Supporting Information

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SI materials and Methods

Single-cell TCR sequencing using multiplex PCR

To obtain paired TCRα and TCRβ sequences, we performed PCR with multiplexed primers covering all TCRα and TCRβ V genes according to the published protocol (1). However, different from the protocol published by Han et al, we performed cDNA synthesis and the first PCR reaction in two separate steps. We sorted single cells into 96-well plates containing 5 µl capture buffer (20 mM Tris-HCl pH8, 1% NP-40, 1 U/µl RNase Inhibitor (optional)). The plates were stored at -70ºC until cDNA synthesis to facilitate cell lysis. For cDNA synthesis, we added 5 µl cDNA mix (1X FS buffer, 1 mM dNTP, 2.5 mM DDT, 1 µM oligo d(T) (5'-CTGAATTCT$_{(16)}$-3'), 1 µM reverse *TRAC* (5'-AGTCAGATTTGTTGCTCCAGGCC-3') and *TRBC* (5'-TTCACCCACCAGCTCAGCTCC-3') primers, 1.5 U/µl RNase Inhibitor, 2.5 U/µl Superscript II in final 10 µl reaction volume). The cDNA synthesis was carried out at 42ºC for 50 min followed by an inactivation step at 72ºC for 10 min. The cDNA plates were stored at -20ºC. Each of the three nested PCR steps was carried out in a total volume of 10 µl using 1 µl cDNA/PCR template and KAPA HiFi HotStart ReadyMix (Kapa Biosystems). For the two first nested PCR reactions, the final concentration of each TCR V-gene and C-gene primers was 0.06 µM and 0.3 µM, respectively. In the final barcoding PCR step, we added 5'-barcoding primers (0.044 µM) and 1:4 ratio of the 3'-barcoding primers, *TRBC* (0.044 µM) and *TRAC* (0.18 µM). In addition, Illumina Paired-End primers were added to the master mix (0.5 µM each). Primer sequences and cycling conditions for all three PCR reactions are provided in the original protocol (1).

Bulk TCR sequencing by PCR amplification of template-switched cDNA

When feasible due to high cell numbers, we sorted in bulk 150-3000 T cells in an eppendorf tube containing 50-100 µl TCL lysis buffer (Qiagen) supplemented with 1% β-mercaptoethanol. We stored the tubes at -70°C until cDNA synthesis. Total RNA was extracted by incubation with 2.2x volume of RNAclean XP beads (Agencourt) for 10 min at room temperature before tubes were placed on a magnet (DynaMag-2, Invitrogen) and washed three times with 80% ethanol. We allowed the beads to dry while still on magnet and eluted in H_2O. A modified SMART protocol (2) was used in first-strand cDNA synthesis. The eluted RNA was transferred to

