry was performed to analyze the expression of the CD69. To compare data across different TCRs, results were normalized with the DMSO group as 0% activation and the KRAS^{G12D} group as 100% activation.

The design and Screening of TCR library

The workflow includes a three-stage process.

Stage-I: Design of the TCR Library. Based on structural data from the TCR JDI, amino acid residues within the CDR region critical for the interaction with pHLA were identified. For the construction of mutation libraries, two regions of the CDR were selected. The first library, named TCR1 Lib1, encompassed a saturation mutation library targeting four consecutive sites (G111 to N113) proximal to the peptide interaction within the CDR-3B. The second library, TCR1 Lib2, consisted of a saturation mutation library at three consecutive sites (D29 to T36) nearest to the HLA interaction within CDR-1A. The DNA for the two TCR libraries was synthesized and subsequently cloned into the pWPXL plasmid by GenScript. Extraction of TCR library plasmids was also prepared by GenScript. The IMGT numbering scheme was employed to describe the positions of amino acids within the TCR (Supplementary Table 7), facilitating direct comparisons across different T cell receptors.

Stage-II: TCR Library Display by Jurkat Cells. Recombinant lentiviruses encoding the TCR library were generated through the transfection of HEK293T cells with the TCR library plasmids and packaging plasmids (psPAX2 and pMD2.G). Viral titer was determined to achieve an approximate 10% positive expression of mouse TCR in CD8⁺ Jurkat cells, ensuring each cell expressed only one copy of TCR variant. The saturation mutation library across four sites contained 1.6E5 TCR variants. To prepare a TCR library Jurkat cells covering 100X the library capacity, an initial cell count of 1.6E8 CD8⁺ Jurkat cells was utilized for lentiviruses infection. 24 hours later post-transfection, TCR library Jurkat cells were harvested and resuspended at a concentration of 2E5/ml in G-Rex 100 (Wilson Wolf). Two days post-transfection, 50% of the culture medium volume was replaced with fresh medium. Three days post-transfection, TCR library Jurkat cells were harvested for downstream screening procedure.

Stage-III: Screening of the TCR Library. The screening of the TCR library was performed over five rounds to ensure the enrichment and selection of functional TCR clones with specificity for

the KRAS^{G12D} mutation. Round 01: Enrichment for TCR Expression. 2.0E7 TCR library Jurkat cells were stained with APC-anti-mouse TCR β -chain antibody. Utilizing the EasySep™ APC Positive Selection Kit (STEMCELL Technologies), TCR clones exhibiting normal TCR expression on the cell membrane were enriched following the manufacturer's protocol. Round 02: Specificity for KRAS^{G12D} Tetramer. 2.0E7 TCR library Jurkat cells was stained with both the APC-anti-mouse TCR β chain antibody and PE-KRAS^{G12D} Tetramer. mTCR⁺ KRAS^{G12D} Tet⁺ TCR clones were sorted. Round 03 and Round 04: Enrichment for Functional clones. HLA-A*11:01⁺ K562 cells were pulsed with 10 μ M of the KRAS^{G12D} peptide and then co-cultured with the TCR library Jurkat cells. Six hours post-co-culture, the cells were stained with PE-anti-mouse TCR β chain antibody, APC-anti-human CD69 antibody and BV421-anti-human CD62L antibody. This panel could distinguish between specific activated (CD62L⁻ CD69⁺) and non-specific activated (CD62L⁺ CD69⁺) cells. The top 10% of CD62L⁻ CD69⁺ cells displaying the highest MFI of CD69 were sorted. Each enrichment process required 10 to 14 days to propagate sufficient cells for subsequent round. Round 05: Isolation of Specific Clones. clones were stained with PE-SMC1A₂₉₋₃₈ Tetramer and APC-KRAS^{G12D} Tetramer, KRAS^{G12D} Tetramer⁺ SMC1A Tetramer⁻ TCR clones were sorted into a 96-well PCR plate via single-cell FACS. The TCR α and TCR β chain genes of the single cell were amplified under previously described conditions, with specific primers (Supplementary Table 12). The TCR repertoire of these clones was then analyzed using the IMGT/HighV-QUEST tool.

Supplementary Figure Legend

Supplementary Fig. 1 Flow cytometry gating strategy in experimental analysis. Gating strategy of single cell sorting for KRAS^{G12D} specific T cells.

Supplementary Fig. 2 Design and expression analysis of minigene-cluster. a. Schematic representation of the minigene-cluster construct is shown. The complete expression framework includes a minigene-cluster, a 2A element, and NGFR. The minigene-cluster comprises 10 minigenes, each encoding a 10-mer homologous peptide flanked by 10 native amino acids from the corresponding protein. Within each minigene-cluster, there is a SARS-CoV-2 NP₃₆₁₋₃₆₉ minigene, encoding the NP₃₆₁₋₃₆₉ peptide from the SARS-CoV-2 N protein known to activate the

P64 TCR. The SARS-CoV-2 NP₃₆₁₋₃₆₉ minigene is utilized to ensure the proper intracellular processing and presentation of MC. NGFR serves as a marker to monitor the expression efficiency of the minigene-cluster construct within cells. b. HLA-A*11:01⁺ K562 cells expressing the MC construct were enriched and then stained with an anti-NGFR antibody to assess the expression efficiency of MC. c. The SMC1A₂₉₋₃₈ peptide exhibits sequence conservation across multiple mammalian species. Panel b represent data from two independent experiments with n = 2. NGFR, nerve growth factor receptor.

Supplementary Fig. 3 Peptide specificity similarities between TCR1 with JDI TCR. TCR Jurkat cells were co-cultured with HLA-A*11:01⁺ K562 cells that were exogenously loaded with various concentrations of the KRAS^{G12D} (a) or SMC1A₂₉₋₃₈ peptide (b). After 6 hours, the expression of CD69 was assessed. c. The reactivity of TCR1 Jurkat cells and TCR1 T cells towards KRAS^{G12D} peptide library were compared. Each point on the graph represents an individual peptide, with the x-axis indicating the reactivity of TCR1 T cells and the y-axis showing the reactivity of TCR1 Jurkat cells to the respective peptides. To facilitate comparison across different detection methods, the percentages of CD69 expression and the concentration of IFN- γ release were normalized, setting the reactivity of the DMSO control group as 0% activation and the reactivity to the KRAS^{G12D} peptide as 100% activation. Peptide specificity profiling of TCR1 Jurkat (d), JDI TCR Jurkat (e) and TIL4373 TCR (f) were conducted using an X-scan assay. To compare data across different TCRs, the result of CD69⁺ percent was normalized with the DMSO group set as 0% activation and the KRAS^{G12D} group set as 100% activation. g. The reactivity of TCR1 and JDI TCR to the KRAS^{G12D} peptide library were compared. Panel a, b and c represents data from two independent experiments with n = 2. Panel d, e and f represent data from two independent experiments with n = 1.

Supplementary Fig. 4 Structural similarities between TCR1 with JDI TCR. a. The AA sequences of the CDR regions from TCR1 and JDI TCR are displayed. The sequences in the CDR-1A, CDR-2A, and CDR-3B regions are identical between the two TCRs (in bold black). b. A top view of the JDI TCR/pHLA complex is presented. Regions of JDI TCR within 5 Å of the KRAS^{G12D} pHLA include 1 α (colored in orange), 3 α (colored in yellow), and 3 β (colored in

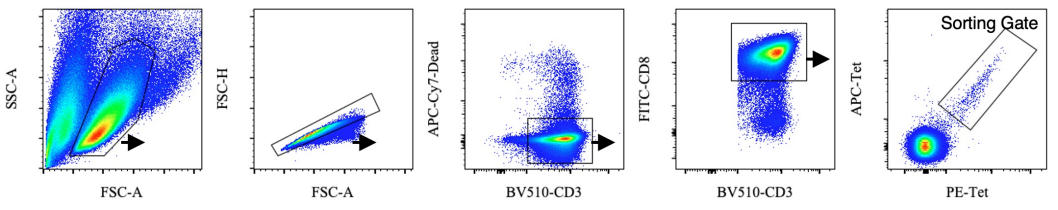
green). c. A detailed residue interactions between JDI TCR and the KRAS^{G12D} peptide-HLA is shown. Hydrogen bonds are marked with black dashed lines, and the AA numbers forming Hydrogen bonds are displayed. d. The residue T30 in the CDR-1A region of JDI TCR forms a hydrogen bond with HLA. e. Mutation of the T30 AA site in TCR1 resulted in changes in binding affinity and functional avidity to KRAS^{G12D} pHLA. Panel e represents data from two independent experiments with n = 2. The IMGT numbering scheme (Supplementary Table 7) was used to describe AA positions within the TCR. 1 α , TCR CDR-1A. 3 α , TCR CDR-3A. 3 β , TCR CDR-3B. AA, amino acid.

Supplementary Fig. 5 Structure-guided designing and functional screening of TCR1 libraries. Two regions of JDI TCR interacting with pHLA were targeted to construct TCR libraries. TCR1 Lib1 (a) was established as a saturation mutation library encompassing four sequential sites proximal to the peptide interaction region (CDR-3B: G111 to N113). TCR1 Lib2 (b) included a saturation mutation library covering three sequential sites nearest to the HLA interaction region (CDR-1A: D29 to T36). c. The five rounds of TCR screening were employed to enrich for functional TCR clones. Both libraries underwent the same selection strategy, with the left side illustrating the screening process for TCR1 Lib1 and the right side for TCR1 Lib2. During Round-1, TCR library Jurkat cells were stained with an anti-mouse antibody to enrich clones displaying normal TCR expression on the cell membrane. In Round-2, cells stained with the KRAS^{G12D} Tetramer enabled the enrichment of clones that showed binding activity to the KRAS^{G12D} Tetramer. For Rounds-03 and 04, cells co-cultured with HLA-A*11:01⁺ K562 cells loaded with 10 μ M KRAS^{G12D} for 6 hours and then were stained with anti-CD69 and anti-CD62L antibodies, allowing the sorting of peptide-specifically activated TCR clones (CD62L⁻ CD69⁺). In Round-5, cells were stained with SMC1A₂₉₋₃₈ Tetramer and KRAS^{G12D} Tetramer to eliminate clones capable of cross-recognizing SMC1A₂₉₋₃₈, sorting those binding only to the KRAS^{G12D} Tetramer for TCR cloning and sequencing. Following five rounds of TCR screening, TCR clone sequences were obtained through single-cell TCR cloning and the frequency of TCR clones were analyzed in TCR1 Lib1 (d) and TCR1 Lib2 (e). TCRs sharing the same AAs in CDR-3B in TCR1 Lib1 were classified as a TCR clone and TCRs sharing the same AAs in CDR-1A in TCR1 Lib2 were classified as a TCR clone, with clones appearing not less than twice were used to analyze the

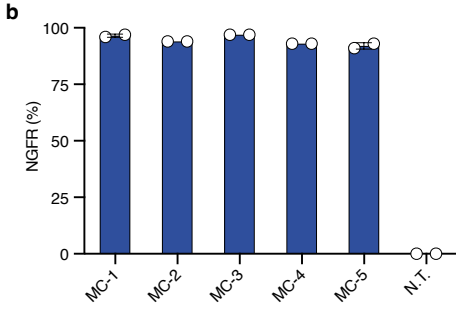
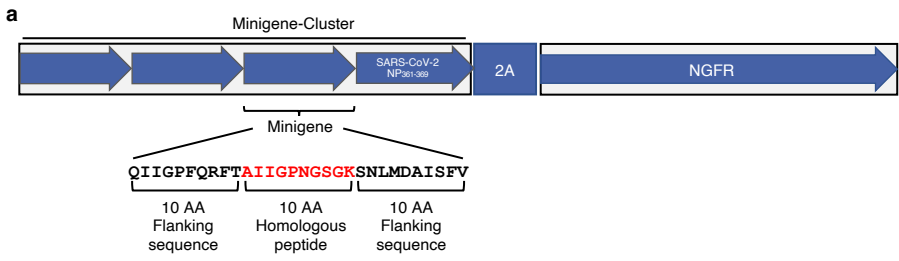
frequency within the TCR library. WebLogo shows enriched peptide sequences from the fifth round of selection, where the size of each AA letter reflects its abundance at specific positions within the CDR region. The libraries screening process was conducted once, with Panel c representing data from a single experiment. The IMGT numbering scheme was used to describe AA positions within the TCR.

Supplementary Fig. 6 Comparison of peptide specificity among three KRAS^{G12D} specific TCR clones. Comparison of TCR1, TCR1a1, and TCR1a7 reactivity to the KRAS^{G12D} peptide library, TCR1a1 and TCR1a exhibited enhanced discrimination capability for the 7th amino acid.

Supplementary Fig. 7 Impact of endogenous TCR knockout on TCR1a7 peptide specificity. a. TCR T cells were stained with anti-mouse TCR antibodies to evaluate the expression efficiency of exogenous TCRs, with anti-human TCR antibodies to assess the efficiency of human TCR knockout, and with KRAS^{G12D} Tetramer to assess the binding capacity to KRAS^{G12D}-HLA complex. b. Results from panel a were quantified (n=3). c. hTCR-KO TCR1a7 T cells were co-cultured with HLA-A*11:01⁺ COS-7 cells endogenously expressing the full-length SMC1A gene. After 24 hours, CD137 expression of TCR T cells was analyzed, with E7 TCR serving as the negative control. d. Comparison of the reactivity of TCR1 and TCR1a7 towards KRAS^{G12D} peptide library belonging to 7th amino acid of the epitope, normalized data are displayed as a heatmap. e. Homologous peptides of TCR recognition (binders) were categorized into those with low binding affinity to HLA-A*11:01 (weak binders) and those with high binding affinity (high binders). Significance was determined using a two-sided Student's t-test (**P < 0.01). Data are presented as mean ± SD. Panel a and c represent data from two independent experiments with n = 3. Panel d represents data from two independent experiments with n = 2.



