Cell Reports, Volume *28*

Supplemental Information

Sensitive Detection and Analysis of Neoantigen-Specific T Cell Populations from Tumors and Blood

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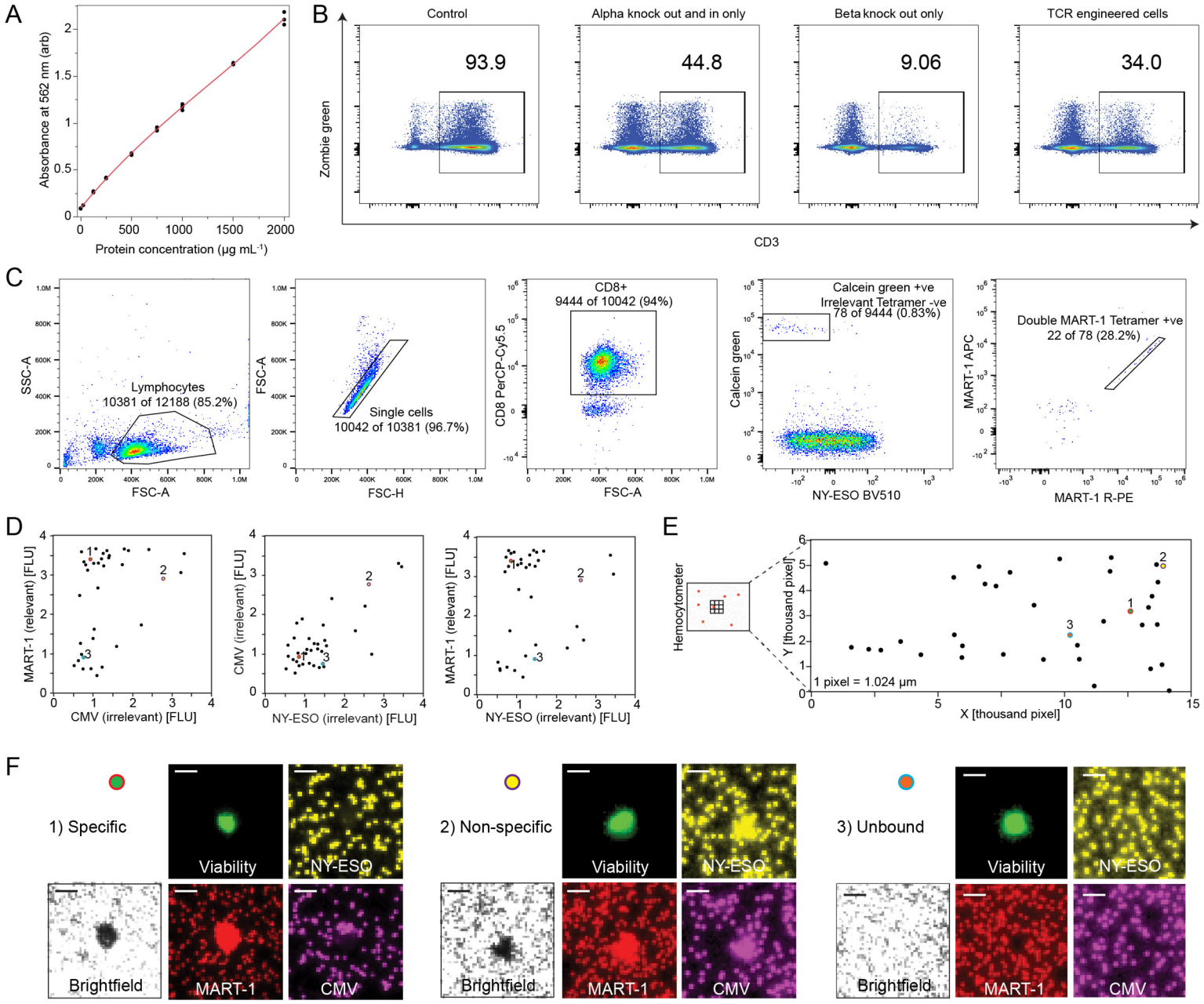

Figure S1: Characterization of NP and engineered T cells and sample analysis of NP-barcoded NACS and flow cytometry. Related to Figure 1.

(A) Plot of bicinchoninic acid assay (BCA) calibration curve fitted using a cubic polynomial (R^2=1.0), resulting in a limit of detection of 1.64 μg/mL. The standards were prepared and analyzed in triplicates. The number of pMHC tetramers per NP was measured to be 20270, assuming that the molecular weight of pMHC tetramer is 236.8 kDa. (B) Flow cytometry analysis of CRISPR-Cas9-based TCR gene-editing T cells. CD3 was used as an indirect measure of TCR gene editing efficiency since TCR-CD3 complexes are presented on the cell surface only when both CD3 and TCR subunits are co-expressed. Density plots of donor cells are shown for no electroporation conditions (control), knock out-knock in at endogenous TCR-alpha locus using F5 TCR homology-directed repair template, knock out at endogenous TCR-beta locus, and simultaneous alpha knock out and in and beta knock out (TCR engineered cells). The gene editing efficiency for the TCR engineered cells is about 34%. Only 2% of these cells expressed endogenous TCR (IP26). (C) Gating scheme for flow cytometry analysis of a spiked specimen. MART-1 specific T cells are defined as Calcein green positive, NY-ESO tetramer negative, and double MART-1 tetramer positive. (D-F) NP-barcoded NACS analysis of a MART-1 spiked specimen. Cells imaged in the hemocytometer can either be (1) specific, (2) non-specific, or (3) unbound. (D) Representative fluorescent plots with each type of cell highlighted. (E) Representative x-y coordinate map of the hemocytometer chip. (F) Representative bright field and fluorescent images. Scale bars are 10 μm. Here, MART-1 pNP (stained red) is accompanied by two irrelevant pNP (stained yellow and purple). Thus, specific cells must be coated with black pNP in bright field microscopy, stain positive for red and Calcein green, and stain negative for yellow and purple.

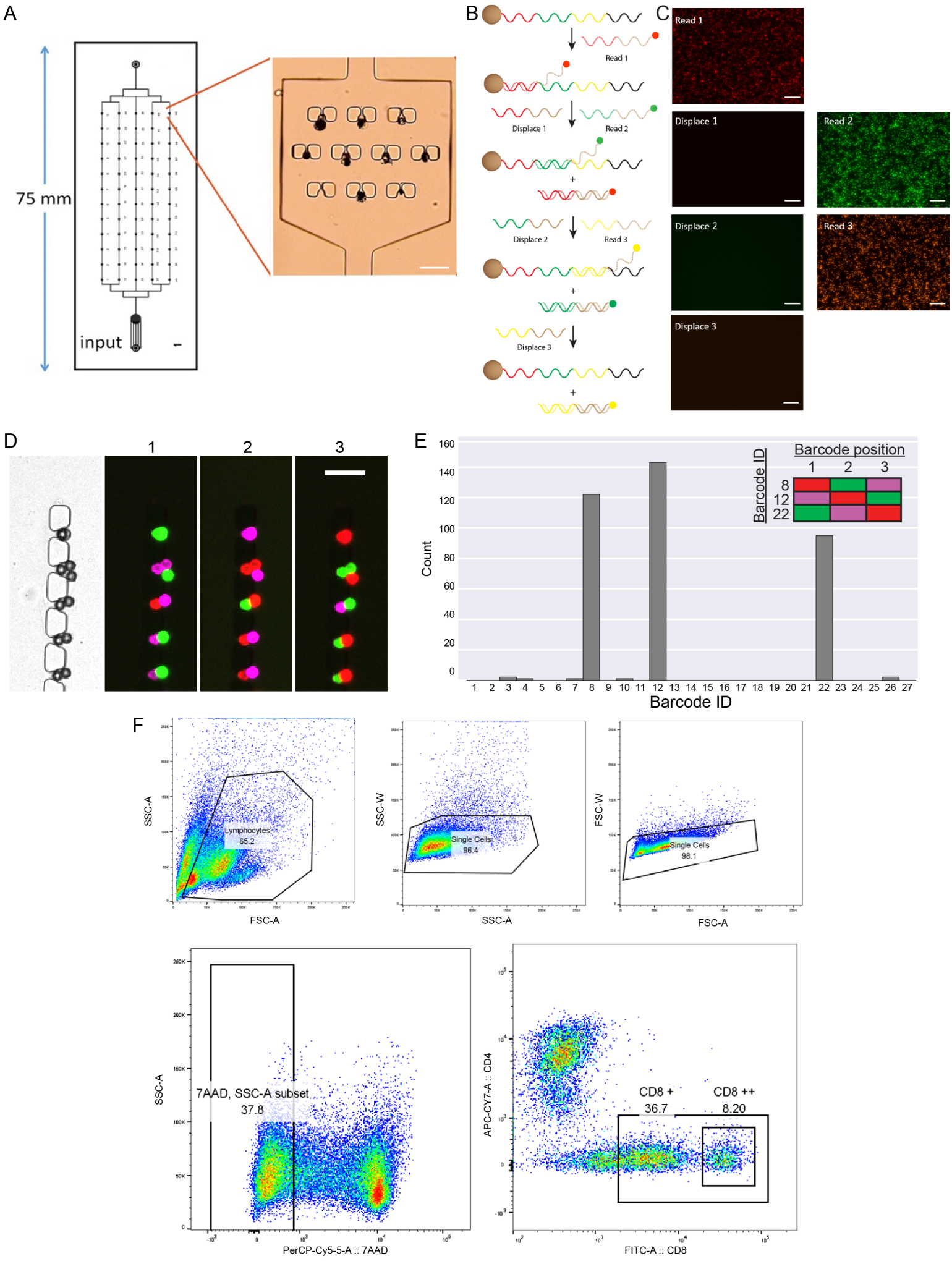
A
75 mm
input
B
Read 1
Displace 1
Read 2
Displace 2
Read 3
Displace 3
C
Read 1
Displace 1
Read 2
Displace 2
Read 3
Displace 3
D
1
2
3
E
Count
Barcode ID
Barcode position
1 2 3
8
12
22
F
SSC-A
FSC-A
Lymphocytes
65.2
SSC-W
SSC-A
Single Cells
96.4
FSC-W
FSC-A
Single Cells
98.1
SSC-A
PerCP-Cy5-5-A :: 7AAD
7AAD, SSC-A subset
37.8
APC-CY7-A :: CD4
FITC-A :: CD8
CD8 +
36.7
CD8 ++
8.20