RT1 mix (20 mM Tris-HCl pH 8, 0.2% Tween-20, 1 mM dNTP, 2 μM oligo d(T), 1 U/μl RNase Inhibitor) in total volume of 20 μl and incubated at 72°C for 3 min followed by 1 min on ice. To complete cDNA synthesis, we added equal volume of the RT2 mix (1X FS buffer, 0.8 M Betaine, 6 mM $MgCl_2$, 2.5 mM DTT, 2 μM TSO (5'-Bio-AAGCAGTGGTATCAACGCAGAGTACrGrGrG-3'), 1 U/μl RNase Inhibitor, 10 U/μl SuperScript II). The cDNA synthesis was carried out at 42°C for 90 min followed by 15 min at 72°C. Subsequently, *TRA* and *TRB* genes were amplified in two rounds of semi-nested PCR reactions. The cDNA from each sample was divided into 3-6 replica and amplified with indexed primers. The reaction mix for the first PCR: 2 µl cDNA template, 200/40 nM forward primer mix (STRT-fwd S/L), 200 nM reverse primer (TRAC_rev1 or TRBC_rev1) with KAPA HiFi HotStart ReadyMix in a total volume of 20 µl was amplified by touchdown PCR to increase specificity. The cycling conditions were: 3 min at 95°C followed by 5 cycles (15s x 98°C, 60s x 72°C), 5 cycles (15s x 98°C, 30s x 70°C, 40s x 72°C) and 8 cycles (15s x 98°C, 30s x 65°C, 40s x 72°C). The second PCR was done in a total volume of 10 µl with 1 µl of first PCR product, 200 nM indexed forward primers (R2_STRT_In01-12), 200 nM barcoded reverse primers (*TRAC*_01-10_rev2 or *TRBC*_01-10_rev2) and KAPA HiFi HotStart ReadyMix for 2 min at 95°C followed by 10 cycles (20s x 98°C, 30s x 65°C, 40s x 72°C) with final elongation at 72°C for 5 min. A final third PCR reaction was carried out in a total volume of 20 µl with 2 µl of second PCR product, 200 nM forward primer (Illumina Seq Primer R2), 200 nM reverse primer (Illumina Seq Primer R1) and KAPA HiFi HotStart ReadyMix to prepare the sequencing library for the Illumina MiSeq platform. The cycling conditions were: 2 min at 95°C followed by 15 cycles (20s x 98°C, 30s x 60°C, 40s x 72°C) with final elongation at 72°C for 5 min. The PCR products were pooled, cleaned and concentrated with Ampure XP beads (Agencourt) or QIAquick PCR purification kit prior to gel extraction and cleaned with QIAquick Gel Extraction kit and QIAquick PCR purification kit (Qiagen). All primer sequences are listed below:

Oligo	Barcode	Sequence (5’-3’)
1st PCR		
fwdS		Bio-CTAATACGACTCACTATAGGGC
fwdL		Bio-CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT
TRAC_rev1		GGAACTTTCTGGGCTGGGGAAGAAGGTGTCTTCTGG
TRBC_rev1		TGCTTCTGATGGCTCAAACACAGCGACCT
2nd PCR fwd	Replica barcode	
R2_bulk01	ATGAGC	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNATGAGCAAGCAGTGGTATCAACGCAGAGT
R2_bulk02	CAACTA	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNCAACTAAAGCAGTGGTATCAACGCAGAGT
R2_bulk03	CTAGCT	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNCTAGCTAAGCAGTGGTATCAACGCAGAGT
R2_bulk04	ACTTGA	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNACTTGAAAGCAGTGGTATCAACGCAGAGT
R2_bulk05	CACTCA	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNCACTCAAAGCAGTGGTATCAACGCAGAGT
R2_bulk06	TACAGC	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNTACAGCAAGCAGTGGTATCAACGCAGAGT
R2_bulk07	CGTGAT	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNCGTGATAAGCAGTGGTATCAACGCAGAGT
R2_bulk08	CACTGT	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNCACTGTAAGCAGTGGTATCAACGCAGAGT
R2_bulk09	TGGTCA	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNTGGTCAAAGCAGTGGTATCAACGCAGAGT
R2_bulk10	ATTGGC	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNATTGGCAAGCAGTGGTATCAACGCAGAGT
R2_bulk11	TACAAG	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNTACAAGAAGCAGTGGTATCAACGCAGAGT
R2_bulk12	GGAACT	GGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNNGGAACTAAGCAGTGGTATCAACGCAGAGT
2nd PCR rev	Sample barcode	
TRAC01_rev2	ACCGTA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNACCGTACAGCTGGTACACGGCAGGGT
TRAC02_rev2	GAGTAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGAGTAGCAGCTGGTACACGGCAGGGT
TRAC03_rev2	TTACGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNTTACGCCAGCTGGTACACGGCAGGGT
TRAC04_rev2	CGTACT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNCGTACTCAGCTGGTACACGGCAGGGT
TRAC05_rev2	GTGAAA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGTGAAACAGCTGGTACACGGCAGGGT
TRAC06_rev2	TAGCTT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNTAGCTTCAGCTGGTACACGGCAGGGT
TRAC07_rev2	ACTGAT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNACTGATCAGCTGGTACACGGCAGGGT
TRAC08_rev2	CCGTCC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNCCGTCCCAGCTGGTACACGGCAGGGT
TRAC09_rev2	GGCTAC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGGCTACCAGCTGGTACACGGCAGGGT
TRAC10_rev2	ATTCCT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNATTCCTCAGCTGGTACACGGCAGGGT
TRBC01_rev2	ATCTCG	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNATCTCGCGACCTCGGGTGGGAACAC
TRBC02_rev2	CAGATC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNCAGATCCGACCTCGGGTGGGAACAC
TRBC03_rev2	TGACGA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNTGACGACGACCTCGGGTGGGAACAC
TRBC04_rev2	GCTGAT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGCTGATCGACCTCGGGTGGGAACAC
TRBC05_rev2	CGATGT	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNCGATGTCGACCTCGGGTGGGAACAC
TRBC06_rev2	ACCACA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNACCACACGACCTCGGGTGGGAACAC
TRBC07_rev2	GATCAG	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGATCAGCGACCTCGGGTGGGAACAC
TRBC08_rev2	TCGGTC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNTCGGTCCGACCTCGGGTGGGAACAC
TRBC09_rev2	GTCTGC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNGTCTGCCGACCTCGGGTGGGAACAC
TRBC10_rev2	AGTCAA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNAGTCAACGACCTCGGGTGGGAACAC
3rd PCR		
R1		AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC
R2		CAAGCAGAAGACGGCATACGAGATCGGTCTCGGCATTCCTGCTGAACCGCTC