Supplementary Fig. 1 Flow cytometry gating strategy in experimental analysis



c

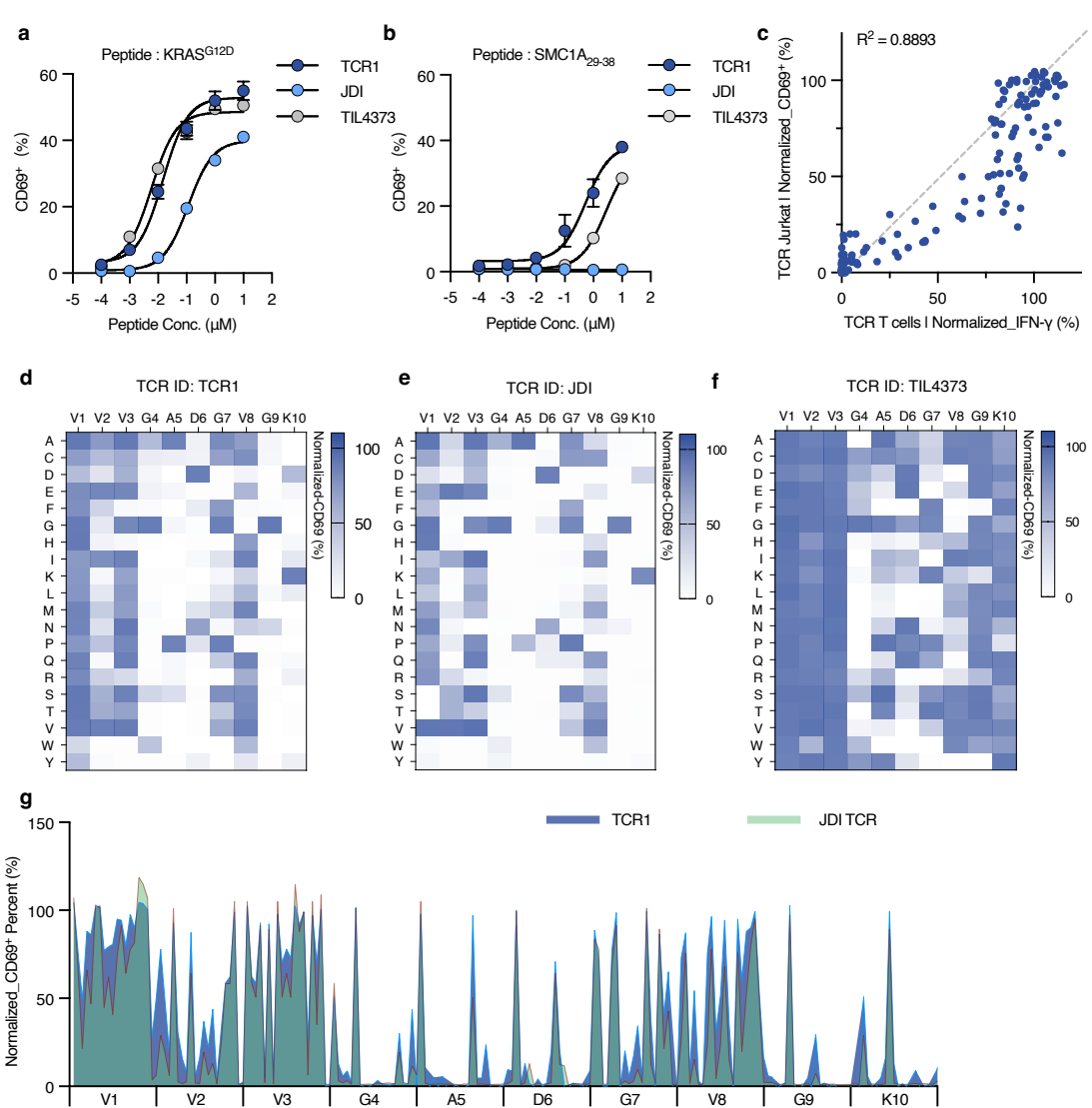
KRAS^{G12D} : V V V G A D G V G K

SMC1A₂₉₋₃₈ : A I I G P N G S G K

SMC1A :

Human	FT A I I G P N G S G K S N L
Monkey	FT A I I G P N G S G K S N L
Rat	FT A I I G P N G S G K S N L
Mouse	FT A I I G P N G S G K S N L
Bovine	FT A I I G P N G S G K S N L
Pig	FT A I I G P N G S G K S N L

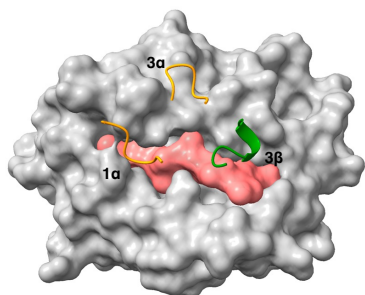
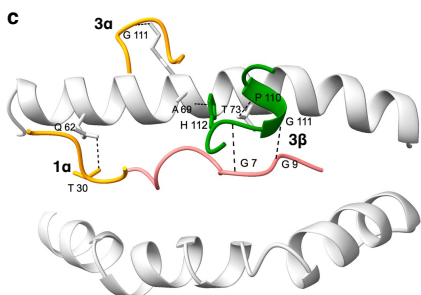
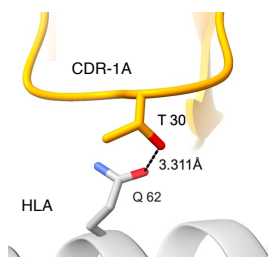
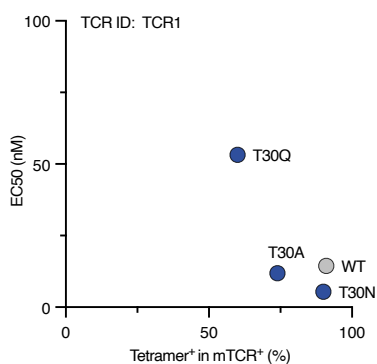
Supplementary Fig. 2 Design and expression analysis of minigene-cluster



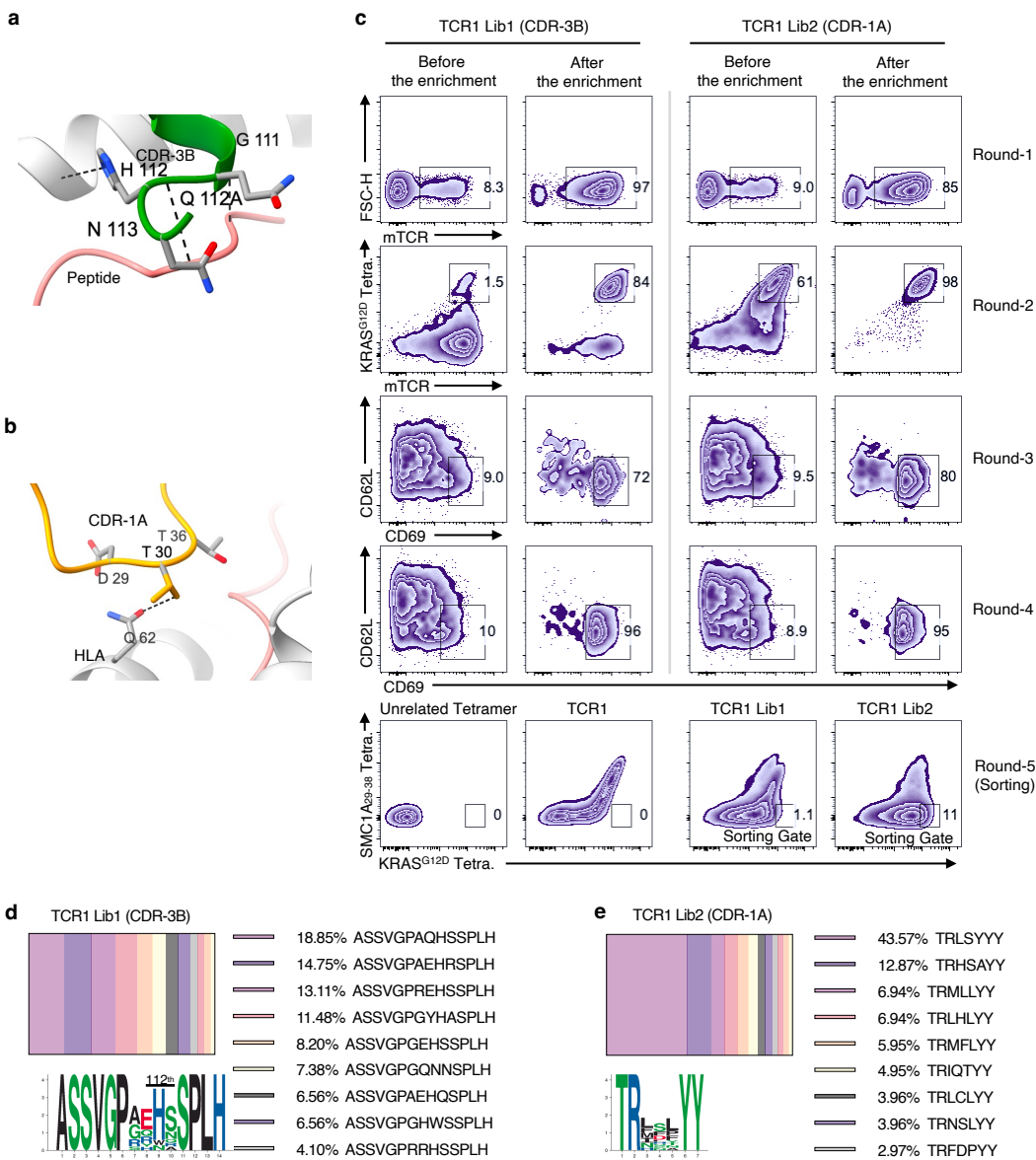
Supplementary Fig. 3 Peptide specificity similarities between TCR1 with JDI TCR

a

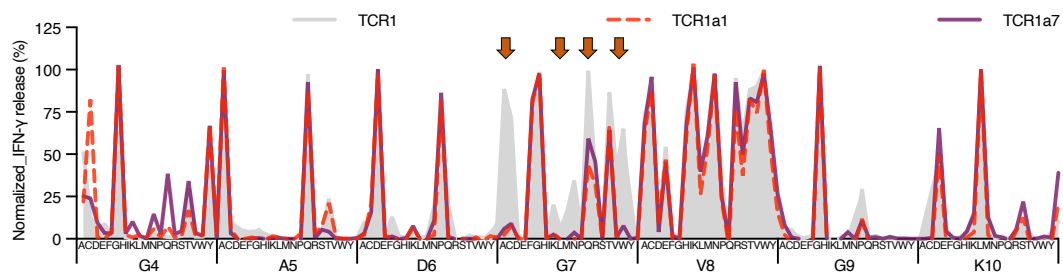
TCR ID	CDR-1A	CDR-2A	CDR-3A	CDR-1B	CDR-2B	CDR-3B
TCR1	TRDTTY	RNSFDEQN	ALSGPSTSGTYKYI	SGDLS	YYNGEE	ASSVGPQQNNSPLH
JDI TCR	TRDTTY	RNSFDEQN	ALSGPSGAGSYQLT	MNHEY	SVGEGT	ASSYGPQQHNSPLH

b**c****d****e**

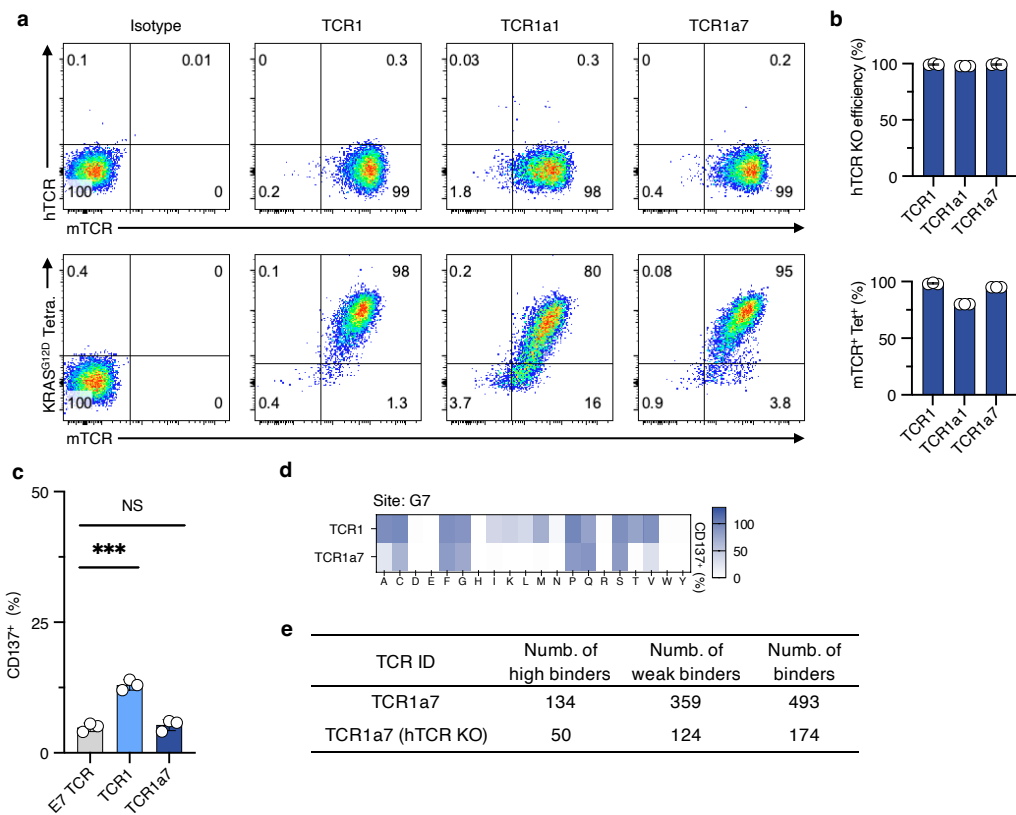
Supplementary Fig. 4 Structural similarities between TCR1 with JDI TCR



Supplementary Fig. 5 Structure-guided designing and functional screening of TCR1 libraries



Supplementary Fig. 6 Comparison of peptide specificity among three KRASG12D specific TCR clones



Supplementary Fig. 7 Impact of endogenous TCR knockout on TCR1a7 peptide specificity

List of Supplementary Tables :

ID	Title
Supplementary Table 1	List of peptides in the study
Supplementary Table 2	List of antibodies used in the flow cytometry
Supplementary Table 3	Sequences of HLA-A*11:01 restricted KRAS ^{G12D} specific TCRs
Supplementary Table 4	The KRAS G12D peptide library used for X-scan analysis
Supplementary Table 5	TCR recognition motifs
Supplementary Table 6	Homologous peptides and minigene-clusters for TCR1 T cells
Supplementary Table 7	The IMGT numbering scheme for TCR1's CDRs
Supplementary Table 8	The information of 24 TCR clones derived from TCR1 libraries
Supplementary Table 9	Functional evaluation process of 24 TCR clones from TCR1 libraries
Supplementary Table 10	Homologous peptides for TCR1a7 T cells
Supplementary Table 11	Homologous peptides and minigene-clusters for hTCR-KO TCR1a7 T cells
Supplementary Table 12	List of primers used for TCR cloning derived from TCR1 libraries

Supplementary Table 1. List of peptides in the study

Peptide ID	Peptide Name	HLA	Peptide sequence	Length	Antigen Type	Uniprot ID	Reference (PMID)	Note
1	KRAS ^{WT}	A0301	VVVGACGVGK	10	Self-antigen	P01116	35474673	wild type KRAS peptide
2	KRAS ^{G12D}	A0301	VVVGADGVGK	10	Neoantigen	P01116	35474673	KRAS ^{G12D} peptide
3	HPV16_E7	A0201	YMLDLQPET	9	Virus, HPV16	P03129	22566864	the epitope of E7 TCR
4	NP ₃₆₁₋₃₆₉	A1101	KTFPPTPEPK	9	Virus, SARS-CoV-2	P0DTC9	34222571	the epitope of P64 TCR
5	DNHD1	A1101	TVLGPNGVGK	10	Self-antigen	Q96M86	this article	10 homologous peptide of TCR1, corresponding to Minigene-cluster 1
6	CMA1A	A1101	MVMGPNTVGK	10	Self-antigen	Q96PU9	this article	
7	SEM3D	A1101	SGTASDFLGK	10	Self-antigen	O95025	this article	
8	ANK3	A1101	KSASPDAAGK	10	Self-antigen	Q12955	this article	
9	SE1L2	A1101	QRTSSNVINK	10	Self-antigen	Q5TEA6	this article	
10	PEX13	A1101	VPVAPDSIGK	10	Self-antigen	Q92968	this article	
11	APC	A1101	SVSSSDGYGK	10	Self-antigen	P25054	this article	
12	SMC1A ₂₉₋₃₈	A1101	AIIGPNGSGK	10	Self-antigen	Q14683	this article	
13	CSF1R	A1101	SCVASNVQGK	10	Self-antigen	P07333	this article	
14	FHDC1	A1101	SVGSSDPENK	10	Self-antigen	Q9C0D6	this article	