Figure S2: Parallel NP-barcoded NACS device design, readout validation, and sample selection. Related to Figures 2 and 3.

(A) Design of microchip for the capture and isolation of antigen-specific T cells. Cells are injected into the input, and flow through one of 5 channels, before exiting to waste. Each channel contains 12 microchambers, each of which has 10 cell traps. The micrograph at right shows one of those microchambers, with 9 of the 10 cell traps filled. The trapped cells appear black because of the pNPs that coat the cell surface. Scale bar is 50 μm. (B) Illustration and (C) test data of the DNA sequential barcode readout process, reflecting 3 fluorescent read-out steps, and 3 displacement steps. The fluorescence images illustrate this process for DNA barcodes appended to NPs. Scale bar is 50 μm. (D) Barcode cross reactivity evaluation. To check for cross reactivity of displacement and read DNA during the decoding process, an equal mixture of three DNA-barcoded 10-μm beads is analyzed after isolating individual beads in the cell traps of a microfluidic chip. Scale bar is 40 μm. (E) Histogram of the three labeled barcode positions as read out from beads isolated within a single column of cell traps in the microchip of panel D. The counts for each of the three barcoded identities 8, 12, and 22 (inset) indicated that each population accounted for approximately 1/3 of the trapped beads, as expected. Negligible reads (<2) were detected from absent barcodes. (F) Sample density plots of CD8+ T cells from patient #1 TILs sorted for parallel NP-barcoded NACS analysis.

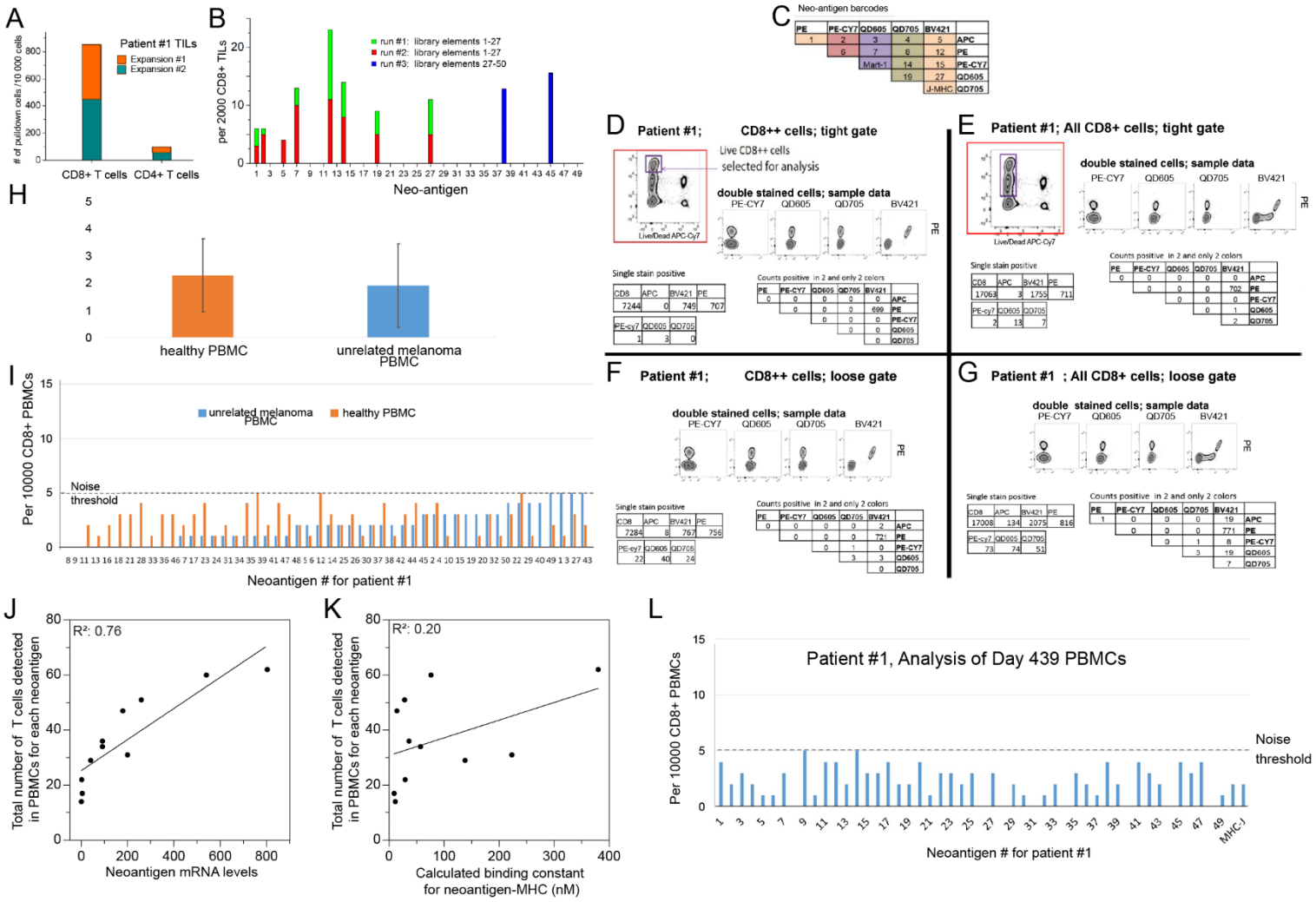

Figure S3. Patient #1 analysis. Related to Figures 3 and 4.

(A) Number of neoantigen-specific CD8+ T cells captured for patient #1 expanded TILs from two independent analyses using pNP library 1-27. Non-selective capture is estimated to be around 0.5%, as gauged by the numbers of CD4+ T cells that were captured using the same method. The two independent captures were carried out more than one week apart. (B) Neoantigen populations detected in expanded TILs from the tumor of patient #1. For each run, approximately 10,000 CD8+ TILs were analyzed by NP-barcoded NACS, resulting in around 500 cells pulled down by pNPs. After free particles are removed using a 5 μm pore transwell membrane, the pNP-bound cells are loaded into the microfluidic chip (Figure S2A), and cells are isolated within the cell capture chambers of the microfluidic chip for fluorescence-based readouts of the attached pNPs. Capture efficiency within the microfluidic chip was about 10% (i.e. of the 500 cells that are loaded, 50 cells can be captured for analysis). Runs #1 and #2 used the same 27-element NP-barcoded NACS library, corresponding to the top-ranked 27 putative neoantigens. All populations shown for runs #1 and #2 were detected in both runs, except neoantigen 5, which was detected in 4 clean reads only in run #2. Run #3 utilized a NP-barcoded NACS library designed to capture CD8+ T cells specific to neoantigens rank ordered 28-50. (C-G) Multiplexed flow cytometry analysis of patient #1 expanded TILs and detection statistics for two selections of CD8+ T cells. (C) Color encoding scheme of neoantigen-MHC tetramers. For example, neoantigen 7 tetramer is stained with QD605 and PE. The CD8++ subpopulation is analyzed in panels D and F, while the CD8+ T cells are analyzed in panels E and G. Each panel incorporated either a tight or loose gating condition for counting those cells that stain with exactly 2 colors. Each panel provides the numbers of cells analyzed (single stain positive for CD8), as well as the numbers of cells that stained positive for single stains and two stains. Note that neoantigen 12 specific CD8+ T cells are almost completely localized within the CD8++ subpopulation.