The sequencing was done at Norwegian Sequencing Centre (NSC), a core facility at the University of Oslo and Oslo University Hospital.

Data processing and analysis

Raw reads from Illumina NGS were processed in a multistep pipeline. Single-cell TCR sequencing data was first pre-processed by using selected steps of the pRESTO toolkit (3). First, low-quality reads with average Phred quality score Q<30 were removed. Sequences were then unmasked according to barcodes (row, plate and column) and gene-specific primers (TRA/TRB), which were then annotated in the read header. Reads without recognizable primer sequences were removed. Subsequently, forward (R2) and reverse (R1) reads were paired according to Illumina coordinates and assembled into full-length TCR sequences. Next, identical duplicate sequences derived from the same cell were collapsed and the number of sequences collapsing as one sequence was denoted as "dupcount". Only sequences with dupcount > 2 were used for further analysis. In the last pre-processing step, we aligned the three highest ranking (in terms of dupcount) sequences on a per-cell, per-chain basis, implemented as a custom python script. Here, the highest-ranking sequence was aligned to the second highest ranking sequence using a dynamic programming algorithm (4). For sequences aligning with < 2% mismatches (relative to the length of the highest-ranking sequence, and ignoring gaps), the highest-ranking sequence was retained and the dupcounts were added up. Remaining sequences were discarded. Subsequently, the third-highest ranking sequence was aligned to the previous outcome, and possibly merged as well. Other pairs of the top three sequences were aligned as needed, always prioritizing the highest-ranking sequence in terms of dupcounts.

Bulk-cell derived sequencing data was pre-processed in much of the same manner as pre-processing of single-cell sequencing data described above. The difference was that sequences were marked according to barcoded gene-specific primers (TRA/TRB) in the R1 reads and the TSO sequence together with replicate barcodes in the R2 reads. The barcoded primers were then annotated in the read header.

We submitted pre-processed TCR sequences to the IMGT/HighV-QUEST online tool (5) for identification of V, D, J genes and alleles and the nucleotide sequences of the CDR3 junctions. Before analyzing the IMGT/HighV-QUEST output, the IMGT annotation was parsed, stored in a relational database and subjected to additional filters before extracting the sequences. This workflow was implemented as an in-house Java program together with a custom MySQL database. First, only productive sequences according IMGT annotation was included. For single-cell data, within each cell and each chain, duplicate sequences that had identical V gene, J gene and nucleotide CDR3 sequences were collapsed. Next, only valid singleton cells containing single TRA and TRB and dual TRA or TRB (maximum 3 chains) with dupcount > 100 were considered for downstream analysis. Within samples taken from the same individual, cells were defined to belong to the same clonotype when they share identical V and J gene (subgroup level) in addition to identical nucleotide CDR3 region for both the TRA and TRB genes. All bulk samples were divided after cDNA synthesis and amplified in independent PCR reactions that were barcoded with 3-6 replicate indices. Within each bulk TCR sample replicate, duplicate sequences defined as identical V gene, J gene and allowing for one nucleotide mismatch in CDR3 regions to account for PCR and sequencing errors were collapsed. Only sequences present in ≥ 2 distinct replicas and cumulative dupcount > 10 were used for downstream analysis.