Supplementary Table 2. List of antibodies used in the flow cytometry

ID	Antibody Name	Supplier	Catalogue number	Final staining Concentration
1	BV510 anti-Human CD3 Antibody (Clone: SK7)	Biolegend	344828	1 µg/ml
2	FITC anti-human CD8a Antibody (Clone: HIT8a)	Biolegend	300906	1 µg/ml
3	BV510 anti-human CD8a Antibody (Clone: HIT8a)	Biolegend	300934	1 µg/ml
4	BV421 anti-human CD62L Antibody (Clone: DREG-56)	Biolegend	304828	1 µg/ml
5	APC anti-human CD69 Antibody (Clone: FN50)	Biolegend	310910	1 µg/ml
6	PE anti-human CD137 (Clone: 4B4-1)	Biolegend	309804	1 µg/ml
7	APC anti-human TCR α/β Antibody (Clone: IP26)	Biolegend	306718	1 µg/ml
8	PE anti-mouse TCR β chain Antibody (Clone: H57-597)	Biolegend	109208	1 µg/ml
9	APC anti-mouse TCR β chain Antibody (Clone: H57-597)	Biolegend	109212	1 µg/ml
10	PE anti-human CD271 (NGFR) Antibody (Clone: ME20.4)	Biolegend	345106	1 µg/ml

Supplementary Table 3. Sequences of HLA-A*11:01 restricted KRAS^{G12D} specific TCRs

ID	TCR Name	TRAV	TRAJ	TRBV	TRBJ	CDR-3A	CDR-3B	PMID
1	TCR1	TRAV19	TRAJ40	TRBV9	TRBJ1-6	ALSGPSTSGTYKYI	ASSVGPGQNNNSPLH	This article
2	TCR2	TRAV19	TRAJ33	TRBV6-1	TRBJ2-7	ALTSPDSNYQLI	ASRVNWAYEQY	This article
3	JDI TCR	TRAV19	TRAJ28	TRBV6-2	TRBJ1-6	ALSGPSGAGSYQLT	ASSYGPGQHNSPLH	36088370
4	TIL4373 TCR	TRAV23	TRAJ18	TRBV5-1	TRBJ2-1	AAEAGNHRGSTLGRLY	ASSLAAGGYFNEQF	34168045

Supplementary Table 4. The KRAS G12D peptide library used for X-scan analysis

ID	Peptide Name	Sequence
1	KS12D-1	AVVGADGVGK
2	KS12D-2	CVVGADGVGK
3	KS12D-3	DVVGADGVGK
4	KS12D-4	EVVGADGVGK
5	KS12D-5	FVVGADGVGK
6	KS12D-6	GVVGADGVGK
7	KS12D-7	HVVGADGVGK
8	KS12D-8	IVVGADGVGK
9	KS12D-9	KVVGADGVGK
10	KS12D-10	LVVGADGVGK
11	KS12D-11	MVVGADGVGK
12	KS12D-12	NVVGADGVGK
13	KS12D-13	PVVGADGVGK
14	KS12D-14	QVVGADGVGK
15	KS12D-15	RVVGADGVGK
16	KS12D-16	SVVGADGVGK
17	KS12D-17	TVVGADGVGK
18	KS12D-18	VVVGADGVGK
19	KS12D-19	WVVGADGVGK
20	KS12D-20	YVVGADGVGK
21	KS12D-21	VAVGADGVGK
22	KS12D-22	VCVGADGVGK
23	KS12D-23	VDVGADGVGK
24	KS12D-24	VEVGADGVGK
25	KS12D-25	VFVGADGVGK
26	KS12D-26	VGVGADGVGK
27	KS12D-27	VHVGADGVGK
28	KS12D-28	VIVGADGVGK
29	KS12D-29	VKVGADGVGK
30	KS12D-30	VLVGADGVGK
31	KS12D-31	VMVGADGVGK
32	KS12D-32	VNVGADGVGK
33	KS12D-33	VPVGADGVGK
34	KS12D-34	VQVGADGVGK
35	KS12D-35	VRVGADGVGK
36	KS12D-36	VSVGADGVGK
37	KS12D-37	VTVGADGVGK
38	KS12D-38	VVVGADGVGK
39	KS12D-39	VWVGADGVGK
40	KS12D-40	VYVGADGVGK
41	KS12D-41	VVAGADGVGK
42	KS12D-42	VVCGADGVGK
43	KS12D-43	VVDGADGVGK

44	KS12D-44	VVEGADGVGK
45	KS12D-45	VVFGADGVGK
46	KS12D-46	VVGGADGVGK
47	KS12D-47	VVHGADGVGK
48	KS12D-48	VVIGADGVGK
49	KS12D-49	VVKGADGVGK
50	KS12D-50	VVLGADGVGK
51	KS12D-51	VVMGADGVGK
52	KS12D-52	VVNGADGVGK
53	KS12D-53	VVPGADGVGK
54	KS12D-54	VVQGADGVGK
55	KS12D-55	VVRGADGVGK
56	KS12D-56	VVSGADGVGK
57	KS12D-57	VVTGADGVGK
58	KS12D-58	VVVGADGVGK
59	KS12D-59	VVWGADGVGK
60	KS12D-60	VVYGADGVGK
61	KS12D-61	VVVAADGVGK
62	KS12D-62	VVVCADGVGK
63	KS12D-63	VVVDADGVGK
64	KS12D-64	VVVEADGVGK
65	KS12D-65	VVVFADGVGK
66	KS12D-66	VVVGADGVGK
67	KS12D-67	VVVHADGVGK
68	KS12D-68	VVVIADGVGK
69	KS12D-69	VVVKADGVGK
70	KS12D-70	VVVLADGVGK
71	KS12D-71	VVVMADGVGK
72	KS12D-72	VVVNADGVGK
73	KS12D-73	VVVPADGVGK
74	KS12D-74	VVVQADGVGK
75	KS12D-75	VVVRADGVGK
76	KS12D-76	VVVSADGVGK
77	KS12D-77	VVVTADGVGK
78	KS12D-78	VVVVADGVGK
79	KS12D-79	VVWADGVGK
80	KS12D-80	VVYADGVGK
81	KS12D-81	VVGADGVGK
82	KS12D-82	VVGCDGVGK
83	KS12D-83	VVGDDGVGK
84	KS12D-84	VVGEDGVGK
85	KS12D-85	VVGFDGVGK
86	KS12D-86	VVGGDGVGK
87	KS12D-87	VVGHDGVGK
88	KS12D-88	VVGIDGVGK

89	KS12D-89	VVVGKDGVGK
90	KS12D-90	VVVGLDGVGK
91	KS12D-91	VVVGMDGVGK
92	KS12D-92	VVVGNDGVGK
93	KS12D-93	VVVGPDGVGK
94	KS12D-94	VVVGQDGVGK
95	KS12D-95	VVVG RDGVGK
96	KS12D-96	VVVGSDGVGK
97	KS12D-97	VVVGTDGVGK
98	KS12D-98	VVVGVDGVGK
99	KS12D-99	VVVGWDGVGK
100	KS12D-100	VVVG YDGVGK
101	KS12D-101	VVVG AAGVGK
102	KS12D-102	VVVGACGVGK
103	KS12D-103	VVVGADGVGK
104	KS12D-104	VVVG AEGVGK
105	KS12D-105	VVVGAFGVGK
106	KS12D-106	VVVGAGGVGK
107	KS12D-107	VVVG AHGVGK
108	KS12D-108	VVVG AIGVGK
109	KS12D-109	VVVG AKGVGK
110	KS12D-110	VVVG ALGVGK
111	KS12D-111	VVVG AMGVGK
112	KS12D-112	VVVG ANGVGK
113	KS12D-113	VVVG APGVGK
114	KS12D-114	VVVG AQGVGK
115	KS12D-115	VVVG ARGVGK
116	KS12D-116	VVVG ASGVGK
117	KS12D-117	VVVG ATGVGK
118	KS12D-118	VVVG AVGVGK
119	KS12D-119	VVVG AWGVGK
120	KS12D-120	VVVG AYGVGK
121	KS12D-121	VVVG ADAVGK
122	KS12D-122	VVVG ADCVGK
123	KS12D-123	VVVG ADDVGK
124	KS12D-124	VVVG ADEVGK
125	KS12D-125	VVVG ADFVGK
126	KS12D-126	VVVG ADGVGK
127	KS12D-127	VVVG ADHVGK
128	KS12D-128	VVVG ADIVGK
129	KS12D-129	VVVG ADKVGK
130	KS12D-130	VVVG ADLVGK
131	KS12D-131	VVVG ADMVGK
132	KS12D-132	VVVG ADNVGK
133	KS12D-133	VVVG ADPVGK

134	KS12D-134	VVVGADQVGK
135	KS12D-135	VVVGADRVGK
136	KS12D-136	VVVGADSVGK
137	KS12D-137	VVVGADTVGK
138	KS12D-138	VVVGADVVGK
139	KS12D-139	VVVGADWVGK
140	KS12D-140	VVVGADYVGK
141	KS12D-141	VVVGADGAGK
142	KS12D-142	VVVGADGCGK
143	KS12D-143	VVVGADGDGK
144	KS12D-144	VVVGADGEGK
145	KS12D-145	VVVGADGFGK
146	KS12D-146	VVVGADGGGK
147	KS12D-147	VVVGADGHGK
148	KS12D-148	VVVGADGIGK
149	KS12D-149	VVVGADGKGK
150	KS12D-150	VVVGADGLGK
151	KS12D-151	VVVGADGMGK
152	KS12D-152	VVVGADGNGK
153	KS12D-153	VVVGADGPGK
154	KS12D-154	VVVGADGQGK
155	KS12D-155	VVVGADGRGK
156	KS12D-156	VVVGADGSGK
157	KS12D-157	VVVGADGTGK
158	KS12D-158	VVVGADGVGK
159	KS12D-159	VVVGADGWGK
160	KS12D-160	VVVGADGYGK
161	KS12D-161	VVVGADGVAK
162	KS12D-162	VVVGADGVCK
163	KS12D-163	VVVGADGVDK
164	KS12D-164	VVVGADGVEK
165	KS12D-165	VVVGADGVFK
166	KS12D-166	VVVGADGVGK
167	KS12D-167	VVVGADGVHK
168	KS12D-168	VVVGADGVIK
169	KS12D-169	VVVGADGVKK
170	KS12D-170	VVVGADGVLK
171	KS12D-171	VVVGADGVMK
172	KS12D-172	VVVGADGVNK
173	KS12D-173	VVVGADGVPK
174	KS12D-174	VVVGADGVQK
175	KS12D-175	VVVGADGVRK
176	KS12D-176	VVVGADGVSK
177	KS12D-177	VVVGADGVTK
178	KS12D-178	VVVGADGVVK

179	KS12D-179	VVVGADGVWK
180	KS12D-180	VVVGADGVYK
181	KS12D-181	VVVGADGVGA
182	KS12D-182	VVVGADGVGC
183	KS12D-183	VVVGADGVGD
184	KS12D-184	VVVGADGVGE
185	KS12D-185	VVVGADGVGF
186	KS12D-186	VVVGADGVGG
187	KS12D-187	VVVGADGVGH
188	KS12D-188	VVVGADGVGI
189	KS12D-189	VVVGADGVGK
190	KS12D-190	VVVGADGVGL
191	KS12D-191	VVVGADGVGM
192	KS12D-192	VVVGADGVGN
193	KS12D-193	VVVGADGVGP
194	KS12D-194	VVVGADGVGQ
195	KS12D-195	VVVGADGVGR
196	KS12D-196	VVVGADGVGS
197	KS12D-197	VVVGADGVGT
198	KS12D-198	VVVGADGVGV
199	KS12D-199	VVVGADGVGW
200	KS12D-200	VVVGADGVGY

Supplementary Table 5.TCR recognition motifs

TCR Name	TCR recognition motif
TCR1	[ACDEFGHIKLMNPQRSTVWY]-[ACDEFGHILMNPRSTV]-[ACDEGIKLMNPQRSTV]-[AGSW]-[APS]-[DN]-[ACFGMPQSTV]-[ACEHIKLMNQRSTVWY]-[GN]-[DIKLY]
TCR1a7	[ACDEFGHIKLMNPQRSTVWY]-[ACDEFGHIKLMNPQRSTVWY]-[ACDEFGHIKLMNPQRSTV]-[ACDGPRSW]-[AKPQRS]-[DIN]-[CFGPQS]-[ACEHIKLMNQRSTVWY]-[AGLN]-[DEFHIKLNQRY]
TCR1a7 (hTCR KO)	[ACDEFGHIKLMNPQRSTVWY]-[ACDEFGHIKLMNPQRSTVW]-[ACDEFGHIKLMNPQRSTV]-[ACDGPSW]-[APRS]-[DN]-[ACFGPQSV]-[ACDEHIKLMNQRSTVWY]-[AGN]-[DEFHIKLNQRY]