(H and I) Results of serial NP-barcoded NACS control experiments in which the pNP library designed for patient #1 was used to capture CD8+ T cells from a different patient with melanoma (blue) and from a healthy donor (orange). (H) Average numbers of pulled-down T cells, per library element, from healthy donor PBMC and PBMC from an unrelated patient with melanoma, on the same clinical trial as patient #1. Data is presented as mean ± standard deviation (n=50). (I) Number of pulled-down T cells for each library element. The numerical labels on the x-axis corresponds to the rank-order of the putative neoantigens. The data has been sorted according to frequency of detection for the patient, so as to illustrate that there is no correlation between these two controls. A correlation would likely indicate capture by non-selective library elements. The noise threshold was set at the average plus two

standard deviations. (J and K) Correlation analysis between the number of neoantigen-specific T-cell populations and measured neoantigen-related mRNA levels (J), or calculated binding constant for neoantigen-MHC (K). The total T-cell numbers are a summation of each neoantigen-specific population counts from PBMCs (day 41, 187, and 207) and TILs at day 187 (Figure 3C). Only neoantigen populations that appeared in more than one analysis are included in this correlation (i.e. neoantigen 1, 9, 30, and 35 were excluded). (L) Analysis of patient #1 PBMCs from a blood draw collected 439 days following the start of anti-PD-1 therapy. No populations above two standard deviations of the mean (2.2±1.4 cells per library element) were recorded.

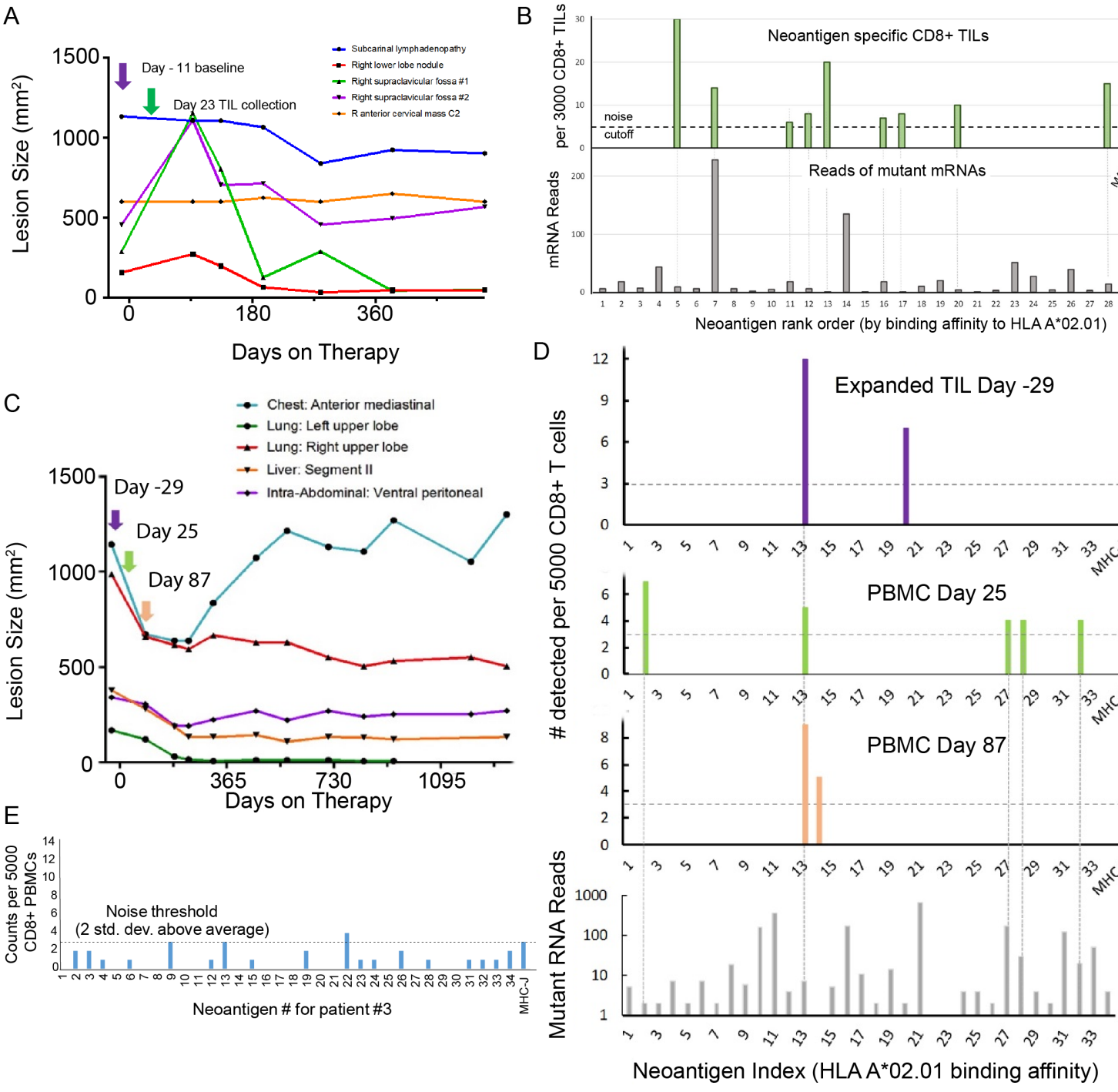

Figure S4. Patient #2, #3, and #4 analysis. Related to Figures 3 and 4.

(A and B) TIL analysis of patient #2. (A) The timeline of the lesion size of subcarinal lymph node, supraclavicular lymph node, and neck in patient #2. Day 0 corresponds to the start of anti-PD-1 therapy. A baseline tumor biopsy (indicated by the purple arrow) was collected for genomic and transcriptomic analysis at day -11. Black markers represent CT-scan measurement dates, while the green arrow corresponds to the time point of analysis. (B) Serial NP-barcoded NACS analysis of patient #2 TILs using a pNP library formed from the top 28 putative neoantigens predicted for patient #2, plus the MART-1 tumor antigen. Only T-cell populations detected at more than 5 cells per 3000 TILs were considered statistically significant. The bottom graph shows the mRNA copies measured for the mutated proteins from which the neoantigens are derived. (C-E) TIL and PBMC analysis of Patient #3 over the course of response to anti-PD-1 therapy. (C) The timeline of the lesion size of chest, lung, liver and intra-abdominal in Patient #3. Day 0 corresponds to the start of anti-PD-1 therapy. A baseline tumor biopsy (indicated by the purple arrow) was collected for genomic and transcriptomic analysis at day -29. Black markers represent CT-scan measurement dates, while the arrows correspond to the time points of analysis, and are color coded for the bar graphs in panel D. (D) Results of serial NP-barcoded NACS analysis using patient #3 specific 34-element pNP library. The plots are neoantigen specific T-cell populations detected from expanded TILs collected from baseline (top graph), PBMCs over the course of the therapy (middle two graphs), and mutation-containing mRNA read counts for the mutant proteins (bottom graph) from the baseline RNA-seq. The horizontal dashed lines in the TIL and PBMC analysis graphs represent the signal threshold above which the identification of a T-cell population is statistically significant, which is determined in panel E. The vertical gray dashed lines indicate T-cell populations detected across the different time points and patient materials, and their correlation with RNA transcripts reads. (E) Results of control experiments in which a patient #3 specific 34-element pNP library was used to capture CD8+ PBMCs from a healthy donor. The average pulled-down T-cell numbers from healthy donor PBMCs was 0.9 ± 1.1 (mean ± standard deviation). The noise threshold was set at average plus two standard deviations. (F-H) Detection and single cell TCR sequencing results of a neoantigen-specific T-cell population from a patient expressing the HLA-A*03:01 allele (patient #4). (F) Of 5 potential neoantigens, the second highest predicted binder was detected above the signal threshold. (G) Micrographs showing a representative neoantigen-specific cell in bright field and fluorescence channels. Scale bars are 10 μm. (H) Cells were tetramer-sorted using the neoantigen SLHAHGLSYK into 24 wells. TCR β chains were identified in 10 wells, and 7 wells shared one of two repeated TCR β sequences.