Area-proportional Venn diagrams were drawn by using free software available from Bioinforx (http://apps.bioinforx.com) and eulerAPE (6).

References

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2. Quigley MF, Almeida JR, Price DA, Douek DC. Unbiased molecular analysis of T cell receptor expression using template-switch anchored RT-PCR. *Curr Protoc Immunol.* 2011;Chapter 10:Unit10 33.

3. Vander Heiden JA, Yaari G, Uduman M, et al. pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. *Bioinformatics.* 2014;30(13):1930-1932.

4. Needleman SB, Wunsch CD. A general method applicable to the search for similarities in the amino acid sequence of two proteins. *J Mol Biol.* 1970;48(3):443-453.

5. Alamyar E, Duroux P, Lefranc MP, Giudicelli V. IMGT((R)) tools for the nucleotide analysis of immunoglobulin (IG) and T cell receptor (TR) V-(D)-J repertoires, polymorphisms, and IG mutations: IMGT/V-QUEST and IMGT/HighV-QUEST for NGS. *Methods Mol Biol.* 2012;882:569-604.

6. Micallef L, Rodgers P. eulerAPE: drawing area-proportional 3-Venn diagrams using ellipses. *PLoS One.* 2014;9(7):e101717.

Fig. S1: Gating strategy. For PBMCs, cells within the singlet lymphocyte population were further gated to isolate tetramer-binding $CD4^+$ effector-memory gut-homing T cells that were: $CD3^+$, $CD11c^-$, $CD14^-$, $CD15^-$, $CD19^-$, $CD56^-$, $CD45RA^-$, $CD62L^-$, integrin $\beta7^+$ and $CD4^+$. For lamina propria cell suspensions of duodenal biopsies, live cells within the singlet lymphocyte population were further gated to obtain tetramer-binding $CD4^+$ T cells that were: $CD3^+$, $CD11c^-$, $CD14^-$, $CD15^-$, $CD19^-$, $CD56^-$, $CD8^-$ and $CD4^+$. For T-cell lines, live cells within the singlet lymphocyte population were further gated to obtain tetramer-binding $CD4^+$ T cells that were: $CD3^+$, $CD8^-$ and $CD4^+$.