Supplementary Table 6. Homologous peptides and minigene-clusters for TCR1

ID	Uniprot ID	Protein Name	Peptide Sequence	30-mer Minigene Sequence	Minigene-Cluster ID	Minigene-Cluster Sequence
1	Q96M86	DNHD1	TVLGPNGVGK	LLALEEVACGTVLGPNGVGKRAIVNSLAQA	TCR1_MC-1	LLALEEVACGTVLGPNGVGKRAIVNSLAQATPGP AAYMLPMVMGPNVTGKASQPSFSIKGASVMTDE YLYSGTASDFLGKDTAFTRSLGPKLEVANLLQK SASPDAAAGKSGLTPLHVAIKQYLSHILEQRTSS NVINKRENLEKKNKNEAFESVFNKVPVAPD SIGKDGKEQDLYKRSSNDLSNSVSSDGYGKRG QMKPSIESQIIGPFQRTAIIIGPNSGKSNLMDAISF FVQVDFQHAGNYSCVASNVQGHSTSMFFRVV PDEPGSAALGSGSSDPENKDRPLFCISDILLN KHIDAYKTFPPTEPKDKKKKKADET
2	Q96PU9	CMA1A	MVMGPNVTGK	TPGPAAYMLPMVMGPNVTGKASQPSFSIKG		
3	Q95025	SEM3D	SGTASDFLGK	ASVMTDEYLYSGTASDFLGKDTAFTRSLGP		
4	Q12955	ANK3	KSASPDAAAGK	KLEVANLLQKSASPDAAAGKSGLTPLHVAA		
5	Q5TEA6	SE1L2	QRTSSNVINK	IKQYLSHILEQRTSSNVINKRENLEKKN		
6	Q92968	PEX13	VPVAPDSIGK	EAFESVFNKVPVAPDSIGKDGKEQDQL		
7	P25054	APC	SVSSSDGYGK	YKRSSNDLSNSVSSDGYGKRGQMKPSIES		
8	Q14683	SMC1A	AIIGPNSGSK	QIIGPFQRTAIIIGPNSGKSNLMDAISFV		
9	P07333	CSF1R	SCVASNVQGH	QVDFQHAGNYSCVASNVQGHSTSMFFRVV		
10	Q9C0D6	FHDC1	SVGSSDPENK	PDEPGSAALGSGSSDPENKDRPLFCISD		
11	Q53EP0	FND3B	RLTASNTEGK	NLKRSTQYKFRLTASNTEGKSCPSEVLVCT	TCR1_MC-2	NLKRSTQYKFRLTASNTEGKSCPSEVLVCTIRLH QELGRQKSLWADVHGKLRSHIDALREMSLKLQA SNVTNKNPKSINSRVFIGNLNTEVLDASVKEVG SSSSDVSQKESVPEEPLRNSVGPASVIVISA DPENKEVEEERIAGTTMIGVAVDTVGILGNSVEG KQVLQKTGTRFTYVTEGNSFLIITGNMSSGKSTYL KQIALCEFGIDLDTRVALVGPNGAGKSTLLKLLTG ETFTLRPGEVTVLGPNGSGKSTVAALLQNLCEC GGDKGRVKVITGNSSGKSYLQVGLIILLNKHID AYKTFPPTEPKDKKKKKADET
12	Q8TDR4	TCP1L	KSLWADVHGK	IRLHQELGRQKSLWADVHGKLRSHIDALRE		
13	Q9UKM9	RALY	KLQASNVTNK	MSLKLQASNVTNKNDPKSINSRVFIGNLN		
14	Q5T5Y3	CAMP1	GSSSDVSGK	EVLDAVKEVGSSSDVSQKESVPEEPLR		
15	Q99650	OSMR	IVISADPENK	NSVGPASVIVISADPENKEVEEERIAGT		
16	Q16401	PSMD5	GILGNSVEGK	TMIGVAVDTVGILGNSVEGKQVLQKTGTRF		
17	O15457	MSH4	IITGNMSSGK	TYVTEGNSFLIITGNMSSGKSTYLKQIALC		
18	Q9UG63	ABC2	ALVGPNGAGK	EFGIDLDTRVALVGPNGAGKSTLLKLLTGE		
19	Q03518	TAP1	ALVGPNGSGK	TFTLRPGEVTVLGPNGSGKSTVAALLQNL		
20	Q43196	MSH5	VITGNSSGK	ECGGDKGRVKVITGNSSGKSYLQVGLI		
21	Q60264	SMCA5	ASGGSNSNNK	SAPSKPAASIASGGSNSNNKGGPEGVAAQANLN	TCR1_MC-3	SAPSKPAASIASGGSNSNNKGGPEGVAAQANLN FYEGHITSLGPNAGKTTTISMLTGLYTDLNYSI NNLSISANVENKSYLYVGLVAHHNIGSPYCLRL ASADVNGKIIWVDAAGVENLLDEVMKSLSVSS DFLGKDKPVCGLARVNSRASPNLIGATGANS GKVMPTKSPPPPVEEVKKNHSIILSAPNPEGKI ELEDLNKRAAWSPYEDAVPAANARGKSKAKAK APAPFETLNLGNENTDSSANMLGKTQSRLLIWTK SEDEVVLLKFLSFGSDVQNKLESAQCVGDILLN KHIDAYKTFPPTEPKDKKKKKADET
22	Q86UK0	ABCAC	SLLGPNAGK	NLNFYEGHITSLGPNAGKTTTISMLTGL		
23	Q6NVV3	NIP3	LSISANVENK	YTDLNYSINLNSISANVENKSYLYVGLVA		
24	Q9BZH6	WDR11	RLASADVNGK	HHNIGSPYCLRLASADVNGKIIWVDAAGV		
25	Q3V6T2	GRDN	LSVSSDFLGK	ENLLDEVMKSLSVSSDFLGKDKPVCGLAR		
26	Q02078	MEF2A	GATGANSGLK	VNSRASPNLIGATGANSGLKVMPTKSPPPP		
27	P32856	STX2	ILSAPNPEGK	VEEVKKNHSIILSAPNPEGKIIELEDLNK		
28	Q8NEG4	FA83F	AVPAANARGK	LRAAWSPYEDAVPAANARGKSKAKAKAPAP		
29	Q92628	K0232	TDSSANMLGK	FETLNLGNENTDSSANMLGKTQSRLLIWTK		
30	Q9Y5X2	SNX8	SFSGSDVQNK	SEDEVVLLKFLSFGSDVQNKLESAQCVGD		
31	Q9H3R2	MUC13	RSSSNFLNY	TVTEKINKAIRSSSNFLNYDLTLRCDYYG	TCR1_MC-4	TVTEKINKAIRSSSNFLNYDLTLRCDYYG GAILSSNIVGNSNYGKRNAVEVLKREDFGIDMDS RICIVGPNVGVKSTLLLLTGKCVRSVNTGRSCV LGSNAENKPIKNQLGLTLDLNLNATEGNLSPGN VKNKSSPCEDMGIAATAARRHTVLEGPDGIG KTTLLRQVMDLQIITFFSPLTILVGPNGAGKTTIEC LKYYAAHLVDSGNYTCMASNSIGKSNLVISLHVQ QVIGPFRFTCIIGPNSGKSNVMDALSFVFLQV KVIRAEGMAADVTKGSDPFCVVELNILLNKHIDA YKTFPPTEPKDKKKKKADET
32	P10997	IAPP	TNVGSNTYK	SNNFGAILSSNIVGNSNYGKRNAVEVLKRE		
33	Q8NE71	ABC1	CIVGPNVGVK	DFGIDMDSRICIVGPNVGVKSTLLLLTGK		
34	Q8N9Z0	ZN610	CVLGSNAENK	CVRSVNTGRSCVLSNAENKPIKNQLGLTL		
35	P33032	MC5R	NLSGPNVKNK	LDLNLNATEGNLSPGNVKNKSSPCEDMGIA		
36	Q7RTR0	NLRP9	VLEGPDGIGK	YTAARRHTVLEGPDGIGKTTLLRQVMDL		
37	Q92878	RAD50	ILVGPNGAGK	QIITFFSPLTILVGPNGAGKTTIECLKYI		
38	A6NDA9	LRIT2	TCMASNSIGK	AAHLVDSGNYTCMASNSIGKSNLVISLHVQ		
39	Q8NDV3	SMC1B	CIIGPNSGSK	QVIGPFRFTCIIGPNSGKSNVMDALSFV		
40	Q6DN14	MCTP1	GLMAADVTKG	FLQVKVIRAEGMAADVTKGSDPFCVVELN		
41	Q8NCS7	CTL5	LGIAANGINK	GNGGTRSVVVELGIAANGINKLLDAKSLGLK	TCR1_MC-5	GNGGTRSVVVELGIAANGINKLLDAKSLGLKALQ DSNRGVRLKAADALGKLSIHIKVDPSFCVQEGEI LGLLGPNGAGKSSSIRMISGIEGESVTEIDISFLES PNPENKDYEEPKNVKGALAGLGGPLGVPVGPDP GKGLDFPEGVFAVSLDAKLLLQRRAAADSAG KNGLTPLHVAIFWLNAAETWVDISSNTAGKTLF GKMMDYLRQHSDSGNVYTCIASNMEGKAQKYY FLSIQILLNKHIDAYKTFPPTEPKDKKKKKADET
42	Q92616	GCN1	RLKAADALGK	KALQDSNRGVRLKAADALGKLSIHIKVD		
43	Q8N139	ABCA6	GLLGPNAGK	SFCVQEGEILGLLGPNAGKSSSIRMISGI		
44	Q9UBV2	SE1L1	FLESPNPENK	EGESVTEIDISFLESPNPENKDYEEPKNVVK		
45	Q14526	HIC1	GVPGPDGKGGK	GALAGLGGPLGVPGPDGKGLDFPEGVFAV		
46	Q01484	ANK2	RRAAADSAGK	SLDVAKLLLQRRAAADSAGKNGLTPLHVAA		
47	Q14697	GANAB	VDISSNTAGK	IFWLNAAETWVDISSNTAGKTLFGKMMDYL		
48	Q96RW7	HMCN1	TCIASNMEGK	RSQHSDSGNVYTCIASNMEGKAQKYYFLSIQ		

Supplementary Table 7. The IMGT numbering scheme for TCR1's CDRs

CDR Region	IMGT number	AA.	TCR Libraries		
TCR1 CDR-3B	105	A			
	106	S			
	107	S			
	108	V			
	109	G			
	110	P			
	111	G		TCR1 Lib1 (G111 to N113)	
	112.1	Q			
	112	N			
	113	N			
	114	S			
	115	P			
	116	L			
	117	H			
TCR1 CDR-1A	27	T			
	28	R			
	29	D			TCR1 Lib2 (D29 to T36)
	30	T			
	36	T			
	37	Y			
	38	Y			

Note: AA., amino acid. The IMGT numbers, which are standardized identifiers for immunogenetics data, were acquired through detailed analysis using the International ImMunoGeneTics information system (IMGT) database available at <https://www.imgt.org/>.

Supplementary Table 8. The information of 24 TCR clones derived from TCR libraries

ID	TCR Name	CDR sequence	Count	TCR Libraries
1	TCR1b1	ASSVGP <u>AOHS</u> SPLH	20	TCR1 Lib1
2	TCR1b2	ASSVGP <u>REHS</u> SPLH	16	
3	TCR1b3	ASSVGP <u>AEHS</u> SPLH	4	
4	TCR1b4	ASSVGP <u>AEHS</u> SPLH	4	
5	TCR1b5	ASSVGP <u>ARHN</u> SPLH	4	
6	TCR1b6	ASSVGP <u>AEHQ</u> SPLH	3	
7	TCR1b7	ASSVGP <u>GEHS</u> SPLH	2	
8	TCR1b8	ASSVGP <u>GHWS</u> SPLH	2	
9	TCR1b9	ASSVGP <u>GYHA</u> SPLH	2	
10	TCR1b10	ASSVGP <u>RRHS</u> SPLH	2	
11	TCR1b11	ASSVGP <u>SEHS</u> SPLH	2	
12	TCR1a1	TR <u>LCL</u> YY	4	TCR1 Lib2
13	TCR1a2	TR <u>MLL</u> YY	4	
14	TCR1a3	TR <u>NSL</u> YY	4	
15	TCR1a4	TR <u>FDP</u> YY	3	
16	TCR1a5	TR <u>LSP</u> YY	3	
17	TCR1a6	TR <u>LSY</u> YY	3	
18	TCR1a7	TR <u>MFL</u> YY	3	
19	TCR1a8	TR <u>FFF</u> YY	2	
20	TCR1a9	TR <u>INF</u> YY	2	
21	TCR1a10	TR <u>LHL</u> YY	2	
22	TCR1a11	TR <u>HS</u> AYY	2	
23	TCR1a12	TR <u>IQT</u> YY	2	
24	TCR1a13	TR <u>RND</u> YY	2	

Note: This table summarizes the cloning and sequencing process of TCRs from single-cell sorted TCR Jurkat cells, analyzing CDR sequences from 100 samples in each library. 24 Clones that were identified at least twice were used for further validation.

Supplementary Table 9. Functional evaluation process of 24 TCR clones from TCR libraries

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
		TCR1 Lib1 (CDR-3B)											TCR1 Lib2 (CDR-1A)												
		TCR1b1	TCR1b2	TCR1b3	TCR1b4	TCR1b5	TCR1b6	TCR1b7	TCR1b8	TCR1b9	TCR1b10	TCR1b11	TCR1a1	TCR1a2	TCR1a3	TCR1a4	TCR1a5	TCR1a6	TCR1a7	TCR1a8	TCR1a9	TCR1a10	TCR1a11	TCR1a12	TCR1a13
Filter_01	Functional avidity (EC50)	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Stop	Pass	Pass	Stop	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Filter_02	SMC1A ₂₉₋₃₈ Tetramer binding	Stop	Pass	Stop	Pass	Pass	Pass	Stop	Stop	Stop	Pass	Pass	Pass		Pass	Pass		Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Filter_03	SMC1A ₂₉₋₃₈ recognition		Stop		Stop	Stop	Pass				Stop	Pass	Pass		Pass	Stop		Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Filter_04	HLA-A*11:01 [*] K562 recognition						Pass					Pass	Pass		Pass			Stop	Pass	Stop	Stop	Pass	Pass	Pass	Pass
Filter_05	X-scan assay					Stop					Stop	Pass			Stop				Pass			Stop	Stop	Stop	Stop

Supplementary Table 10. Homologous peptides for TCR1a7 T cells

ID	Uniprot ID	Protein Name	Peptide Sequence
1	Q9Y6R7	FCGBP	AAAPSNCSGR
2	Q9Y603	ETV7	RVVDPNGLAR
3	Q9Y5F6	PCDGM	LQVSSDGTLK
4	Q9Y3F4	STRAP	ATAAADFTAK
5	Q9Y366	IFT52	RSNWKIQSLK
6	Q9Y305	ACOT9	VMVARDSENK
7	Q9Y2M0	FAN1	MLFSPDFTLR
8	Q9Y2K5	R3HD2	MSGAKIQWLK
9	Q9Y2B5	VP9D1	KLLPQNPEAK
10	Q9Y275	TN13B	GNSSQNSRNK
11	Q9Y238	DLEC1	AVGCPISLR
12	Q9Y217	MTMR6	VMDAAIFLAK
13	Q9UQC9	CLCA2	SIAGPICNLK
14	Q9UQ53	MGT4B	SLAGKIQKLLK
15	Q9UQ35	SRRM2	SDSSPDSKAK
16	Q9UQ35	SRRM2	FESSPDPELK
17	Q9UQ05	KCNH4	LGADPNFVLK
18	Q9UPN3	MACF1	IKTSQIFLAK
19	Q9UP65	PA24C	GSTWAISSLY
20	Q9UNY4	TTF2	KVEPSDPVAR
21	Q9ULN7	PNM8B	YTDPSDPWAR
22	Q9ULM3	YETS2	TTNSKNPSGK
23	Q9ULL5	PRR12	GVGPPNSEGK
24	Q9ULI4	KI26A	ASFDSDCSLR
25	Q9UKZ4	TEN1	LTISSNGVLK
26	Q9UKY1	ZHX1	RYAWKNGNLK
27	Q9UK73	FEM1B	IIAARNGHAK
28	Q9UK05	GDF2	TKLSPISVLY
29	Q9UJ71	CLC4K	TLNAQIPELK
30	Q9UHW9	S12A6	LVKDRNSMLR
31	Q9UHV7	MED13	ATVPSIPEAH
32	Q9UG63	ABCF2	ALVGPNAGAGK
33	Q9UF33	EPHA6	RIVSSIQTLR
34	Q9UBZ9	REV1	HTPSSNGALK
35	Q9UBZ9	REV1	ASVPKNPLLH
36	Q9UBV2	SE1L1	FLESPNPENK
37	Q9UBS9	SUCO	KILANPEAK
38	Q9UBL0	ARP21	SSTSDSSNR

39	Q9UBF8	PI4KB	SVPARIPENR
40	Q9P2K3	RCOR3	VQTSKIGLGR
41	Q9P2J2	TUTLA	GSGSPDSVAK
42	Q9P2I0	CPSF2	AAFDKIQQLK
43	Q9P2E3	ZNFX1	SLVRSNQEGK
44	Q9P267	MBD5	RRVDQNGVLY
45	Q9NZV7	ZIM2	SKQSKDPLGK
46	Q9NZU1	FLRT1	RTIARDSLAR
47	Q9NZJ4	SACS	IIHDANSRLK
48	Q9NYV4	CDK12	SVTAAIPHLK
49	Q9NYL2	M3K20	VVIAADGVLK
50	Q9NY47	CA2D2	FIEDPNFKNK
51	Q9NXD2	MTMRA	KVLGPNQKLK
52	Q9NX70	MED29	VIKAQISCAK
53	Q9NVX2	NLE1	VSGSSDSTLK
54	Q9NVT9	ARMC1	RDLAADPLNR
55	Q9NRX2	RM17	SVAAAISHGR
56	Q9NRC6	SPTN5	SWTDSISLAR
57	Q9NR48	ASH1L	LTAAPIGLGY
58	Q9NR23	GDF3	TKLSPISMLY
59	Q9NQS1	AVEN	GGRGPIFELK
60	Q9NPG3	UBN1	LSFSADSSAK
61	Q9HCK5	AGO4	MVGGPDPYLK
62	Q9HC52	CBX8	SLIARIPVAR
63	Q9HC21	TPC	RLSRSDPSAK
64	Q9HAR2	AGRL3	STESSIGSGK
65	Q9HAP2	MLXIP	PSTAQDPLGK
66	Q9H6S3	ES8L2	SLGRSDGVAK
67	Q9H582	ZN644	TTFPKNSALK
68	Q9H3R2	MUC13	RSSSNFLNY
69	Q9H2U9	ADAM7	GIADPNQSAK
70	Q9H2K2	TNKS2	LAHGADPTLK
71	Q9H269	VPS16	ATADKIQRAR
72	Q9H223	EHD4	ALEDADFENK
73	Q9H1A4	APC1	SILSKDGVLY
74	Q9H0G5	NSRP1	KESSPNSRAK
75	Q9H0E3	SP130	ISEARDSMLK
76	Q9H095	DRC9	KVDSKDSKGK
77	Q9C0F0	ASXL3	RQMGSDGILR
78	Q9C0D6	FHDC1	SVGSSDPENK