Table S1. Patient Information. Related to Figures 2, 3, and 4.

	Patient #1	Patient #2	Patient #3
irRECIST	Partial Response	Partial Response	Partial Response
Study	Merck MK-3475-001	Merck MK-3475-001	Merck MK-3475-001
Age at Tx start	61	70	70
Sex	M	M	M
ECOG Status at Baseline	0	0	0
Disease Status at Baseline	M1c	M1b	M1c
BRAF/NRAS	BRAF V600E	NRAS G13D	NRAS Q61K
Melanoma Sub-Type	Cutaneous	Cutaneous	Cutaneous
HLA Type	HLA-A*02:01, HLA-A*68:01 HLA-B*15:07, HLA-B*44:02 HLA-C*03:03, HLA-C*07:04	HLA-A*02:01, HLA-A*24:02 HLA-B*51:01, HLA-B*58:01 HLA-C*01:02, HLA-C*03:02	HLA-A*02:01, HLA-A*03:01 HLA-B*07:02, HLA-B*51:01 HLA-C*02:02, HLA-C*07:02
Prior Systemic Therapies	1. Vemurafenib 2. Ipilimumab 3. Chemotherapy+IL-2 4. TIL adoptive cell transfer	1. Adjuvant GM-CSF	1. Ipilimumab
Date of first evidence of tumor regression	Day 166	Day 134	Day 87
Date of first irRECIST Response (-50%)	Day 250	Day 280	Day 186
Site of Baseline Biopsy	Left Chestwall	Subclavicular Lymph Node	Right Chestwall
Date of Baseline Biopsy for Exome/RNA-seq	Day -28	Day -11	Day -29
# Somatic Nonsynonymous Mutations	350	745	660
Date of Biopsy for TIL collection	Day 187	Day 23	Day -29
Date of PBMCs Sampled	Day 41, Day 187, Day 208, Day 439	N/A	Day 25, Day 87
SRA Run ID, tumor WES	SRR3083863	SRR3083845	SRR3083847
SRA Run ID, normal WES	SRR3083864	SRR3083846	SRR3083848
Accession ID, WES	SRP067938	SRP067938	SRP067938
SRA Run ID, tumor RNA	SRR3184283	SRR3184291	SRR3184293
Accession ID, RNAseq	GSE78220	GSE78220	GSE78220

Table S2. Analysis of binding affinity and gene expression of putative neoantigens in patients. Related to Figures 2, 3, and 4.