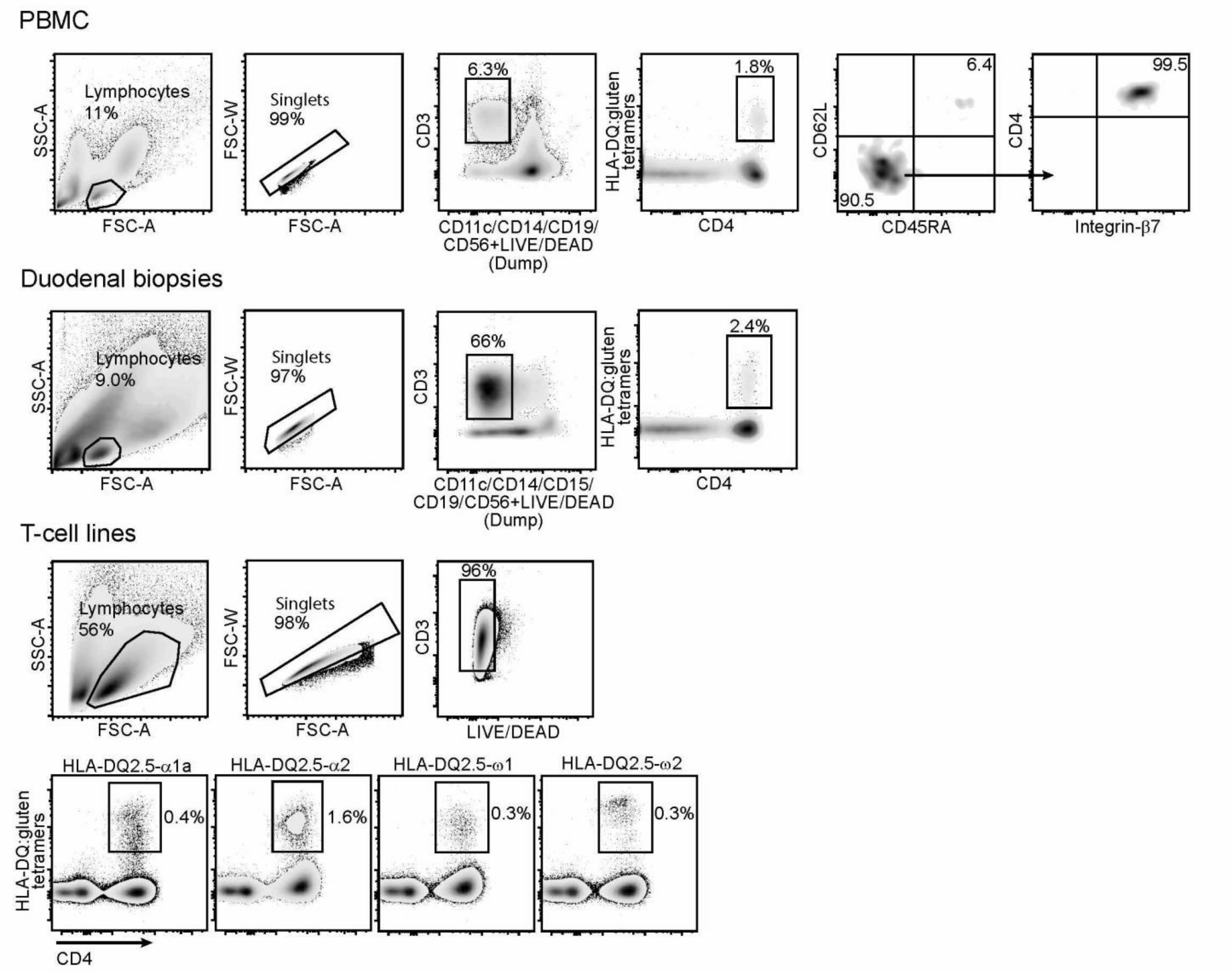


Fig. S2: Clonotype sharing of gluten-specific $CD4^+$ T cells across anatomical compartments and within the same sample. Panel A shows clonotype sharing of HLA-DQ:gluten tetramer-sorted cells from matched blood and gut biopsy samples of untreated CD patients that were subjected to bulk TCRβ sequencing. TCRβ clonotype is defined by nucleotide sequence and the overlap is depicted in area-proportional Venn diagrams. Degree of sharing was calculated by dividing the number of shared clonotypes by the total clonotype number in the blood sample. Panel B shows the range of maximum expected clonotype overlap between two independent sequencing experiments (single-cell and bulk TCR sequencing) of the same sample. Percentages of TCRβ clonotype overlap was calculated by dividing the number of shared clonotypes by the total clonotype number in the smallest sample. Median is depicted as a line and 95% confidence interval is depicted as stippled lines.