79	Q9BZE1	RM37	AWVDSDQLLY
80	Q9BZC7	ABCA2	RCLGSIQHLK
81	Q9BYG4	PAR6G	AVSSANPLLR
82	Q9BXW9	FACD2	LRLDPNFKLK
83	Q9BXP5	SRRT	SLPSQNPILK
84	Q9BXI3	5NT1A	GGNSPICYLK
85	Q9BXA6	TSSK6	RRAPPDFVNK
86	Q9BX40	LS14B	AGFPSIPVGK
87	Q9BTD3	TM121	SRVSAIFVGK
88	Q9BTA9	WAC	TVVPQNSSAR
89	Q9BSJ8	ESYT1	SSSGPNSRLY
90	Q9BQI7	PSD2	LNSASDPSLK
91	Q99973	TEP1	VSVSRDGTLLK
92	Q99942	RNF5	SQKPQDPRLK
93	Q99941	ATF6B	LLLPAISHNK
94	Q99698	LYST	MSTDSNSLAR
95	Q99677	LPAR4	ATLSQIGTNK
96	Q99650	OSMR	IVISADPENK
97	Q99551	MTEF1	VLDSSISTLK
98	Q99424	ACOX2	RLRPSDPEAK
99	Q99259	DCE1	KIIPADFEAK
100	Q96RR4	KKCC2	SETRKIFSGK
101	Q96RN5	MED15	IPSSSIPLGR
102	Q96RL6	SIG11	STLGPISQGH
103	Q96RK4	BBS4	KYVAAISCLK
104	Q96QV1	HHIP	TILCSDSNGK
105	Q96Q89	KI20B	YVFSADPIAR
106	Q96Q15	SMG1	KVVDRIFSLY
107	Q96Q05	TPPC9	GICWRIPSLK
108	Q96PN7	TREF1	KARGAIPSGK
109	Q96P66	GP101	RMEAKDGSLK
110	Q96P26	5NT1B	GGKDPIGYLK
111	Q96NW7	LRRC7	QLPDSIGLLK
112	Q96NW7	LRRC7	VLPGSIGKLLK
113	Q96N23	CFA54	KITCRNFIGK
114	Q96N11	INT15	LVPGSIQTLK
115	Q96MR9	ZN560	TSSGRIQHLR
116	Q96M86	DNHD1	TVLGPNGVGK
117	Q96L91	EP400	ATFSANPEAK
118	Q96KR4	LMLN	GISDADFVLY

119	Q96K78	AGRG7	FTFARIPVGR
120	Q96JM4	LRIQ1	ETNWRDSSLK
121	Q96JB1	DYH8	STAPKDPKLY
122	Q96HA8	NTAQ1	RVIRADSYLK
123	Q96H86	ZN764	QTDPADSRNK
124	Q96DU9	PABP5	SSFGSISRAK
125	Q96CV9	OPTN	RTSDSDQQAY
126	Q96CM8	ACSF2	ILASPIFNGK
127	Q96BY9	SARAF	RRLDPIPQLK
128	Q96B01	R51A1	SVKSPNQSLR
129	Q96AY4	TTC28	AVDPQNCILY
130	Q96AH8	RAB7B	IIVGAIGVGK
131	Q93070	NAR4	YLTSAIQLLR
132	Q93052	LPP	IPVAPIGTLK
133	Q93009	UBP7	KTDPKDPANY
134	Q92993	KAT5	SVFPQNGAAR
135	Q92968	PEX13	VPVAPDSIGK
136	Q92887	MRP2	KVLGPNGLLK
137	Q92878	RAD50	ILVGPNGAGK
138	Q92636	FAN	FTTSQDSTLK
139	Q92625	ANS1A	RSSDQDSTNK
140	Q92598	HS105	AKIAADFRNK
141	Q92583	CCL17	RAICSDPNNK
142	Q92547	TOPB1	ESAPSNGSGK
143	Q92529	SHC3	AYVAKDPVNR
144	Q8WZ42	TITIN	TTVSSDSVAK
145	Q8WZ42	TITIN	PVFAKDPIAK
146	Q8WXH0	SYNE2	GLQAKIQEAK
147	Q8WX94	NALP7	SLFSSNSNLK
148	Q8WVF1	OSCP1	ESIAPNPLAK
149	Q8WUY9	DEP1B	RMMARICLNK
150	Q8WU76	SCFD2	AVGGPDCHLR
151	Q8TDJ6	DMXL2	FSCGADGTLK
152	Q8TD55	PKHO2	ASAASDGLLR
153	Q8TCB0	IFI44	LLLGPIGAGK
154	Q8TC44	POC1B	ITASSDGTLLK
155	Q8TC21	ZN596	KTFKNSNLR
156	Q8TBC3	SHKB1	LLSGRISTLK
157	Q8TB96	TIP	TTVDANGYLK
158	Q8TAT5	NEIL3	RVVGKDGENTK

159	Q8TAC1	RFESD	SINPKDPSAK
160	Q8NI35	INADL	SVADRDQRLK
161	Q8NHV4	NEDD1	KIADSIGNNR
162	Q8NHM5	KDM2B	KKVPPDGLLR
163	Q8NG31	KNL1	NSSAPICENK
164	Q8NFD5	ARI1B	IAHWQDSLAK
165	Q8NEZ4	KMT2C	SVTPKIGMGK
166	Q8NEY8	PPHLN	RSHPSDGYNR
167	Q8NE71	ABCF1	CIVGPNGVGK
168	Q8NDY3	ARHL1	RKISKDSENK
169	Q8NDV3	SMC1B	CIIGPNGSGK
170	Q8NCS7	CTL5	LGIAANGINK
171	Q8NBT0	POC1A	ITASSDSTLK
172	Q8NBP0	TTC13	EVAGKIPKGK
173	Q8NBF6	AVL9	KDFSQISILK
174	Q8N7X1	RMXL3	RSLDANSSGR
175	Q8N6F1	CLD19	RVGDSNPIAK
176	Q8N5U6	RNF10	FIEAAIQELK
177	Q8N4H0	SPA6L	KQGDADFHGK
178	Q8N456	LRC18	NLISPNSMAK
179	Q8N3U4	STAG2	RQIDKIQCAK
180	Q8N3K9	CMYA5	SSARSDQMLK
181	Q8N371	KDM8	QLFDQIPELK
182	Q8N2K0	ABD12	AALDADCRLK
183	Q8N2C9	UMAS1	MVLGAISLLY
184	Q8N1W1	ARG28	CSSPKISLGK
185	Q8N1G2	CMTR1	FTNPRDSYGK
186	Q8N139	ABCA6	GLLGPNGAGK
187	Q8N136	DAW1	ATASADGTAR
188	Q8N122	RPTOR	RLDDQIFLNR
189	Q8IZL2	MAML2	KIAPQDQINR
190	Q8IZH2	XRN1	RFTGSIFIGR
191	Q8IYL2	TRM44	TRSSRNGSLK
192	Q8IXK0	PHC2	GTAPQNGENK
193	Q8IXF0	NPAS3	GPSASNSLLY
194	Q8IWX8	CHERP	CTKDAISAGK
195	Q8IWW8	HOT	YVSAPIGKGK
196	Q8IWU9	TPH2	GLLSSIGELK
197	Q8IWC1	MA7D3	GLPSPISTNR
198	Q8IVS8	GLCTK	KVRDRNFQLR

199	Q86YW9	MD12L	NVMPANSNLR
200	Q86YA3	ZGRF1	SKVWQDGILK
201	Q86XM0	CTSRD	TLFSSIFEAK
202	Q86XK2	FBX11	IKTDSNPTLR
203	Q86XA9	HTR5A	ALESPNPLLR
204	Q86V48	LUZP1	GSVPSDPLGR
205	Q86UV5	UBP48	LLVSANQTLK
206	Q86UU0	BCL9L	QISPSNSSLK
207	Q86UK0	ABCAC	SLLGPNGAGK
208	Q86TC9	MYPN	TIMAANPQGR
209	Q86SR1	GLT10	YVSDKISLNR
210	Q7Z7K0	COXM1	ALDPADQHLLR
211	Q7Z7G8	VP13B	KLFAPDPENK
212	Q7Z7G8	VP13B	NAIASIFQAK
213	Q7Z745	MRO2B	RGAGAIGLLK
214	Q7Z5Q5	DPOLN	ITTPKNFKGK
215	Q7Z589	EMSY	AGNSSIQEGK
216	Q7Z4P5	GDF7	ARLSPISILY
217	Q7Z3Q1	S46A3	IGIAPIFILY
218	Q7Z3G6	PRIC2	RRSAKIGKNK
219	Q7Z309	PBIR2	SGLSSDPLAK
220	Q7Z2Y5	NRK	KIQAADPVNR
221	Q7Z2K8	GRIN1	RTAPPDGAAK
222	Q7Z2E3	APTX	QLLPSIPQLK
223	Q7RTX1	TS1R1	AVIGPDSTNR
224	Q7RTR2	NLRC3	HALCANSTLK
225	Q7RTR0	NLRP9	VLEGPDGIGK
226	Q7LG56	RIR2B	GSFAAIFWLK
227	Q7LDG7	GRP2	LSHSSISRLK
228	Q7L9B9	EEPD1	ESSPSNGHGK
229	Q7L1I2	SV2B	LLMDRIGRLK
230	Q6ZUX3	TGRM2	IVIPPIPKAR
231	Q6ZUB1	S31E1	SRSRKISALK
232	Q6ZT07	TBCD9	STLPPIPHLH
233	Q6ZRQ5	MMS22	ATIPPISSLK
234	Q6ZNL6	FGD5	SEVGPIFHLY
235	Q6ZNG1	ZN600	KTFGSDSHLK
236	Q6ZMI0	PPR21	KLRAQNQVLK
237	Q6ZMC9	SIG15	TCTAANSLGR
238	Q6XZF7	DNMBP	LSVSANQKLLK

239	Q6V0I7	FAT4	FTVDKNGVLK
240	Q6UXT8	ALKL1	EIFPRDSNLK
241	Q6TFL4	KLH24	LLRAAPIAK
242	Q6SZW1	SARM1	SDIGAIQSLK
243	Q6QHC5	DEGS2	ALMRPDPRLK
244	Q6P474	PDXD2	GHTDKIGRLK
245	Q6P2Q9	PRP8	FMHGKIPTLK
246	Q6P1S2	CC033	KTTGSDFSLK
247	Q6NXN4	D19P1	SSPGRIPNLK
248	Q6NUT2	D19L2	SSPGRIQSLK
249	Q6NUN9	ZN746	SSACSDGTLK
250	Q6NUM9	RETST	RAQSPIPNLY
251	Q6NUJ5	PWP2B	APSASIPKPK
252	Q6IQ21	ZN770	KVFPSSISLKL
253	Q6IMN6	CAPR2	STLPKDPVLR
254	Q6IMI4	ST6B1	KLPGSIFENK
255	Q6AHZ1	Z518A	LLNDKDGTLK
256	Q68DU8	KCD16	LVCGRISLAK
257	Q68DI1	ZN776	KLFRSNSHLK
258	Q68D10	SPT2	SISGSIPAGR
259	Q66K14	TBC9B	SVSPPIPHLR
260	Q63HN8	RN213	KRISSNPVAK
261	Q5VYP0	S31A3	LLASPDPQAK
262	Q5VU92	DC121	GHIARIPLLR
263	Q5VU65	P210L	ASTASIFLAY
264	Q5VTB9	RN220	LPSSKNSLLK
265	Q5T9G4	ARM12	CSNSPICIAR
266	Q5T5Y3	CAMP1	SSGDSISLAR
267	Q5T2R2	DPS1	FTSCSDQMGK
268	Q5T011	SZT2	GVSRAIQALR
269	Q5SZD4	GLYL3	DNTASISLLK
270	Q5SYE7	NHSL1	SVSPANGKGG
271	Q5SRN2	TSBP1	KSCSKIQILK
272	Q5KSL6	DGKK	GTLSSISLKL
273	Q5JUQ0	FA78A	AISDSDGVNY
274	Q5HYK9	ZN667	KKLPPNQC�K
275	Q5H9R4	ARMX4	AIHRANSQAK
276	Q5H8A4	PIGG	QVIAADFCLK
277	Q5GH76	XKR4	STLRSISNNR
278	Q5GH73	XKR6	ALFASIFQLY

279	Q5BKT4	AG10A	HVVCSIGMLR
280	Q587J7	TDR12	VESSSIFCLK
281	Q53HC5	KLH26	STADKNGALK
282	Q53GS7	GLE1	LTNSKDSQAK
283	Q53FE4	CD017	VKLPPNFTAK
284	Q502W7	CCD38	ASQGRDSQGK
285	Q4V348	Z658B	KAFAQNSTLR
286	Q4LDE5	SVEP1	NVTWQIPTAK
287	Q4KWH8	PLCH1	ATRDQDGVLR
288	Q4G0U5	PCDP1	SILRKIGQAK
289	Q4G0S7	CC152	LSVGKDSHLK
290	Q49AH0	CDNF	KLDSQICELK
291	Q495X7	TRI60	KSFRRNPQLR
292	Q495D7	CL036	RIAWRIQRLK
293	Q460N5	PAR14	LVSDKIPKAK
294	Q3V6T2	GRDN	SGSSPIQYLK
295	Q3V6T2	GRDN	LSVSSDFLGK
296	Q2TAZ0	ATG2A	DTMRPDSLLK
297	Q2M3X9	ZN674	RFFDPNQRGK
298	Q1MSJ5	CSPP1	VDLDAIPSAK
299	Q17R31	TATD3	VLIRQIQLAK
300	Q16586	SGCA	MVASPDSHAR
301	Q16288	NTRK3	RAFAKNPHLR
302	Q15846	CLUL1	ILPSSNFTLK
303	Q15813	TBCE	LIASIGQLK
304	Q15517	CDSN	AAGPPISEGK
305	Q15517	CDSN	SSGSSISSAR
306	Q15392	DHC24	MVPPKISLLK
307	Q15388	TOM20	RRSDPNFKNR
308	Q15276	RABE1	EEIASISSLK
309	Q15274	NADC	ARQAADFTLK
310	Q15154	PCM1	RSIGSDSQGR
311	Q15032	R3HD1	SSTDSDSSLR
312	Q15020	SART3	VQIRPIFSNR
313	Q14766	LTBP1	CQCPPNFTGK
314	Q14696	MESD	GSDRAIFMLR
315	Q14683	SMC1A	AIIGPNGSGK
316	Q14667	BLTP2	SVTRPICRGK
317	Q14563	SEM3A	SGTAADFMGR
318	Q14526	HIC1	GVPGPDGK GK