Patient #	HLA	neoantigen	Gene	Protein_Change	FPKM	Mut_RNA_Reads_	pepLen	mutantpep Position	peptideTumor	K_D (nM)	peptideNormal	K_D (nM)	DeltaAbs (nM)
1	A2:01	1	DYM	p.S434F	20.5835	53	9	1	FLGSLLILV	5	SLGSLLILV	13	-8
1	A2:01	2	SLC8A2	p.P719S	0.025223	4	9	3	RLSSCFDYV	9	RLPSCFDYV	15	-6
1	A2:01	3	IFNA7	p.P133S	0	0	9	1	SLMNEDFIL	11	PLMNEDFIL	820	-809
1	A2:01	4	DYM	p.S434F	20.5835	53	10	1	FLGSLLILVV	11	SLGSLLILVV	33	-22
1	A2:01	5	IFNA7	p.P133S	0	0	10	1	SLMNEDFILA	11	PLMNEDFILA	550	-539
1	A2:01	6	RFTN1	p.G348D	5.27924	36	9	4	SLHDLTDGV	12	SLHGLTDGV	36	-24
1	A2:01	7	PRRC2C	p.S2260F	27.70395	179	9	6	KAWENFPNV	14	KAWENSPNV	22	-8
1	A2:01	8	FASTKD1	p.S159F	10.8846	26	9	6	LLSEFFSCL	18	LLSEFSSCL	26	-8
1	A2:01	9	FASTKD1	p.S159F	10.8846	26	10	7	KLLSEFFSCL	20	KLLSEFSSCL	32	-12
1	A2:01	10	LDHD	p.R148Q	4.41145	20	10	2	LQDSGLWFPV	21	LRDSGLWFPV	2629	-2608
1	A2:01	11	IFNA7	p.P133S	0	0	11	1	SLMNEDFILAV	25	PLMNEDFILA	94	-69
1	A2:01	12	USP7	p.D789Y	41.2267	259	9	1	YLYHRVDVI	28	DLYHRVDVI	10865	-10837
1	A2:01	13	PLS1	p.P376L	4.53658	19	10	10	FVANLFNTYL	29	FVANLFNTYP	3399	-3370
1	A2:01	14	CPVL	p.R25H	5.87024	2	10	4	GLFHSLYRSV	29	GLFRSLYRSV	49	-20
1	A2:01	15	PCDHB6	p.G327E	11.7725	91	9	4	GLSEKCSLV	36	GLSGKCSLV	132	-96
1	A2:01	16	LDHD	p.R148Q	4.41145	20	11	3	HLQDSGLWFPV	39	HLRDSGLWF	126	-87
1	A2:01	17	GOSR1	p.P213S	14.3655	84	9	7	TLANRFSAV	45	TLANRFPAV	13	32
1	A2:01	18	CHD8	p.A866V	10.04205	64	10	5	FLVIVPLSTI	48	FLVIAPLSTI	38	10
1	A2:01	19	PCDHB6	p.G327E	11.7725	91	10	4	GLSEKCSLVV	57	GLSGKCSLVV	107	-50
1	A2:01	20	ENTHD2	p.P110F	2.401075	47	11	1	FLHGNSLYQKV	61	PLHGNSLYQK	1934	-1873
1	A2:01	21	PPFIA4	p.S43F	0.305613	6	9	1	FLRESQETL	65	SLRESQETL	522	-457
1	A2:01	22	FASTKD1	p.S159F	10.8846	26	10	6	LLSEFFSCLA	66	LLSEFSSCLA	133	-67
1	A2:01	23	LGALS8	p.P29S	11.86285	6	9	4	QLDSGTLIV	67	QLDPGTLIV	70	-3
1	A2:01	24	OSGIN1	p.P233L	7.949295	84	9	5	WMGLLDLEV	67	WMGLPDLEV	202	-135
1	A2:01	25	NUMA1	p.D136E	29.5143	144	9	4	FVLEHEDGL	71	FVLDHEDGL	79	-8
1	A2:01	26	PCLO	p.P2787L	0.07751	0	10	2	TLVSLATETV	75	TPVSLATETV	20558	-20483
1	A2:01	27	SNRNP200	p.H1175Y	51.15825	540	10	7	KMGKTIYKYV	76	KMGKTIHKYV	117	-41
1	A2:01	28	PLS1	p.P376L	4.53658	19	9	7	NLFNTYLCL	77	NLFNTYPCL	42	35
1	A2:01	29	MCM6	p.A630V	11.7303	33	9	5	RLSEVMARM	82	RLSEAMARM	117	-35
1	A2:01	30	DYM	p.S434F	20.5835	53	10	6	VLTEIFLGSL	105	VLTEISLGSL	185	-80
1	A2:01	31	IGSF1	p.G718E	0.029302	0	11	6	ALYKEEEQEPV	133	ALYKEGEQEP	133	0
1	A2:01	32	TAOK1	p.D299V	9.740685	32	11	11	VLIDLIQRTKV	134	VLIDLIQRTKD	21537	-21403
1	A2:01	33	QSER1	p.R1185C	9.301975	41	10	3	MVCTFCPPPL	138	MVRTFCPPPL	1307	-1169
1	A2:01	34	FAM83B	p.P127S	0.003497	0	10	5	LLFHSPRAHL	139	LLFHPPRAHL	222	-83
1	A2:01	35	KIF1C	p.M81V	26.47415	744	11	1	VLLHAFEGYNV	147	MLLHAFEGYN	73	74
1	A2:01	36	PCLO	p.P2787L	0.07751	0	9	8	VTSSIVTLV	158	VTSSIVTPV	57	101
1	A2:01	37	C8orf86	p.P192L	0	0	10	2	SLAPPRTPEL	212	SPAPPRTPEL	26625	-26413
1	A2:01	38	RETSAT	p.S492F	55.40045	200	9	1	FFVEASMSV	223	SFVEASMSV	2721	-2498
1	A2:01	39	ADCK1	p.C379S	4.45008	22	11	1	SMLTARSWDSV	248	CMLTARSWD	729	-481
1	A2:01	40	NUMA1	p.D136E	29.5143	144	11	4	FVLEHEDGLNL	261	FVLDHEDGLN	358	-97
1	A2:01	41	RPL13	p.A112T	403.4245	23	9	4	SLQTNVQRL	273	SLQANVQRL	152	121
1	A2:01	42	COPS7A	p.Y113F	48.0616	372	9	7	KVKCIPFAV	313	KVKCIPYAV	465	-152
1	A2:01	43	LYST	p.R395C	36.5952	55	10	7	FVFSKYCHRA	366	FVFSKYRHRA	1426	-1060
1	A2:01	44	SLC39A10	p.N393S	20.23725	86	10	1	SLVPEDEANI	368	NLVPEDEANI	1530	-1162
1	A2:01	45	DUSP4	p.L203F	54.64275	803	10	5	ILPFFYLGSA	380	ILPFLYLGSA	786	-406
1	A2:01	46	SNTG1	p.N127I	0	0	11	2	RIAGEEVTLTV	416	RNAGEEVTLT	7235	-6819
1	A2:01	47	TTC34	p.A88T	0.016071	1089	10	3	VLTRLALLQL	418	VLARLALLQL	146	272
1	A2:01	48	F13A1	p.S305I	0.51986	0	11	6	LLEYRISENPV	440	LLEYRSSENP	813	-373
1	A2:01	49	PIAS2	p.P138Q	7.271005	27	11	7	MQQPSPQIPPV	449	MQQPSPPIPP	367	82
1	A2:01	50	CPVL	p.R25H	5.87024	2	9	4	GLFHSLYRS	463	GLFRSLYRS	1048	-585
2	A2:01	1	LRBA	p.S1325L	1.881915	6	9	8	LLTDLLFLI	4	LLTDLLFSI	4	0
2	A2:01	2	TK2	p.H137Y	4.86209	18	10	8	RLMERSIYSA	7	RLMERSIHSA	19	-12
2	A2:01	3	PKD1	p.S3220L	6.81945	7	9	8	FLVNDWLLV	8	FLVNDWLSV	7	1
2	A2:01	4	ATMIN	p.S715C	8.58103	43	10	5	FLDSCPHLPL	8	FLDSSPHLPL	9	-1
2	A2:01	5	CASK	p.H512Y	2.38613	9	9	7	KMNELNYCI	10	KMNELNHCI	24	-14
2	A2:01	6	LRBA	p.S1325L	1.88192	6	10	9	RLLTDLLFLI	10	RLLTDLLFSI	8	2
2	A2:01	7	PIGT	p.R570W	161.945	228	9	7	RLANLIWRA	11	RLANLIRRA	763	-752
2	A2:01	8	LRBA	p.S1325L	1.881915	6	9	9	RLLTDLLFL	12	RLLTDLLFS	909	-897
2	A2:01	9	EPHB1	p.R90C	1.78296	2	10	7	RIYTEMCFTV	13	RIYTEMRFTV	41	-28
2	A2:01	10	TRAPPC9	p.P181L	5.145625	5	9	2	VLFEKKDFV	16	VPFEKKDFV	18017	-18001
2	A2:01	11	MROH2A	p.S1064F	0.257644	18	9	7	KIFCASFRI	17	KIFCASSRI	261	-244
2	A2:01	12	LRBA	p.S1325L	1.881915	6	9	2	FLIETDIQM	17	FSIETDIQM	4758	-4741
2	A2:01	13	ELOVL3	p.P17L	0.64389	1	10	5	QLFQLYNFEL	23	QLFQPYNFEL	35	-12
2	A2:01	14	POMT2	p.H664N	8.53243	135	10	5	VLYFNHYFPA	24	VLYFHHYFPA	22	2
2	A2:01	15	SLC5A8	p.S76F	0.112721	1	9	7	TVLGTPFEV	26	TVLGTPSEV	391	-365
2	A2:01	16	TK2	p.H137Y	4.86209	18	10	3	SIYSARYIFV	26	SIHSARYIFV	205	-179
2	A2:01	17	DYDC2	p.H39Y	0.328192	1	9	8	YLAHWLYYY	27	YLAHWLYHY	99	-72
2	A2:01	18	SASH1	p.P981S	3.694035	10	9	3	KISSQPPPV	28	KIPSQPPPV	51	-23
2	A2:01	19	TERF1	p.S252L	7.794875	20	9	2	KLSTFLMKA	29	KSSTFLMKA	9473	-9444
2	A2:01	20	TTC39B	p.S634F	1.13525	4	9	8	FTLFELAFL	31	FTLFELASL	55	-24
2	A2:01	21	CDK12	p.S433I	3.62697	1	10	8	FLPRKENISV	31	FLPRKENSSV	75	-44
2	A2:01	22	EPB41L4A	p.R127C	3.31517	3	10	5	VLQGCLPCPV	31	VLQGRLPCPV	75	-44
2	A2:01	23	CCDC61	p.S469F	10.9458	51	9	1	FLANSGGWV	33	SLANSGGWV	300	-267
2	A2:01	24	EPDR1	p.D100N	18.869	27	9	7	YILLYKNGV	37	YILLYKDGV	59	-22
2	A2:01	25	TTC39B	p.S634F	1.13525	4	9	1	FLYKSQGEI	40	SLYKSQGEI	286	-246
2	A2:01	26	TUBG1	p.P350S	30.40205	39	9	3	FISWGPASI	44	FIPWGPASI	74	-30
2	A2:01	27	PCDHA4	p.S608L	0.590446	3	9	2	LLYELQPGT	44	LSYELQPGT	11654	-11610
2	A2:01	28	B3GALNT	p.H304Y	5.16678	14	9	3	NLYEEDALL	45	NLHEEDALL	273	-228
3	A2:01	1	DDHD1	p.S873F	0.71471	5	9	1	FLDVALFLL	6	SLDVALFLL	19	-13
3	A2:01	2	TTC28	p.S1823F	2.30807	2	9	1	FLLGLPNPA	7	SLLGLPNPA	34	-27
3	A2:01	3	STAG3	p.P212S	0.88299	2	9	1	SMDDLISLL	7	PMDDLISLL	371	-364
3	A2:01	4	KLHL13	p.G441E	2.77748	7	9	4	ALKEYLYAV	7	ALKGYLYAV	12	-5
3	A2:01	5	TTC28	p.S1823F	2.30807	2	10	1	FLLGLPNPAL	8	SLLGLPNPAL	26	-18
3	A2:01	6	SUSD2	p.M155I	20.3220	7	9	3	SMIEKSELV	9	SMMEKSELV	5	4