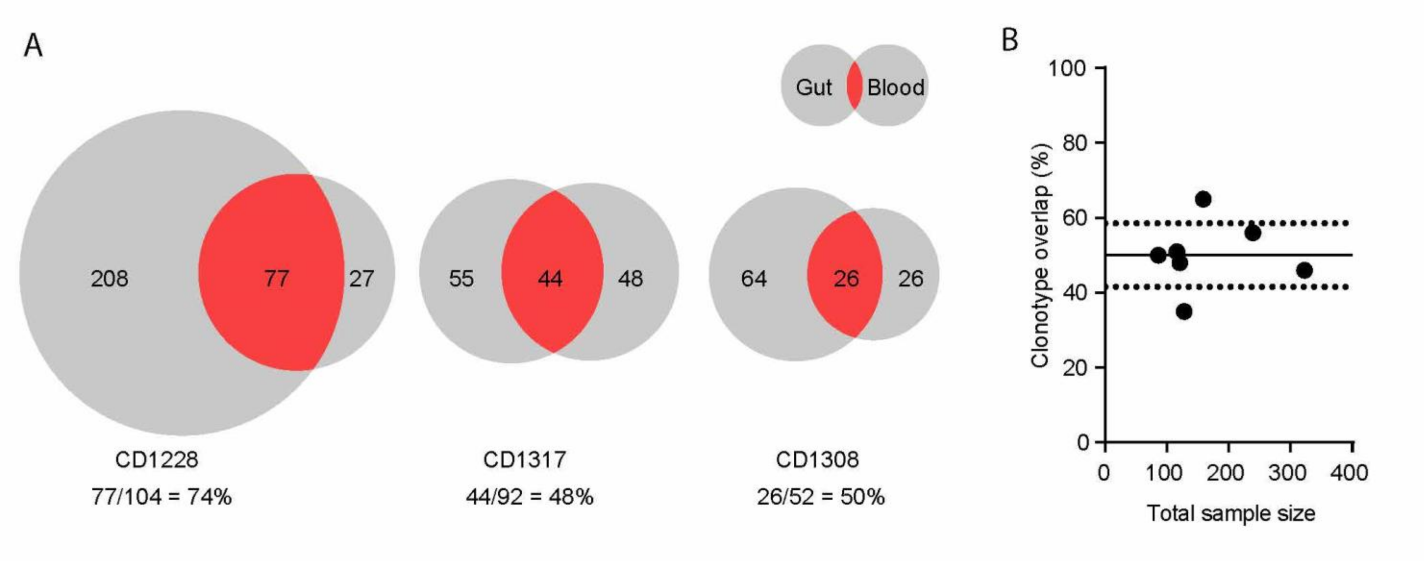


Fig. S3. Clonal distribution and diversity in CD patients. Panel A shows clonal distribution of TCRαβ clonotypes obtained by single-cell TCR sequencing of gluten-specific T cells from four CD patients during the first weeks (w) and 1-2 years (yr) after commencement of gluten-free diet (GFD). Panel B shows clonal diversity as sample-corrected non-parametric estimate of the classic Shannon entropy in samples with >20 cells of the patients represented in Fig 1. Panel C shows clonal distribution of TCRαβ clonotypes obtained by single-cell TCR sequencing of gluten-specific T cells from five CD patients during 14-day gluten challenge; at baseline (B), on day 6 (D6), day 14 (D14) and day 28 (D28) after the onset of gluten challenge. Panel D shows clonal diversity as sample-corrected non-parametric estimate of the classic Shannon entropy in samples with >20 cells of the patients represented in Fig 2. Panels A and C show the distribution of clonotypes consisting of at least two cells plotted as stacked boxes in percentage of total number of cells. The clonal size of the most dominant clonotype is displayed with number inside the box. The total number of clonotypes and cells in each sample are shown below each stacked bar. For panel C, the colored boxes represent the three most dominant clonotypes at D6 that were also observed at other time points. The isolated and non-stacked colored boxes represent shared clonotypes with clonal size one.