319	Q14439	GP176	YIGSADFQAK
320	Q14244	MAP7	AVSPSNPKAR
321	Q14146	URB2	RSEGAIQSLR
322	Q14005	IL16	SPSAPISTAK
323	Q13835	PKP1	VYIPPISCNK
324	Q13630	FCL	KKTASNSKLR
325	Q13620	CUL4B	RVLAKNPKGK
326	Q13546	RIPK1	VVLWAIKANK
327	Q13496	MTM1	KRTSRDGVNR
328	Q13459	MYO9B	AITARDSMAK
329	Q13136	LIPA1	ALEDKNSLLR
330	Q13106	ZN154	REVGKDFLAK
331	Q13087	PDIA2	QTSAKIFAAR
332	Q13045	FLII	GSGPKDPMAR
333	Q13042	CDC16	SIKSSICLLR
334	Q13017	RHG05	DVVSPIPANK
335	Q12891	HYAL2	PTAPPIFTGR
336	Q0P6H9	TMM62	HVSGPIFVLK
337	Q09019	DMWD	SKAPRNPLAK
338	Q08AH3	ACS2A	TVTGGKIQRAK
339	Q07002	CDK18	EDTASIFSLK
340	Q05519	SRS11	QSLAADQLLK
341	Q05193	DYN1	AQQRSNQMNK
342	Q05048	CSTF1	LSSGKDSVAK
343	Q03518	TAP1	ALVGPNGSGK
344	Q02880	TOP2B	VVIPRDSLLR
345	Q02363	ID2	ELVPSIPQNK
346	Q02078	MEF2A	GATGANSLGK
347	Q02045	MYL5	KMLDPDGK GK
348	Q01974	ROR2	GQDGPIPTLK
349	Q01484	ANK2	RRAAADSAGK
350	P82094	TMF1	EESSEISSLK
351	P80192	M3K9	RRTPSDGALK
352	P78312	F193A	SINWSNFSLK
353	P59045	NAL11	SLISPDCVLK
354	P58304	VSX2	TVSGPDSLAR
355	P55087	AQP4	VCTRKISIAK
356	P55056	APOC4	FLESKDSLLK
357	P54886	P5CS	AASSQDSVGR
358	P53396	ACLY	TAVAKNQALK

359	P53355	DAPK1	LLDPPDPLGK
360	P51816	AFF2	NSVPQNPNNK
361	P50613	CDK7	RSEAKDGINR
362	P50542	PEX5	QHTASDFVAK
363	P49005	DPOD2	STQSRDSINK
364	P48230	T4S4	FIISAISINK
365	P48165	CXA8	IAVSSIQKAK
366	P46100	ATRX	KSMSKIGAAR
367	P43357	MAGA3	MEVDPIGHLV
368	P42772	CDN2B	AGADPNGVNR
369	P41212	ETV6	RIVDPNGLAR
370	P40926	MDHM	MISDAIPELK
371	P39880	CUX1	QLSAKNSTLK
372	P36871	PGM1	RIAAANGIGR
373	P35670	ATP7B	SIEDRISNLK
374	P35520	CBS	KVQPSDQVGK
375	P33993	MCM7	REVRADSVGK
376	P33981	TTK	GLNSPNSILK
377	P32856	STX2	ILSAPNPEGK
378	P32004	L1CAM	VTMGQNGNLY
379	P31937	3HIDH	AYSGANGILK
380	P31785	IL2RG	RTMPRIPTLK
381	P31350	RIR2	GSFASIFWLK
382	P31327	CPSM	RLRDADPILR
383	P31150	GDIA	IIIPQNQVNR
384	P29474	NOS3	RCVGRIQWGK
385	P28347	TEAD1	QQRDPDSYNK
386	P25054	APC	SVSSSDGYGK
387	P23381	SYWC	GFTDSDCIGK
388	P22607	FGFR3	NPTPSISWLK
389	P22105	TENX	RTCPSNCHGR
390	P20702	ITAX	VSHPQNPSLR
391	P20248	CCNA2	SLIDADPYLK
392	P20020	AT2B1	KILSANGEAK
393	P17752	TPH1	GLLSSISELK
394	P17301	ITA2	NTFGAIQYAR
395	P17020	ZNF16	KTFSQNSVLK
396	P17020	ZNF16	KAFSQNSSLK
397	P16499	PDE6A	QMKSQNPLAK
398	P15863	PAX1	AAAPAIGTGR

399	P15516	HIS3	SMTGADSHAK
400	P14679	TYRO	SANDPIFLLH
401	P14410	SUIS	LPSDPISTLR
402	P13667	PDIA4	KRSPPIPLAK
403	P12270	TPR	TTSSQDGQGK
404	P12110	CO6A2	FAVAPNQNLK
405	P11172	UMPS	ALGPSICMLK
406	P0DP23	CALM1	RVFDKDGNGY
407	P0DJD0	RGPD1	MLMRRDQVLK
408	P0CB47	UBFL1	MTGGPDPRLK
409	P09471	GNAO	MLFDSICNNK
410	P09238	MMP10	LSFDAISTLR
411	P08151	GLI1	SSSSSISSAY
412	P07451	CAH3	MTVSSDQMAK
413	P05556	ITB1	ASNGQICNGR
414	P05549	AP2A	NAVSAIPINK
415	P05155	IC1	AAASAVISVAR
416	P04899	GNAI2	KLFDSICNNK
417	P04114	APOB	TTKAQIPILR
418	P04114	APOB	ILTDPDGK GK
419	P01106	MYC	RVLRQISNNR
420	P01031	CO5	KMTDKNFLGR
421	O95837	GNA14	VRAARDFILK
422	O95793	STAU1	SRLAQIQQAK
423	O95490	AGRL2	KQNSRNLAK
424	O95405	ZFYV9	VTLDSDQVGY
425	O95359	TACC2	VAQDRIPSGK
426	O95359	TACC2	ASDAKNQEGK
427	O95302	FKBP9	GVIPPNSVLH
428	O95025	SEM3D	SGTASDFLGK
429	O94911	ABCA8	RCIGSIQHLK
430	O94885	SASH1	PTASRISLGK
431	O94804	STK10	QLLDRDFVAK
432	O75970	MPDZ	SPAGKNGTLK
433	O75923	DYSF	GLQPKDPNGK
434	O75864	PPR37	ASPPADGRLK
435	O75764	TCEA3	RVRSRISNLK
436	O75626	PRDM1	ARSSPDQSLK
437	O75592	MYCB2	SVISKDGELY
438	O75427	LRCH4	GPSSPDSVLR

439	O75427	LRCH4	GAPRKDSLLK
440	O75367	H2AY	IAFPSIGSGR
441	O60687	SRPX2	IISAPDPSNR
442	O60673	REV3L	GYTSANFSGR
443	O60613	45550	YVRGSDPVLK
444	O60504	VINEX	VLQPSNQVLR
445	O60499	STX10	MVSGSIQVLK
446	O60343	TBCD4	KLERANSQLK
447	O60331	PI51C	TVFRKNSSLK
448	O60303	KATIP	YVNGANSELK
449	O60287	NPA1P	AVRSSIFRLY
450	O60264	SMCA5	ASGGSNSSNK
451	O43752	STX6	LVSGSIGVLK
452	O43583	DENR	VTIAKIPRAK
453	O43493	TGON2	KQTPKDGSNK
454	O43491	E41L2	KHQASISELK
455	O43196	MSH5	VITGPNSSGK
456	O43148	MCES	RSQSRIFYLR
457	O15446	RPA34	FSCPPNFTAK
458	O15079	SNPH	MEVAQNGMAK
459	O15072	ATS3	TAFGKDFHLR
460	O15040	TCPR2	AVGSSIGMLY
461	O15018	PDZD2	SSKGSSELK
462	O14965	AURKA	SSKPSNCQNK
463	O14964	HGS	RACGQIFCGK
464	O14818	PSA7	AVMRRDQSLK
465	O14802	RPC1	TVISPDPNLR
466	O14795	UN13B	AAQDADSVLR
467	O14793	GDF8	KFSSKIQYNK
468	O14727	APAF	ASCSADGTLK
469	O14715	RGPD8	IVMRRDQVLK
470	O14686	KMT2D	GVLAKNPQLR
471	O14646	CHD1	SDSDSISEGK
472	O14645	IDLC	MIPPADSLLK
473	O14617	AP3D1	LIEDSDQNLK
474	C9JBD0	KRBX1	RIVSKIFRNR
475	B7Z6K7	ZN814	KSFSSIGHLR
476	B6SEH8	ERVV1	STRDSISKLK
477	B2RTY4	MYO9A	NTESSNPVLK
478	A8K8P3	SFI1	ACVARIQALR

479	A8CG34	P121C	SSNAPDPCAK
480	A6NN90	CB081	GGVDRIPLGR
481	A6NKT7	RGPD3	ILMRRDQVLK
482	A6NGD5	ZSA5C	KESDPIQALR
483	A6NFN9	ANKUB	ATPSADFLK
484	A6NDA9	LRIT2	TCMASNSIGK
485	A4UGR9	XIRP2	ASNSQNSQAK
486	A4FU69	EFCB5	SQSRKDSILK
487	A4D1E9	GTPBA	GANSKISALK
488	A3QJZ7	PRA27	SQCPSISQLK
489	A2RRP1	NBAS	LSIWAIPSLK
490	A0PK05	TMM72	SLEPADSLAK
491	A0A494C086	SPD21	KTRSRIPLLR
492	A0A0A6YYK4	TVB71	RSEGSISTLK
493	A0A096LP49	CC187	GSFPQNPLGK

Supplementary Table 11. Homologous peptides and minigene-clusters for hTCR-KO TCR1a7 T cells