3	A2:01	7	NAV2	p.V2374I	23.3417	2	10	6	YLLEAIREGL	9	YLLEAVREGL	10	-1
3	A2:01	8	ABCC1	p.R1046C	7.15493	18	9	5	ILASCCLHV	10	ILASRCLHV	26	-16
3	A2:01	9	KIAA0556	p.S707L	2.72127	6	9	2	TLMGDMPSA	10	TSMGDMPSA	4711	-4701
3	A2:01	10	MCHR1	p.P377S	65.2719	164	9	4	CLNSFVYIV	12	CLNPFVYIV	14	-2
3	A2:01	11	RAC1	p.P29S	158.091	363	9	2	FSGEYIPTV	14	FPGEYIPTV	294	-280
3	A2:01	12	NBPF1	p.V1130I	1.31404	4	10	10	TLMGTSLHLI	14	TLMGTSLHLV	6	8
3	A2:01	13	SLC22A23	p.E456K	3.92437	7	9	6	SMMGHKVKV	15	SMMGHEVKV	9	6
3	A2:01	14	UTRN	p.G1513R	1.29967	1	9	1	RMDEQLTSL	15	GMDEQLTSL	17	-2
3	A2:01	15	SLC7A4	p.A348V	1.366	5	10	2	MVADGLFFQV	15	MAADGLFFQV	34	-19
3	A2:01	16	SLC9A1	p.P598L	23.1068	176	9	3	KILSAVSTV	16	KIPSAVSTV	107	-91
3	A2:01	17	SULT1A2	p.P19L	0.06452	11	9	1	LLIKYFAEA	17	PLIKYFAEA	917	-900
3	A2:01	18	SNX14	p.P253S	4.52371	2	10	8	KLTELLFSYI	19	KLTELLFPYI	10	9
3	A2:01	19	IQGAP3	p.S1429F	9.07844	14	10	6	SLTAHFLLPL	21	SLTAHSLLPL	27	-6
3	A2:01	20	STAG3	p.P212S	0.88299	2	9	2	FSMDDLISL	22	FPMDDLISL	603	-581
3	A2:01	21	UQCC2	p.E15K	47.996	660	10	7	FLKLCEKWPV	26	FLKLCEEWPV	13	13
3	A2:01	22	NUBPL	p.L266F	1.84902	1	10	6	KLAQTFGLEV	27	KLAQTLGLEV	30	-3
3	A2:01	23	AKR1B15	p.R46C	0.03659	1	9	3	LLCPYPASL	28	LLRPYPASL	135	-107
3	A2:01	24	GRIK2	p.P6S	0.74939	4	10	8	IIFSILSNPV	31	IIFPILSNPV	31	0
3	A2:01	25	NBPF1	p.V1130I	1.31404	4	9	9	LMGTSLHLI	32	LMGTSLHLV	9	23
3	A2:01	26	ABCB4	p.G1054R	0.94703	2	9	4	VLQRLSLEV	32	VLQGLSLEV	19	13
3	A2:01	27	SLC9A1	p.P598L	23.1068	176	9	6	GMGKILSAV	41	GMGKIPSAV	125	-84
3	A2:01	28	RXRG	p.A425V	17.8726	29	9	8	KLLLRLPVL	43	KLLLRLPAL	19	24
3	A2:01	29	NBPF1	p.V1130I	1.31404	4	10	5	SLHLIFQMGV	45	SLHLVFQMGV	49	-4
3	A2:01	30	STAG3	p.P212S	0.88299	2	10	2	FSMDDLISLL	45	FPMDDLISLL	688	-643
3	A2:01	31	PPAN	p.P165S	35.152	123	10	8	TMFQNLFSSI	46	TMFQNLFPSI	20	26
3	A2:01	32	NBAS	p.R2365C	2.47855	20	9	3	ALCAAQHWV	49	ALRAAQHWV	301	-252
3	A2:01	33	TLN1	p.S714F	46.3297	50	9	1	FQLVACTKV	50	SQLVACTKV	783	-733
3	A2:01	34	ISLR	p.E163K	117.196	4	10	4	TLAKGTFTPL	50	TLAEGTFTPL	14	36
4	A3:01	1	PHF1	p.L356F	N/A	N/A	10	3	RLFSALNSHK	7	RLLSALNSHK	12	-5
4	A3:01	2	F5	p.E1728K	N/A	N/A	10	10	SLHAHGLSYK	8	SLHAHGLSYE	8527	-8519
4	A3:01	3	HPN	p.E393K	N/A	N/A	9	9	KMFCAGYPK	16	KMFCAGYPE	12755	-12739
4	A3:01	4	SLC4A3	p.P411L	N/A	N/A	10	2	KLHVASLSFR	47	KPHVASLSFR	9042	-8995
4	A3:01	5	A2M	p.E1248K	N/A	N/A	9	9	KAPVGHFYK	244	KAPVGHFYE	21524	-21280

Table S3. DNA sequence for library construction and barcoding. Related to Figure 2.

DNA for NP modification (5'-biotin-)					
Barcode	Name	DNA sequence	Fluorescence		
1	D1-D4-D7	AA AAA AAA A GTG ATG AGT TTC AA ATC AGT CAA GAG AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D1	D4	D7
2	D1-D4-D8	AA AAA AAA A GTG ATG AGT TTC AA ATC AGT CAA GAG AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D1	D4	D8
3	D1-D4-D9	AA AAA AAA A GTG ATG AGT TTC AA ATC AGT CAA GAG AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D1	D4	D9
4	D1-D5-D7	AA AAA AAA A GTG ATG AGT TTC AA GTA TTC GTC ATC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D1	D5	D7
5	D1-D5-D8	AA AAA AAA A GTG ATG AGT TTC AA GTA TTC GTC ATC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D1	D5	D8
6	D1-D5-D9	AA AAA AAA A GTG ATG AGT TTC AA GTA TTC GTC ATC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D1	D5	D9
7	D1-D6-D7	AA AAA AAA A GTG ATG AGT TTC AA GTC AGA TAG TTC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D1	D6	D7
8	D1-D6-D8	AA AAA AAA A GTG ATG AGT TTC AA GTC AGA TAG TTC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D1	D6	D8
9	D1-D6-D9	AA AAA AAA A GTG ATG AGT TTC AA GTC AGA TAG TTC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D1	D6	D9
10	D2-D4-D7	AA AAA AAA A CTA TGT CGA TAC AA ATC AGT CAA GAG AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D2	D4	D7
11	D2-D4-D8	AA AAA AAA A CTA TGT CGA TAC AA ATC AGT CAA GAG AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D2	D4	D8
12	D2-D4-D9	AA AAA AAA A CTA TGT CGA TAC AA ATC AGT CAA GAG AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D2	D4	D9
13	D2-D5-D7	AA AAA AAA A CTA TGT CGA TAC AA GTA TTC GTC ATC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D2	D5	D7
14	D2-D5-D8	AA AAA AAA A CTA TGT CGA TAC AA GTA TTC GTC ATC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D2	D5	D8
15	D2-D5-D9	AA AAA AAA A CTA TGT CGA TAC AA GTA TTC GTC ATC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D2	D5	D9
16	D2-D6-D7	AA AAA AAA A CTA TGT CGA TAC AA GTC AGA TAG TTC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D2	D6	D7
17	D2-D6-D8	AA AAA AAA A CTA TGT CGA TAC AA GTC AGA TAG TTC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D2	D6	D8
18	D2-D6-D9	AA AAA AAA A CTA TGT CGA TAC AA GTC AGA TAG TTC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D2	D6	D9
19	D3-D4-D7	AA AAA AAA A TAC ATC CAA GAC AA ATC AGT CAA GAG AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D3	D4	D7
20	D3-D4-D8	AA AAA AAA A TAC ATC CAA GAC AA ATC AGT CAA GAG AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D3	D4	D8
21	D3-D4-D9	AA AAA AAA A TAC ATC CAA GAC AA ATC AGT CAA GAG AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D3	D4	D9
22	D3-D5-D7	AA AAA AAA A TAC ATC CAA GAC AA GTA TTC GTC ATC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D3	D5	D7
23	D3-D5-D8	AA AAA AAA A TAC ATC CAA GAC AA GTA TTC GTC ATC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D3	D5	D8
24	D3-D5-D9	AA AAA AAA A TAC ATC CAA GAC AA GTA TTC GTC ATC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D3	D5	D9
25	D3-D6-D7	AA AAA AAA A TAC ATC CAA GAC AA GTC AGA TAG TTC AA CTC GTT CAC TAT AA CTG AAT CCT CGG GAT GCC TA	D3	D6	D7
26	D3-D6-D8	AA AAA AAA A TAC ATC CAA GAC AA GTC AGA TAG TTC AA CTT ACG AGT GTA AA CTG AAT CCT CGG GAT GCC TA	D3	D6	D8

27	D3-D6-D9	AA AAA AAA A TAC ATC CAA GAC AA GTC AGA TAG TTC AA TGT CTC TAA GTG AA CTG AAT CCT CGG GAT GCC TA	D3	D6	D9

DNA for barcoding	
Name	DNA sequence
M1	5-Cy5-AGC ACA GGG AAA CTC ATC AC
M2	5-Cy3(or Alex Fluor 750)- GCA TCA TCG TAT CGA CAT AG
M3	5-Alex488-ATG GTT CGG TCT TGG ATG TA
M4	5-Cy5-CGC CAA TGC TCT TGA CTG AT
M5	5-Cy3(or Alex Fluor 750)- AGG ACT TCG ATG ACG AAT AC
M6	5-Alex488-ATC CTT GCG AAC TAT CTG AC
M7	5-Cy5-GCC GTA TCA TAG TGA ACG AG
M8	5-Cy3(or Alex Fluor 750)- CCA GCG ATT ACA CTC GTA AG
M9	5-Alex488-CAG ACC TGC ACT TAG AGA CA
DNA for displacement	
Name	DNA sequence
M1 comp	GTG ATG AGT TTC CCT GTG CT
M2 comp	CTA TGT CGA TAC GAT GAT GC
M3 comp	TAC ATC CAA GAC CGA ACC AT
M4 comp	ATC AGT CAA GAG CAT TGG CG
M5 comp	GTA TTC GTC ATC GAA GTC CT
M6 comp	GTC AGA TAG TTC GCA AGG AT
M7 comp	CTC GTT CAC TAT GAT ACG GC
M8 comp	CTT ACG AGT GTA ATC GCT GG
M9 comp	TGT CTC TAA GTG CAG GTC TG
DNA for streptavidin labeling	
Name	DNA sequence
DNA-SAC	5-NH_2-AAA AAA AAA A TAG GCA TCC CGA GGA TTC AG

Table S4: **Single cell TCRα and TCRβ cloning primers. Related to STAR Methods.**