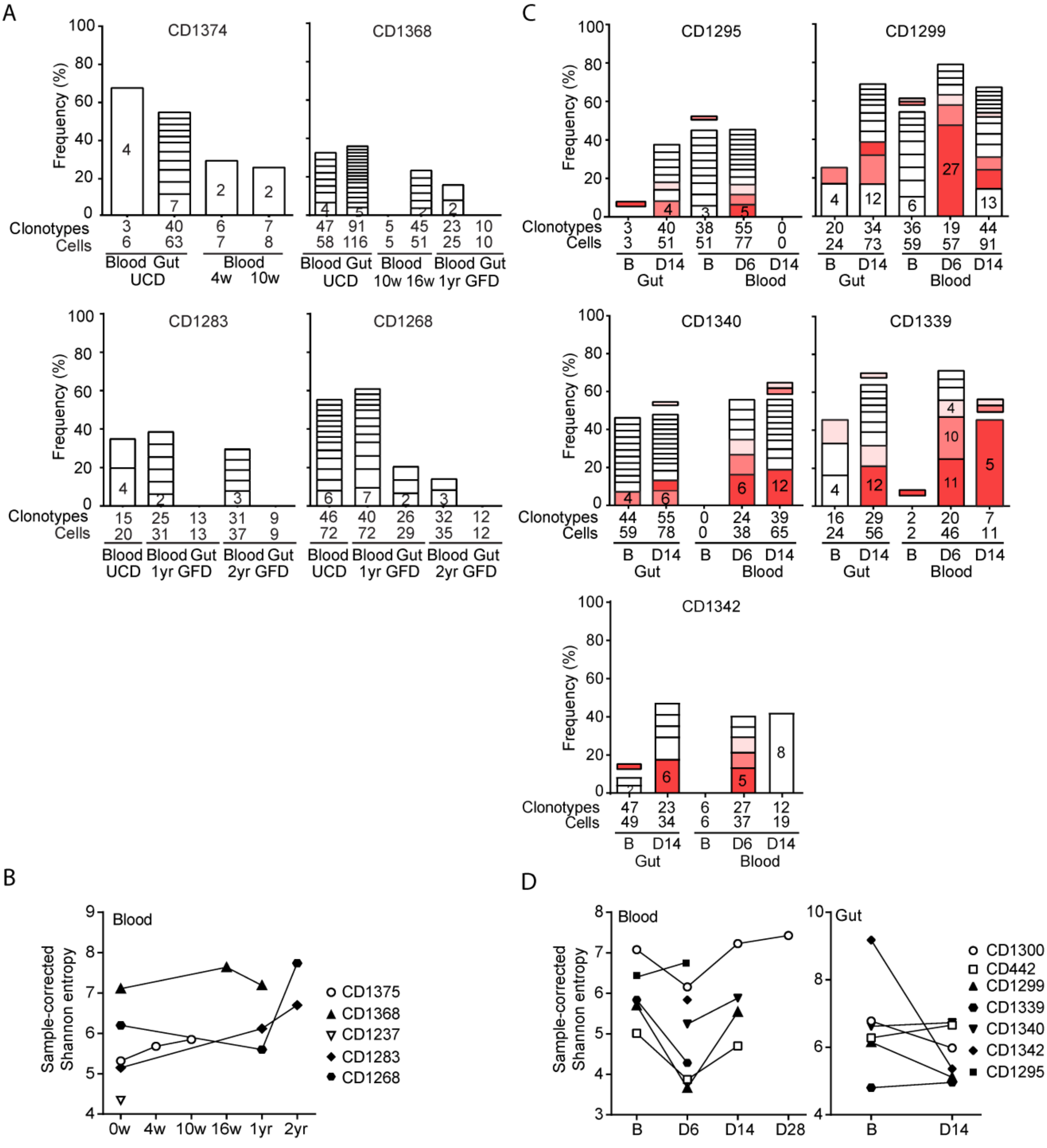
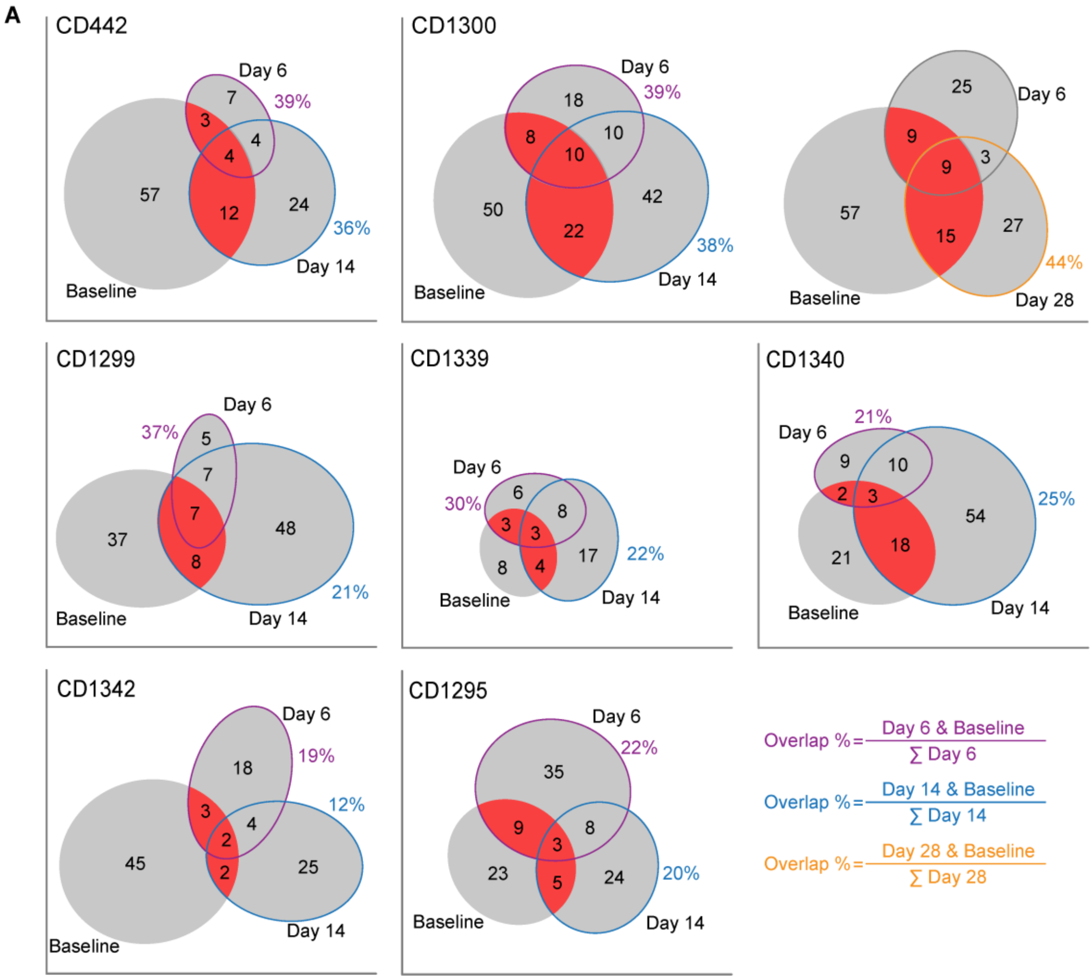