ID	Uniprot ID	Protein Name	Peptide Sequence	30-mer Minigene Sequence	Minigene-Cluster ID	Minigene-Cluster Sequence
1	Q7Z7M9	GALT5	RTIPPDVIAK	IFVWPMNFGWRTIPPDVIAKNRIKETDIR	TCR1a7_MC-01	IFVWPMNFGWRTIPPDVIAKNRIKETDIRRAGPGRS GSVRTAPPDGAARPPGLFRALLQGPLRGRPIIATF SANPEAKAAAAFPQTSQVLSVVMGKCTRVDGSDNPI AKGRVAIAGGALGNMSSLLAGKVQPSDQVGVKQKQIR QFKQIRHKPQGNFSFKSTNSSDVSAKSGAVTFSSYQ GLLALIEEVACGTVLGPNVGVKRAIVNSLAQAVILAG NLLSHSTQSRDSINKAKYLTKKTOAATLNKDATKAA TAAADFTAKVWDVSGDELASVMTDEYLYSGTASD FLGKDTAFTRSLGPILLNKHIDAYKTFPTEPKKDKK KKADET
2	Q7Z2K8	GRIN1	RTAPPDGAAK	RAGPGRSGSVRTAPPDGAARPPGLFRALL		
3	Q96L91	EP400	ATFSANPEAK	QGQLRGRPIIATFSANPEAKAAAAFPQTSQ		
4	Q8N6F1	CLD19	RVGDSNPIAK	VLSVVMGKCTRVDGSDNPIAKGRVAIAGGAL		
5	P35520	CBS	KVQPSDQVGVK	GNMSSLLAGKVQPSDQVGVKQKQKQIR		
6	Q75717	WDHD1	STNSSDVSIAK	HKPGQNSFSKSTNSSDVSAKSGAVTFSSYQ		
7	Q96M86	DNHD1	TVLGPNGVGVK	LLALEEVACGTVLGPNVGVKRAIVNSLAQA		
8	P49005	DPD02	STQSRDSINK	VILAGNLLSHSTQSRDSINKAKYLTKKTOA		
9	Q9Y3F4	STRAP	ATAAADFTAK	ATLNKDATKAAATAAADFTAKVWDVSGDEL		
10	Q95025	SEM3D	SGTASDFLGK	ASVMTDEYLYSGTASDFLGKDTAFTRSLGP		
11	P07358	CO8B	HSFGSNAVNAK	SLPGSRGERPHSFGSNAVNSKFAKSRQMR	TCR1a7_MC-02	SLPGSRGERPHSFGSNAVNSKFAKSRQMRSTYIKPI SKLQATNARDALAKHIYAKLNFYIYHICIIHFSNP PNVNRNKRIRSRVMDTIKPFVITGLQDTSVSSDVAK FAVKATGEPLREDSYDVAFHSSKAYIASAGADALAK VFKWEDKDAKIFRVDVDPNGLARLWGNHKNRNV GKSAAPALGSGSPDVAKLKLGQSPVSKLEVAN LLLQKASPDAAAGKSLTPLHVAAMQWVLPKTIKLF APDPENKGTVCMSVSELLIISMTGVAALDSNVSGK IGLRAVVYFILLNKHIDAYKTFPTEPKKDKKDKK ET
12	Q9Y411	MY05A	ATNARDALAK	TYIKFISKLQATNARDALAKHIYAKLNFWI		
13	Q6PIJ6	FBX38	FSNPPNVRNK	YPYHICIIHFSNPVNRNKRIRSRVMDTI		
14	Q8WZ42	TITIN	TVVSSDVAK	KPVIITGLQDTSVSSDVAKFAVKATGEPR		
15	Q13033	STRN3	ASAGADALAK	LDESIVDVAFHSSKAYIASAGADALAKVFF		
16	Q9Y603	ETV7	RVDVDPNGLAR	KWEDKDAKIFRVDVDPNGLARLWGNHKNRNV		
17	Q9P2J2	TUTLA	GSGSPDVAK	TGKSAAPALGSGSPDVAKLKLGQSPVPS		
18	Q12955	ANK3	KSASPDAAAGK	KLEVANLLQKASPDAAAGKSLTPLHVAAMQWVLPKTIKLF		
19	Q7Z7G8	VP13B	KLFAPDPENK	MQWVLPKTIKLFAPDPENKGTVCMSVSELL		
20	P43005	EAA3	AALDSNVSGK	LIISMITGVAALDSNVSGKIGLRAVVYFILLNKHIDAYKTFPTEPKKDKKDKK ET		
21	Q7RTX1	TS1R1	AVIGPDSTNR	DLLHYSPTVLAVIGPDSTNRAATTAALLSP	TCR1a7_MC-03	DLLHYSPTVLAVIGPDSTNRAATTAALLSPIKQYLSHI LEQRTSSNVINKRENLEKKNKILPYLSSEAITAR DSMAKLSYALFDWIEPLPAPDGTGVGPPNSEGK DPAGAYRSPSEAFESVFTETNKVVPADSIGKDG KQDLVILIKNERGKIIPADFEAKLEAKQGVYKRS SNDSLNSVSSDGYKGRGMKPSIESVVDVSKGIV NAVKDPDSSGKFAFVGYKRSYQIISLTSFSSSNAP DPAKETVLSALKEKRIRIFEDIRRLIQPSDVIKVVAF SLDEPWILLNKHIDAYKTFPTEPKKDKKDKKKADET
22	Q5TEA6	SE1L2	QRTSSNVINK	IKQYLSHILEQRTSSNVINKRENLEKKNK		
23	Q13459	MY09B	AITARDSMAK	KLILPYLSSEAITARDSMAKLSYALFDWIE		
24	Q9ULL5	PRR12	GVGPPNSEGK	EPLPAPDGTGVGPPNSEGKDPAGAYRSPS		
25	Q92968	PEX13	VPVAPDSIGK	EAAFESVFTETNKVVPADSIGKDGKQDL		
26	Q99259	DCE1	KIIPADFEAK	VILIKNERGKIIPADFEAKLEAKQGVY		
27	P25054	APC	SVSSSDGYGK	YKRSNSDLSNVSSDGYKGRGMKPSIES		
28	Q16795	NDUA9	AVKDPDANGK	VVDVSKGIVNAVKDPDANGKSAFVGPSTRY		
29	Q96HA1	P121A	SSNAPDPCAK	QIISSTLSSPSSNAPDPAKETVLSALKEK		
30	Q96MI9	CBPC4	LIQPSDVINK	RIRIFEDIRRLIQPSDVINKVVFSLDEPWP		
31	Q14683	SMC1A	AIIGPNGSGK	QIIGPFQRTFAIGPNGSGKSNLMDAISFV	TCR1a7_MC-04	QIIGPFQRTFAIGPNGSGKSNLMDAISFVSNPPIKIC GHVISRDALNKLINGGKLCPCYDEYHPEEDLQHTAS DFVAKVDDPKLANSEQVDVQFHAGNYSCVASNVQ KHSTSMFFRVVTEPILPEHFLNPKASKDSRGIADPN QSAKIFRPLTVESAVDARDIAKVLVYALLFSWL DKESKIFRIVDPNGLARLWGNHKNRNTNVKPMTR PQAVNARDALAKKIYALHDFDICIVDLLKEPMTVSS DQMAKRLSLSAENPTMNLISODKRISSNPVAKII YGDVPTVILLNKHIDAYKTFPTEPKKDKKDKKKADET
32	Q96G75	RMD5B	HVISRDALNK	SNPPIKICGHVISRDALNKLINGGKLCPC		
33	P50542	PEX5	QHTASDFVAK	YDEYHPEEDLQHTASDFVAKVDDPKLANSE		
34	P07333	CSF1R	SCVASNVQGK	QVDFQHAGNYSCVASNVQGKHSSTSMFFRVV		
35	Q9H2U9	ADAM7	GIADPNQSAK	TEPILPEHFLNPKASKDSRGIADPNQSAK		
36	Q9UKN7	MYO15	AVDARDAIAK	KIFTPLTVESAVDARDIAKVLVYALLFSWL		
37	P41212	ETV6	RIVDPNGLAR	RWEDKESKIFRIVDPNGLARLWGNHKNRNT		
38	Q9NQX4	MY05C	AVNARDALAK	TVVKPMTRPQAVNARDALAKKIYALHDFDI		
39	P07451	CAH3	MTVSSDQMAK	CIVWLLLEKPMVSSDQMAKRLSLSSAEN		
40	Q63HN8	RN213	KRISSNPVAK	PTMNLISODKRISSNPVAKIIYGDVPTVILLNKHIDAYKTFPTEPKKDKKDKKKADET		
41	Q9C0D6	FHDC1	SVGSSDPENK	PDEPGSAAALGSGSSDPENKDRPPLFCISD	TCR1a7_MC-05	PDEPGSAAALGSGSSDPENKDRPPLFCISDVGAA LRAFTSETPPDVTAKACQVCSAWIAALTPVPVFLKS VSPANGKPKPKVPERKSSKNLASVQSEIAPN PLAKEELNFLARLIRLHQLGRQKSLWADVHGK RSHIDALREVLFTSGTRRAVSPNPKARQARSRL WLPMSLKLQASNVNTKRAVSPNPKARQARSRLWDP EVAKCQTQTPDADSRNKKERQREGTEVLDAV KEVSSSDVSGKESVPEEPLRRTWDDSDPES ETDPDAQAKAYVARVLSPPILLNKHIDAYKTFPTEP KKDKKDKKKADET
42	Q86XA9	HTR5A	SETPPDVTAK	VGAALRPAFTSETPPDVTAKACQVCSAWIA		
43	Q5SYE7	NHSL1	SVSPANGKPK	ALTPVPVFLKSVPANGKPKPKVPERKS		
44	Q8WVF1	OSCP1	ESIAPNPLAK	SSKNLASWVTEQESIAPNPLAKEELNFLARL		
45	Q8TDR4	TCP1L	KSLWADVHGK	IRLHQLGRQKSLWADVHGKLRSHIDALRE		
46	Q14244	MAP7	AVSPNPKAR	VFLFTSGTRRAVSPNPKARQARSRLWLP		
47	Q9UKM9	RALY	KLQASNVTKN	MSLKLQASNVTKNPKSINSRVFIGNLNT		
48	Q96H86	ZN764	QTDPADSRNK	QDPEVAKCQTQTPDADSRNKKERQREGTG		
49	Q5T5Y3	CAMP1	GSSSDVSGK	EVLDAVKEVSSSDVSGKESVPEEPLR		
50	Q5XUX1	FBXW9	SETDPDAQAK	RTWDDSDPESETDPDAQAKAYVARVLSPP		
51	Q99650	OSMR	IVISADPENK	NSVGASPASVIVISADPENKEVEEERAGT	TCR1a7_MC-06	NSVGASPASVIVISADPENKEVEEERAGTANMDFV DRMFTNPRDSYGKPLVKDRAELAQEHSTKVLGTV SGPDSLARSTEKPEEEELREVLHWPITANSSKPS NCQNKESASKQSEEPQAGDARFSCPNNFTAKPPA SESPRFSVTRTGEQAPASAPRNQVARMLSATTMIQ VQVPSASVSGKLESPDVPVARRVYLTQLKQREL HLQDNNVRIARDLARIFLLEKHLHLEINNLESKFK SRASNAQAKPSSFFLQMQKTMIGVAVDVTGILGNSV EGKQVLTQGTFRILLNKHIDAYKTFPTEPKKDKK KADET
52	Q8N1G2	CMTR1	FTNPRDSYGK	ANMDFVDRMFTNPRDSYGKPLVKDRAEL		
53	P58304	VX2	TVSGPDSLAR	AQEHSTKVLGTVSGPDSLARKMFGKPEEEEA		
54	O14965	AURKA	SSKPSNCQNK	LREVLEHPWITANSSKPSNCQNKESASKQS		
55	O15446	RPA34	FSCPPNFATK	EPEQAGDAARFSCPNNFTAKPPASESPRFS		
56	Q13332	PTPRS	ASAPRNQVQR	VVTRTGEQAPASAPRNQVARMLSATTMIQ		
57	Q9UNY4	TTF2	KVEPSDVAR	KVSPASVSGKLESPDVPVARRVYLTQLKQ		
58	Q9NZU1	FLRT1	RTIARDSLAR	RELHLQDNNVRIARDSLARIFLLEKHLHLD		
59	Q53SF7	COBL1	KSRASNAQAK	EINNILESKFKSRASNAQAKPSSFFLQMQK		
60	Q16401	PSMD5	GILGNSVEGK	TMIGVAVDVTGILGNSVEGKQVLTQGTFR		
61	Q76FK4	NOL8	ISNSSDVSIAK	REIKTDFLSISNSSDVSIAKDKHAEDNEKR	TCR1a7_MC-07	REIKTDFLSISNSSDVSIAKDKHAEDNEKRSCFDYT GKLIATASADGTARIFAATRKICIEFGIDLTRVALV GNGAGKSTLLKLLTGNNYASVECGAKILANPEAK STSAIENMTTRTFSDTHGSPNSDPLGRADKASDT SSEDAIVFTVQGRAICSDPNPKRVKNVAVYLRVV DTRHEVTVFAADAMARLSGTVGAAVWTSASSW AVRKLTPADQVNYYSRRGRNNSGFTLRPEVETAL VGPNGSGKSTVAALLQNLSDILGSSSSSGLSSDPL AKGSATAESPVAILLNKHIDAYKTFPTEPKKDKK KADET
62	Q8N136	DAW1	ATASADGTAR	SCFDYTGKLIATASADGTARIFAATRKICI		
63	Q9UG63	ABC2F	ALVGPNGAGK	EFGLDTRVALVGPNGAGKSTLLKLLTG		
64	Q9UBS9	SUCO	KILANPEAK	NNYASVECGAKILANPEAKSTSAIENMT		
65	Q86V48	LUZP1	GSPVSDPLGR	TTRTFSDTHGSPVSDPLGRADKASDTSS		
66	Q92583	CCL17	RAICSDPNNK	DAIVFTVQGRAICSDPNPKRVKNVAVYLRV		
67	A1L0T0	HACL2	AVFAADAMAR	RVVDTRHEVTVFAADAMARLSGTVGVAAV		
68	Q99590	SCAFB	KTLPADVQNY	WTSASSWAVRKLTPADVQNYYSRRGRNNSG		
69	Q03518	TAP1	ALVGPNGSGK	TFTLRPEVETALVGPNGSGKSTVAALLQNL		
70	Q7Z309	PBIR2	SGLSSDPLAK	SDILDGSSSSSGLSSDPLAKGSATAESPVA		
71	P53355	DAPK1	LLDPPDPLGK	NLLTRRKLRLDPPDPLGKDWCLLAMNLGN	TCR1a7_MC-08	NLLTRRKLRLDPPDPLGKDWCLLAMNLGNLGN MKLVCGHISRDALNKMFNGSKLCPVVALILALMLS MTGADSHAKRHHGKRFHECGGDKGRVKVITGP NSGKSIYLVKQGLISAPSKPAASIASGGSNSNKG GPEGVAAQANLNFYEGHITSLGPNAGKTTTISML TGLGTVAIKVDDRARRAPPDFVNFKLPRELILRQELS ETILTMVANCNSVMNKARQPPGMPYDNLNYSIN NLSISANVENKYSYLVGLVALQPNLMLSLLEPA DSLAKKKQVHFEDNILLNKHIDAYKTFPTEPKKDK KKADET
72	Q9H871	RMD5A	HIISRDALNK	NNPMLKVCGHISRDALNKMFNGSKLCP		
73	P15516	HIS3	SMTGADSHAK	VFALILALMLSMTGADSHAKRHHGKRFK		
74	Q43196	MSH5	VITGPNSSGK	ECGGDKGRVKVITGPNSSGKSIYLVKQGLI		
75	Q06264	SMCA5	ASGGSNSNKG	SAPSKPAASIASGGSNSNKGPEGVAQA		
76	Q86UK0	ABCAC	SLGPNAGGAK	NLNFYEGHITSLGPNAGKTTTISMLTGL		
77	Q9BXA6	TSSK6	RRAPPDFVNK	GTVAIKVDDRARRAPPDFVNFKLPRELSILR		
78	A5YK66	CNOT1	VANCNSVMNK	QELSETILTMVANCNSVMNKARQPPGMP		
79	Q6NVV3	NIPAF3	LSISANVENK	YTDLNYISNLSISANVENKYSYLVGLVAL		
80	A0PK05	TMM72	SLEPADSLAK	LQPPNLMELSEPADSLAKKQVHFEDNILLNKHIDAYKTFPTEPKKDKK KKADET		