Vα-gene-specific primers for cloning TCRα genes		
TRAV gene	**Signal peptide sequence**	**TRAV gene-specific sequence**
TRAV1-1*01	5'-TACAGGAAGCCTCAGCA	GGACAAAGCCTTGAGCAGCCCTC-3'
TRAV1-2*01	5'-TACAGGAAGCCTCAGCA	GGACAAAACATTGACCAGCCCACTG-3'
TRAV2*01	5'-TACAGGAAGCCTCAGCA	AAGGACCAAGTGTTTCAGCCTTCCAC-3'
TRAV3*01	5'-TACAGGAAGCCTCAGCA	GCTCAGTCAGTGGCTCAGCCGGA-3'
TRAV4*01	5'-TACAGGAAGCCTCAGCA	CTTGCTAAGACCACCCAGCCCATC-3'
TRAV5*01	5'-TACAGGAAGCCTCAGCA	GGAGAGGATGTGGAGCAGAGTCTTTTCC-3'
TRAV6*01	5'-TACAGGAAGCCTCAGCA	AGCCAAAAGATAGAACAGAATTCCGAGGC-3'
TRAV6*03	5'-TACAGGAAGCCTCAGCA	GAGGCCCTGAACATTCAGGAGGG-3'
TRAV7*01	5'-TACAGGAAGCCTCAGCA	GAAAACCAGGTGGAGCACAGCCC-3'
TRAV8-1*01	5'-TACAGGAAGCCTCAGCA	GCCCAGTCTGTGAGCCAGCATAACC-3'
TRAV8-2*01	5'-TACAGGAAGCCTCAGCA	GCCCAGTCGGTGACCCAGCTTG-3'
TRAV8-2*02	5'-TACAGGAAGCCTCAGCA	GCCCAGTCGGTGACCCAGCTTAG-3'
TRAV8-3*01	5'-TACAGGAAGCCTCAGCA	GCCCAGTCAGTGACCCAGCCTG-3'
TRAV8-4*06	5'-TACAGGAAGCCTCAGCA	CTCTTCTGGTATGTGCAATACCCCAACC-3'
TRAV8-4*07	5'-TACAGGAAGCCTCAGCA	GTTGAACCATATCTCTTCTGGTATGTGCAATACC-3'
TRAV8-6*01	5'-TACAGGAAGCCTCAGCA	GCCCAGTCTGTGACCCAGCTTGAC-3'
TRAV8-7*01	5'-TACAGGAAGCCTCAGCA	ACCCAGTCGGTGACCCAGCTTG-3'
TRAV9-1*01	5'-TACAGGAAGCCTCAGCA	GGAGATTCAGTGGTCCAGACAGAAGGC-3'
TRAV9-2*01	5'-TACAGGAAGCCTCAGCA	GGAAATTCAGTGACCCAGATGGAAGG-3'
TRAV9-2*02	5'-TACAGGAAGCCTCAGCA	GGAGATTCAGTGACCCAGATGGAAGG-3'
TRAV10*01	5'-TACAGGAAGCCTCAGCA	AAAAACCAAGTGGAGCAGAGTCCTCAGTC-3'
TRAV11*01	5'-TACAGGAAGCCTCAGCA	CTACATACACTGGAGCAGAGTCCTTCATTCC-3'
TRAV12-1*01	5'-TACAGGAAGCCTCAGCA	CGGAAGGAGGTGGAGCAGGATCC-3'
TRAV12-2*01	5'-TACAGGAAGCCTCAGCA	CAGAAGGAGGTGGAGCAGAATTCTGG-3'
TRAV12-2*03	5'-TACAGGAAGCCTCAGCA	GGACCCCTCAGTGTTCCAGAGGG-3'
TRAV12-3*01	5'-TACAGGAAGCCTCAGCA	CAGAAGGAGGTGGAGCAGGATCCTG-3'
TRAV13-1*02	5'-TACAGGAAGCCTCAGCA	GGAGAGAATGTGGAGCAGCATCCTTC-3'
TRAV13-2*01	5'-TACAGGAAGCCTCAGCA	GGAGAGAGTGTGGGGCTGCATCTTC-3'
TRAV14/DV4*01	5'-TACAGGAAGCCTCAGCA	GCCCAGAAGATAACTCAAACCCAACCAG-3'
TRAV14/DV4*04	5'-TACAGGAAGCCTCAGCA	CAGAAGATAACTCAAACCCAACCAGGAATG-3'
TRAV16*01	5'-TACAGGAAGCCTCAGCA	GCCCAGAGAGTGACTCAGCCCGA-3'
TRAV17*01	5'-TACAGGAAGCCTCAGCA	AGTCAACAGGGAGAAGAGGATCCTCAGG-3'
TRAV18*01	5'-TACAGGAAGCCTCAGCA	GGAGACTCGGTTACCCAGACAGAAGG-3'
TRAV19*01	5'-TACAGGAAGCCTCAGCA	GCTCAGAAGGTAACTCAAGCGCAGACTG-3'
TRAV20*01	5'-TACAGGAAGCCTCAGCA	GAAGACCAGGTGACGCAGAGTCCC-3'
TRAV21*01	5'-TACAGGAAGCCTCAGCA	AAACAGGAGGTGACGCAGATTCCTGC-3'
TRAV22*01	5'-TACAGGAAGCCTCAGCA	GGAATACAAGTGGAGCAGAGTCCTCCAG-3'
TRAV23/DV6*01	5'-TACAGGAAGCCTCAGCA	CAGCAGCAGGTGAAACAAAGTCCTCA-3'
TRAV23/DV6*04	5'-TACAGGAAGCCTCAGCA	CAGCAGGTGAAACAAAGTCCTCAATCTTTG-3'
TRAV24*01	5'-TACAGGAAGCCTCAGCA	ATACTGAACGTGGAACAAAGTCCTCAGTCAC-3'
TRAV25*01	5'-TACAGGAAGCCTCAGCA	GGACAACAGGTAATGCAAATTCCTCAGTACC-3'
TRAV26-1*01	5'-TACAGGAAGCCTCAGCA	GATGCTAAGACCACCCAGCCCCC-3'
TRAV26-1*02	5'-TACAGGAAGCCTCAGCA	GATGCTAAGACCACCCAGCCCACC-3'
TRAV26-2*01	5'-TACAGGAAGCCTCAGCA	GATGCTAAGACCACACAGCCAAATTCAATG-3'
TRAV27*01	5'-TACAGGAAGCCTCAGCA	ACCCAGCTGCTGGAGCAGAGCC-3'
TRAV29/DV5*01	5'-TACAGGAAGCCTCAGCA	GACCAGCAAGTTAAGCAAAATTCACCATC-3'
TRAV30*01	5'-TACAGGAAGCCTCAGCA	CAACAACCAGTGCAGAGTCCTCAAGC-3'
TRAV34*01	5'-TACAGGAAGCCTCAGCA	AGCCAAGAACTGGAGCAGAGTCCTCAG-3'
TRAV35*01	5'-TACAGGAAGCCTCAGCA	GGTCAACAGCTGAATCAGAGTCCTCAATC-3'
TRAV36/DV7*01	5'-TACAGGAAGCCTCAGCA	GAAGACAAGGTGGTACAAAGCCCTCTATCTC-3'
TRAV36/DV7*02	5'-TACAGGAAGCCTCAGCA	GAAGACAAGGTGGTACAAAGCCCTCAATC-3'
TRAV38-1*01	5'-TACAGGAAGCCTCAGCA	GCCCAGACAGTCACTCAGTCTCAACCAG-3'
TRAV38-1*04	5'-TACAGGAAGCCTCAGCA	GCCCAGACAGTCACTCAGTCCCAGC-3'
TRAV38-2/DV8*01	5'-TACAGGAAGCCTCAGCA	GCTCAGACAGTCACTCAGTCTCAACCAGAG-3'
TRAV39*01	5'-TACAGGAAGCCTCAGCA	GAGCTGAAAGTGGAACAAAACCCTCTGTTC-3'
TRAV40*01	5'-TACAGGAAGCCTCAGCA	AGCAATTCAGTCAAGCAGACGGGC-3'
TRAV41*01	5'-TACAGGAAGCCTCAGCA	AAAAATGAAGTGGAGCAGAGTCCTCAGAAC-3'
Vβ-gene-specific primers for cloning TCRα genes		
TRBV gene	**Signal peptide sequence**	**TRBV gene-specific sequence**
TRBV1*01	5'-CAGGAGGGCTCGGCA	GATACTGGAATTACCCAGACACCAAAATACCTG-3'
TRBV2*01	5'-CAGGAGGGCTCGGCA	GAACCTGAAGTCACCCAGACTCCCAG-3'
TRBV3-1*01	5'-CAGGAGGGCTCGGCA	GACACAGCTGTTTCCCAGACTCCAAAATAC-3'
TRBV3-2*01	5'-CAGGAGGGCTCGGCA	GACACAGCCGTTTCCCAGACTCCA-3'
TRBV4-1*01	5'-CAGGAGGGCTCGGCA	GACACTGAAGTTACCCAGACACCAAAACAC-3'

TRBV4-1*02	5'-CAGGAGGGCTCGGCA	CACCTGGTCATGGGAATGACAAATAAGAAG-3'
TRBV4-2*01	5'-CAGGAGGGCTCGGCA	GAAACGGGAGTTACGCAGACACCAAG-3'
TRBV4-3*04	5'-CAGGAGGGCTCGGCA	AAGAAGTCTTTGAAATGTGAACAACATCTGGG-3'
TRBV5-1*01	5'-CAGGAGGGCTCGGCA	AAGGCTGGAGTCACTCAAACTCCAAGATATC-3'
TRBV5-1*02	5'-CAGGAGGGCTCGGCA	AGGGCTGGGGTCACTCAAACTCC-3'
TRBV5-3*01	5'-CAGGAGGGCTCGGCA	GAGGCTGGAGTCACCCAAAGTCCC-3'
TRBV5-4*01	5'-CAGGAGGGCTCGGCA	GAGACTGGAGTCACCCAAAGTCCCAC-3'
TRBV5-4*03	5'-CAGGAGGGCTCGGCA	CAGCAAGTGACACTGAGATGCTCTTCTCAG-3'
TRBV5-4*04	5'-CAGGAGGGCTCGGCA	ACTGTGTCCTGGTACCAACAGGCCCT-3'
TRBV5-5*01	5'-CAGGAGGGCTCGGCA	GACGCTGGAGTCACCCAAAGTCC-3'
TRBV5-8*01	5'-CAGGAGGGCTCGGCA	GAGGCTGGAGTCACACAAAGTCCCAC-3'
TRBV5-8*02	5'-CAGGAGGGCTCGGCA	AGGACAGCAAGCGACTCTGAGATGC-3'
TRBV6-1*01	5'-CAGGAGGGCTCGGCA	AATGCTGGTGTCACTCAGACCCCA-3'
TRBV6-4*01	5'-CAGGAGGGCTCGGCA	ATTGCTGGGATCACCCAGGCAC-3'
TRBV6-4*02	5'-CAGGAGGGCTCGGCA	ACTGCTGGGATCACCCAGGCAC-3'
TRBV7-1*01	5'-CAGGAGGGCTCGGCA	GGTGCTGGAGTCTCCCAGTCCCTG-3'
TRBV7-2*01	5'-CAGGAGGGCTCGGCA	GGAGCTGGAGTCTCCCAGTCCCC-3'
TRBV7-2*04	5'-CAGGAGGGCTCGGCA	GGAGCTGGAGTTTCCCAGTCCCC-3'
TRBV7-3*01	5'-CAGGAGGGCTCGGCA	GGTGCTGGAGTCTCCCAGACCC-3'
TRBV7-3*05	5'-CAGGAGGGCTCGGCA	TGGGAGCTCAGGTGTGATCCAATTTC-3'
TRBV7-4*01	5'-CAGGAGGGCTCGGCA	GGTGCTGGAGTCTCCCAGTCCC-3'
TRBV7-6*01	5'-CAGGAGGGCTCGGCA	GGTGCTGGAGTCTCCCAGTCTCCC-3'
TRBV7-9*01	5'-CAGGAGGGCTCGGCA	GATACTGGAGTCTCCCAGAACCCCAG-3'
TRBV7-9*03	5'-CAGGAGGGCTCGGCA	GATACTGGAGTCTCCCAGGACCCCAG-3'
TRBV7-9*04	5'-CAGGAGGGCTCGGCA	ATATCTGGAGTCTCCCACAACCCCAGAC-3'
TRBV7-9*07	5'-CAGGAGGGCTCGGCA	CACAACCGCCTTTATTGGTACCGACAG-3'
TRBV9*01	5'-CAGGAGGGCTCGGCA	GATTCTGGAGTCACACAAACCCCAAAGC-3'
TRBV10-1*01	5'-CAGGAGGGCTCGGCA	GATGCTGAAATCACCCAGAGCCCAAG-3'
TRBV10-2*01	5'-CAGGAGGGCTCGGCA	GATGCTGGAATCACCCAGAGCCCA-3'
TRBV10-2*02	5'-CAGGAGGGCTCGGCA	AAGGCAGGTGACCTTGATGTGTCACC-3'
TRBV11-1*01	5'-CAGGAGGGCTCGGCA	GAAGCTGAAGTTGCCCAGTCCCC-3'
TRBV11-2*01	5'-CAGGAGGGCTCGGCA	GAAGCTGGAGTTGCCCAGTCTCCCAG-3'
TRBV11-3*01	5'-CAGGAGGGCTCGGCA	GAAGCTGGAGTGGTTCAGTCTCCCAGA-3'
TRBV11-3*03	5'-CAGGAGGGCTCGGCA	GGTCTCCCAGATATAAGATTATAGAGAAGAAACAGC-3'
TRBV12-1*01	5'-CAGGAGGGCTCGGCA	GATGCTGGTGTTATCCAGTCACCCAGG-3'
TRBV12-2*01	5'-CAGGAGGGCTCGGCA	GATGCTGGCATTATCCAGTCACCCAAG-3'
TRBV12-3*01	5'-CAGGAGGGCTCGGCA	GATGCTGGAGTTATCCAGTCACCCC-3'
TRBV12-5*01	5'-CAGGAGGGCTCGGCA	GATGCTAGAGTCACCCAGACACCAAGG-3'
TRBV13*01	5'-CAGGAGGGCTCGGCA	GCTGCTGGAGTCATCCAGTCCCC-3'
TRBV14*01	5'-CAGGAGGGCTCGGCA	GAAGCTGGAGTTACTCAGTTCCCCAGC-3'
TRBV15*01	5'-CAGGAGGGCTCGGCA	GATGCCATGGTCATCCAGAACCCAAG-3'
TRBV16*01	5'-CAGGAGGGCTCGGCA	GGTGAAGAAGTCGCCCAGACTCCA-3'
TRBV17*01	5'-CAGGAGGGCTCGGCA	GAGCCTGGAGTCAGCCAGACCC-3'
TRBV18*01	5'-CAGGAGGGCTCGGCA	AATGCCGGCGTCATGCAGAAC-3'
TRBV19*01	5'-CAGGAGGGCTCGGCA	GATGGTGGAATCACTCAGTCCCCAAAG-3'
TRBV20-1*01	5'-CAGGAGGGCTCGGCA	GGTGCTGTCGTCTCTCAACATCCGAG-3'
TRBV20/OR9-2*01	5'-CAGGAGGGCTCGGCA	AGTGCTGTCGTCTCTCAACATCCGAG-3'
TRBV21-1*01	5'-CAGGAGGGCTCGGCA	GACACCAAGGTCACCCAGAGACCTAGAC-3'
TRBV21/OR9-2*01	5'-CAGGAGGGCTCGGCA	GACACCAAGGTCACCCAGAGACCTAGATTTC-3'
TRBV23-1*01	5'-CAGGAGGGCTCGGCA	CATGCCAAAGTCACACAGACTCCAGG-3'
TRBV24-1*01	5'-CAGGAGGGCTCGGCA	GATGCTGATGTTACCCAGACCCCAAG-3'
TRBV25-1*01	5'-CAGGAGGGCTCGGCA	GAAGCTGACATCTACCAGACCCCAAGATAC-3'
TRBV26*01	5'-CAGGAGGGCTCGGCA	GATGCTGTAGTTACACAATTCCCAAGACACAG-3'
TRBV26/OR9-2*01	5'-CAGGAGGGCTCGGCA	GATGCTGTAGTTACACAATTCTCAAGACACAGAATC-3'
TRBV27*01	5'-CAGGAGGGCTCGGCA	GAAGCCCAAGTGACCCAGAACCC-3'
TRBV28*01	5'-CAGGAGGGCTCGGCA	GATGTGAAAGTAACCCAGAGCTCGAGATATC-3'
TRBV29-1*01	5'-CAGGAGGGCTCGGCA	AGTGCTGTCATCTCTCAAAAGCCAAGC-3'
TRBV29-1*03	5'-CAGGAGGGCTCGGCA	ACGATCCAGTGTCAAGTCGATAGCCAAG-3'
TRBV30*01	5'-CAGGAGGGCTCGGCA	TCTCAGACTATTCATCAATGGCCAGCG-3'
TRBV30*04	5'-CAGGAGGGCTCGGCA	ACTATTCATCAATGGCCAGCGACCC-3'