81	Q9BZH6	WDR11	RLASADVNGK	HHNIGSPYCLRLASADVNGKIIVWVDAAGV	TCR1a7_MC-09	HHNIGSPYCLRLASADVNGKIIVWVDAAGVQSSER NQDRKESPPNSRAKDKFLDQERSNASEILKCKFKIL SANGEAKVFRPRDRDDIFNQEGVPRPSYVFSADPIA RPSEINFDGKITVPIVPHVLSFSDADSSAKAGVSKDA IVTASLLIDGELYSGTAAADFMRDFAIFRTLGHSGRT AVLSESDASQGRDSQGKPSRSLTRTPEENLLEVMK SLSVSSDFLGKDKPVSCLGARSQSDHYGGGGRSL DANSSGRLPDAYSQGHDPSPYKAGHDPKQSDSDA CGKGFNHSMEVIHLLNKHIDAYKTFPPEPKDKKK KADET
82	Q9H0G5	NSRP1	KESSPNSRAK	VQSSERNQDRKESPPNSRAKDKFLDQERSN		
83	P20020	AT2B1	KILSANGAEAK	ASEIILKCKFKILSANGAEAKVFRPRDRDDI		
84	Q96Q89	KI20B	YVFSADPIAR	FNQEGVPRPSYVFSADPIARPSEINFDGKI		
85	Q9NPG3	UBN1	LFSADSSAK	ITPVPPIVHLSFSDADSSAKAGVSKDAIVT		
86	Q14563	SEM3A	SGTAADFMGR	ASLLIDGELYSGTAAADFMRDFAIFRTLGH		
87	Q502W7	CCD38	ASQGRDSQGK	SGRTAVLSESDASQGRDSQGKPSRSLTRTPE		
88	Q3V6T2	GRDN	LSVSSDFLGK	ENLLEVMKSLSVSSDFLGKDKPVSCLGAR		
89	Q8N7X1	RMXL3	RSLDANSSGR	SQSDHYGGGGRSLDANSSGRLPDAYSQGH		
90	Q86UD4	ZN329	RTGDSDACGK	PSYPKSYADKRTGDSDACGKGFNHSMEVIH		
91	Q8N456	LRC18	NLISPNSMAK	TTTTPRKTFIPNLISPNSMAKDSWEDWRIRL	TCR1a7_MC-10	TTTTPRKTFIPNLISPNSMAKDSWEDWRIRLVNSRAS PNLIGATGANSLGKVMPTKSPPPPSASPQERSE DSSPDSKAKTRTPLRQRSRVEEVKKNHSILSAPNP EGKIKEELEDLNKPMEDAAPILSLLASPDPAQKHPQ DLASTPSLRAAWSPYEDAVPAANARGKSKAKAP APSASFSTCLKMVASPDSLKMSAQCGQKPLLSRLV EFSAFLEQORPDPSYNKHLFVHIGHANSYQAYIRILA KIQAADPVNRFKRPDELLHLRNGDVSVRKRLVDA NVNAKDMAGRKSSPLLILNKHIDAYKTFPPEPKD KKKKADET
92	Q02078	MEF2A	GATGANSLGK	VNSRASPNLIGATGANSLGKVMPTKSPPPP		
93	Q9UQ35	SRRM2	SDSSPDSKAK	PSASPQERSESDSSPDSKAKTRTPLRQRSR		
94	P32856	STX2	ILSAPNPEGK	VEEVKKNHSILSAPNPEGKIKEELEDLNK		
95	Q5VYP0	S31A3	LLASPDPAK	PMEDAAPILSLLASPDPAQKHPQDLASTPS		
96	Q8NEG4	FAB3F	AVPAANARGK	LRAAWSPYEDAVPAANARGKSKAKAPAP		
97	Q16586	SGCA	MVASPDSHAR	SASPFSTCLKMVASPDSHARCAQGGQPLLS		
98	P28347	TEAD1	QQRPDPSYNK	RLVEFSAFLEQQRPDPSYNKHLFVHIGHAN		
99	Q7Z2Y5	NRK	KIQAADPVNR	SYQAYIRILAKIQAADPVNRFKRPDELLHL		
100	Q95271	TNKS1	LVDAAANVNAK	RNGDVSVRKRLVDAANVNAKDMAGRKSSPL		
101	P22105	TENX	RTCPNSCHGR	EGYVSEDCSIRTCPSNCHGRGRCEEGRCLC	TCR1a7_MC-11	EGYVSEDCSIRTCPSNCHGRGRCEEGRCLCAFQLI DDVLDFTSCSDQMGKPTSADLKLGLSSIQLSANTVK QNSRNLAKLVLFIYRSLGLLEGSPKPGITASSNV GRHSRFGSDPVLGSKASTLRDLFIEDPNFKVNY SYAAVQIDAETILNAFKMLDPDGKGINKEYIKRLL ERIPRERAPPSPSDGYNRLNVIPEKPPSPEDVVL KLFLSFGSDVQNKLESAQCVDGEELGQRLQHYA KIAADFRNKDEKYNHIDESYNLHKAQPAERFFDPNQ RGKALHOKQALRILLNKHIDAYKTFPPEPKDKK KKADET
102	Q5T2R2	DPS1	FTSCSDQMGK	AFQLIDDLVLDFTSCSDQMGKPTSADLKLGL		
103	Q95490	AGRL2	KQNSRNLAK	SSIQLSANTVKQNSRNLAKLVLFIYRSLG		
104	Q13191	CBLB	ITASSNVNGR	LLGEGSPKPGITASSNVNGRHSRFGSDPVL		
105	Q9NY47	CA2D2	FIEDPNFKNK	GSKASTLRDLFIEDPNFKVNYSYAAVQI		
106	Q02045	MYL5	KMLDPDGKGGK	DAEETILNAFKMLDPDGKGINKEYIKRLL		
107	Q8NEY8	PPHLN	RSHPSDGYNR	ERIPRERAPPSPSDGYNRLNVIPEKPPSP		
108	Q9Y5X2	SNX8	SFSGSDVQNK	SEDVVLKFLSFGSDVQNKLESAQCVDGE		
109	Q92598	HS105	AKIAADFRNK	EELGQRLQHYAKIAADFRNKDEKYNHIDES		
110	Q2M3X9	ZN674	RFFDPNQRGK	YNLHKAQPAERFFDPNQRGKALHOKQALR		
111	Q94804	STK10	QLLDRDFAVK	QKMEEHTQKKQLLDRDFAVKQKEDLEAMK	TCR1a7_MC-12	QKMEEHTQKKQLLDRDFAVKQKEDLEAMKVLQT SEQAPSSAPRDVQARMLSTTILVQTYVKTMSLQV INARNALAKHIIYQALFGWICENLRKLEITGVSCR VYAKLLHRYRHILGHPALTHDGRYTCTAANSLGR SEASVYLFRFGLPHLQVATSPDFGKLDIAGEFKE DNFEEIVKLLSHGANVNAKDNELWTPHATVTEKI NKAIRSSSNFLNYDLTRCDYQGRINFDLQORS IGSDSQGRATAANNRQLSSQGFQKSSSGADAF HGKASFATYQHSTILLNKHIDAYKTFPPEPKDKK KADET
112	P23468	PTPRD	SSAPRDVQAR	VLQTSEQAPSSAPRDVQARMLSTTILVQ		
113	Q9ULV0	MY05B	VINARNALAK	TYVKTMSLQVQVINARNALAKHIIYQALFGW		
114	Q5XUX0	FBX31	GVSCRDVYAK	CENLRKLEITGVSCRDVYAKLLHRYRHILG		
115	Q6ZMC9	SIG15	TCTAANSLGR	LPALTHDGRYTCTAANSLGRSEASVYLFRF		
116	Q6DD88	ATLA3	VATSPDFDGK	CFLPHLQVATSPDFDGKLDIAGEFKE		
117	Q96T49	PP16B	LSHGANVNAK	DNFEEIVKLLSHGANVNAKDNELWTPHATV		
118	Q9H3R2	MUC13	RSSSNFLNY	TVTEKINKAIRSSSNFLNYDLTRCDYQGR		
119	Q15154	PCM1	RSIGSDSQGR	QRINFDLQORSIGSDSQGRATAANNRQL		
120	Q8N4H0	SPA6L	KQGDADFHGK	SSQFGKSSSQGDADADFHGKASFATYQHST		
121	Q99424	ACOX2	RLRPSDPEAK	MRYSVIRQRSRLRPSDPEAKVLDYQTTQQK	TCR1a7_MC-13	MRYSVIRQRSRLRPSDPEAKVLDYQTTQQKHLGAC GALKNISFGFRDQDNKIAKNCDDGVPDNPEFVAI VAYTDNPEFVAIAYTDPSDPWAREEMLKIASVI DNPEFVAIAYTDPSDPWAREEMLKIASVI DFGIDMSRIVGPNVGVGKSTLLLLLTGK CARYEAIEYGEKICRNFVIGKQLKINSSTIE LVEKVRQLLEAGADPNGVNRFGRRRAIQVMM CVRVNTGRSCVLSGNAENKPIKNQLGLTL MSTDNSLAREFLTDVNRLCNAVQVREAR NLSLAREFLTDVNRLCNAVQVREARLDLNLNATEG NLSGPNVKNSSPCEDMGIAYMKEAQLIARIAAAN GIGRLVIGNGILSILLNKHIDAYKTFPPEPKDKK KADET
122	Q60716	CTND1	ISFGRDQDNK	HLGACGALKNISFGFRDQDNKIAKNCDDGVP		
123	Q9ULN7	PNM8B	YTDPSDPWAR	DNPEFVAIAYTDPSDPWAREEMLKIASVI		
124	Q8NE71	ABCF1	CIVGPNVGVK	DFGIDMSRIVGPNVGVGKSTLLLLLTGK		
125	Q96N23	CAF54	KITCRNFIGK	CARYEAIEYGEKICRNFVIGKQLKINSSTIE		
126	P42772	CDN2B	AGADPNGVNR	LVEKVRQLLEAGADPNGVNRFGRRRAIQVMM		
127	Q8N9Z0	ZN610	CVLGSNAENK	CVRVNTGRSCVLSGNAENKPIKNQLGLTL		
128	Q99698	LYST	MSTDNSLAR	MSTDNSLAREFLTDVNRLCNAVQVREAR		
129	P33032	MC5R	NLSGPNVKNK	LDLNLNATEGNLSGPNVKNKSSPCEDMGIA		
130	P36871	PGM1	RIAAANGIGR	YMKEAQLIARIAAANGIGRLVIGNGILS		
131	Q7RTR0	NLRP9	VLEGPDGIGK	YTAAARRHTVLEGPDGIGKTLLRKVMLD	TCR1a7_MC-14	YTAAARRHTVLEGPDGIGKTLLRKVMLDLMEMQ SRHGARTSDSQQAYLVQRGAEDRDLKWDHQR AWSSTDSSSNRNLKPAKMTAQIITFSPFLTLVGP NGAGKTTIECLYIAAHLVDSNGYTCMASNSIGKSN LVISLHVQNSHLENESIKRTRSDGVNRDLTEAVPR LPKPTTVKSPPTVLPNFTAKSKVLTRDTEGRDLA TLPREASTPGRNALGRHEYPRLNRIHQEYL SILTPDGKGEKIAELSATQVIGPFRFRFTCIIGP SGKSNVMDALSFVILLNKHIDAYKTFPPEPKDKK KADET
132	Q96CV9	OPTN	RTSDSDQQAY	LMEMQSRHGARTSDSQQAYLVQRGAEDRD		
133	Q9UBL0	ARP21	SSTDSSSNR	LKWDHQRAWSSTDSSSNRNLKPAKMTAKT		
134	Q92878	RAD50	ILVGPNGAGK	QIITFSPFLTLVGPNGAGKTTIECLYI		
135	A6NDA9	LRIT2	TCMASNSIGK	AAHLVDSNGYTCMASNSIGKSNLVISLHVQ		
136	Q13496	MTM1	KRTSRDGVNR	NSHLENESIKRTRSDGVNRDLTEAVPRLP		
137	Q53FE4	CD017	VKLPPNFTAK	KPPTTVKSPPTVLPNFTAKSKVLTRDTEG		
138	Q9P219	DAPLE	STPGRNALGR	RDLATLPREASTPGRNALGRHEYPRLNRIHQ		
139	P04114	APOB	ILTDPDGKGGK	LHRNIQEYLSILTPDGKGEKIAELSATQV		
140	Q8NDV3	SMC1B	CIIGPNSGSK	QVIGPFRFRFTCIIGPNSGSKSNVMDALSFV		
141	Q6DN14	MCTP1	GLMAADVTGK	FLQVKVIRAEGLMAADVTGKSDPFCVVELN	TCR1a7_MC-15	FLQVKVIRAEGLMAADVTGKSDPFCVVELNKPQL HSMVARSCLRNAAGKNYIIFGSPVGGGTRSVVEL GIAANGINKLLDAKSLGLKAGKCKFERILEMDPSNV QKGNLVCVYFEEPGDLAWNFLMKVQARDVTARD SILSHKVLNDGGCCSSRDQCCPPNFTGKLCQIPV HGASQQGQRSTPLIARNGHAKVVRLLLEHYRR HPTDINILTLSDSNGKNRSSARILKQALQDSNR GVRKKAADALGKLSIHIKVDPODFYKORLLISAPD PSNRYKMQISMLQILLNKHIDAYKTFPPEPKDKK KKADET
142	Q8N414	PGBD5	RSLCRNAAGK	NKPQLHSMVARSCLRNAAGKNYIIFGSPSI		
143	Q8NCS7	CTL5	LGAANGINK	GNGGTRSVVELGIAANGINKLLDAKSLGLK		
144	Q6ZXV5	TMT3	EMDPSNVQGGK	GAKKCKFERILEMDPSNVQGGKHNLCVYFEE		
145	Q9BX69	CARD6	KVQARDVTAR	PGDLAWNFLMKVQARDVTARDSILSHKVL		
146	Q14766	LTBP1	CQCPNFTGK	NGGQCSSRDQCCPPNFTGKLCQIPVHGAS		
147	Q9UK73	FEM1B	IIAARNGHAK	QGGQGRSTPLIARNGHAKVVRLLLEHYRR		
148	Q96QV1	HHIP	TILCSDSNGK	RHPTDINILTLSDSNGKNRSSARILQI		
149	Q92616	GCN1	RLKAADALGK	KALQDSNRGVRKKAADALGKLSIHIKVDPO		
150	Q60687	SRPX2	IISAPDPSNR	DQFYEQRLLIISAPDPSNRYKMQISMLQ		
151	Q8VWZ7	ABCA5	GLLGPNGAGK	SFCVKKGEILGLLGPNGAGKSTIINILVGD	TCR1a7_MC-16	SFCVKKGEILGLLGPNGAGKSTIINILVGDIGYCI FDKRRSDPNFKNRLRERRKQKLTILGNQLDGIHLLD PDVVARFQKQRYPDGIIDKEDWLNLYHLTCRVDIGK ELQKQGRQEAFCFVPLDATFVMMVARDSENKGFV NPLIPRRMENIIDQCLQKPADVIGKSMNAQICIPLEG ESVTEIDISFLESPNPNKDYEEPVKRVEDGMTKGL LRVTLSDSQVYQAGSNGOPLPDVDMATMNNKES APNSGSKNDKSKVLTQGMELRDAGSQESSPSN GHGKLAGSPYLGRILLNKHIDAYKTFPPEPKDKK KKADET
152	Q15388	TOM20	RRSDPNFKNR	IGYCIYDFKRRSDPNFKNRLRERRKQKQL		
153	Q86U44	MTA70	HLLDPDVVAR	ITLGNQLDGIHLLDPDVVARFQKQRYPDGI		
154	Q9NQW7	XPP1	HLTCRVDIGK	DKECDWLNLYHLTCRVDIGKELQKQGRQEA		
155	Q9Y305	ACOT9	VMMVARDSENK	EFCFVPLDATFVMMVARDSENKGFVFNPLIP		
156	Q9UJX5	APC4	LQKPADVIGK	RRMENIIDQCLQKPADVIGKSMNAQICIPLEG		
157	Q9UBV2	SE1L1	FLESPNPNK	EGESVTEIDISFLESPNPNKDYEEPVKRVRK		
158	Q95405	ZFYV9	VTLSDSQVGY	EDGMTKGLRVTLDSDQVGYQAGSNGOPLP		
159	Q92547	TOPB1	ESAPNSGSGK	DVDNMATMNNKESAPNSGSKNDKSKVLTQT		
160	Q7L9B9	EEP1	ESSPNSGHGK	GMELRDAGSQESSPSNGHGLAGSPYLGRL		
161	Q14526	HIC1	GVPGPDGKGGK	GALAGLGGPVGVPDGGKGLDFPEGVFAV	GALAGLGGPVGVPDGGKGLDFPEGVFAVGPACP TSCNGAAAPNSNCSGRPCVFGCVIPLPIQFGKIO	
162	Q9Y6R7	FCGBP	AAAPNSCSGR	GPACPTSCNGAAAPNSNCSGRPCVFGCVIPLPIQFGKIO		

163	Q5JUQ0	FA78A	AISDSGVDNY	LPDLQEGKIQAISDSGVDNYPWYGNTTETC	TCR1a7_MC-17	AISDSGVDNYPWYGNTTETCGSSVFLCYKKSVPAS NAIAYKAGLIFRYPEAYRFHEFHSPALEDADFENK MILLVGQYSVHSPITQGTPLTCSNVENRGRSRSHSP AHASTTSDDDGNYTIMAANPQGRISCSGHLMVQSL DVAKLLQRRAAADSAGKNGLTPLHVAAPDALS VQGLGEGFSVYAAKSK APRNP LAKWAVGEGPLNEILLNKHIDAYKTFPPT ET
164	Q5VZ89	DEN4C	SVPASNAIAY	GSSVFLCYKKSVPASNAIAYKAGLIFRYPE		
165	Q9H223	EHD4	ALEDADFENK	AYRFHEFHSPALEDADFENKPMILLVGQYS		
166	P08235	MCR	LTCSPNVENR	VHSPITQGTPLTCSNVENRGRSRSHSPAHA		
167	Q86TC9	MYPN	TIMAANPQGR	STTSDDDGNYTIMAANPQGRISCSGHLMVQ		
168	Q01484	ANK2	RRAAADSAGK	SLDVAKLLQRRAAADSAGKNGLTPLHVAA		
169	Q9NVT9	ARMC1	RDLAADPLNR	PDALSVVQRLDLAADPLNRRRAIVDQGL		
170	Q09019	DMWD	SKAPRNPLAK	GEGFSVYAAKSKAPRNPLAKWAVGEGPLNE		
171	P23381	SYWC	GFTDSDCIGK	VTFNQVKGIFGFTDSDCIGKISFPAIQAAP		
172	Q14439	GP176	YIGSADFQAK	TEDEEESEAKYIGSADFQAKEIFSTCLEGE		
173	Q7Z7A1	CNTRL	IHSPSDVLGK	KLKLGTGEMNIHSPSDVLGKSLADLQKQFS		
174	Q5HYK9	ZN667	KKLPPNQC NK	APDSGSKCETKKLPPNQC NKSGQ SICQKLV		

Supplementary Table 12. List of primers used for TCR cloning derived from TCR1 libraries

ID	Primer Name	Sequence (5' ~ 3')	Usage
1	TCR1_Lib1_Forward_Primer_01	GGACTCCGGCGTGACACAGA	RT&1st PCR primers
2	TCR1_Lib1_Reverse_Primer_01	CGCTGTGCACTTCCTTGCCG	
3	TCR1_Lib2_Forward_Primer_01	GGAGGAAAACCCCGGCCCTA	
4	TCR1_Lib2_Reverse_Primer_01	AGGCACAGGGTGCTGTCCTG	
5	TCR1_Lib1_Forward_Primer_02	ACCGCCACCGGCCAAAGAGT	The nested PCR primers for TCR1 Lib1
6	TCR1_Lib1_Reverse_Primer_02	CCACCAGCTCAGTTCCACGT	
7	TCR1_Lib2_Forward_Primer_02	GAGAGCCGTGATCGCCTCCA	The nested PCR primers for TCR1 Lib2
8	TCR1_Lib2_Reverse_Primer_02	GGTTCTGGATGTTGGCCAGC	