Fig. S4. Pre-existing T-cell clonotypes dominate during gluten challenge. TCRαβ clonotypes obtained by single-cell sequencing at baseline, day 6 and day 14 or day 28 of the gluten challenge were analyzed and compared in area-proportional Venn diagrams (A). The dark red areas represent clonotypes that were observed both at baseline and day 6 or day 14 or day 28. The percentage denotes the proportion of these shared clonotypes on day 6 (purple) or day 14 (blue) or day 28 (orange). Panel B shows overlap of TCRβ clonotypes at baseline, day 6 and day 14 or day 28 of the gluten challenge in patients CD442 and CD1300. The percentage in blue color denotes the proportion of shared clonotypes in the latest sample while purple color denotes the proportion of shared clonotypes in the earliest sample. The TCRβ clonotypes were obtained from compilation of both single-cell and bulk sequencing data and corresponds to panel D in Figure 4.

A



B

Overlap % = Earliest timepoint & latest timepoint / ∑ Earliest timepoint

CD 442	Base line	Day 6	Day 14
Base line		51%	36%
Day 6	55%		43%
Day 14	52%	57%	

Overlap % = Latest timepoint & earliest timepoint / ∑ Latest timepoint

Overlap % = Earliest timepoint & latest timepoint / ∑ Earliest timepoint

CD 1300	Base line	Day 6	Day 14	Day 28
Base line		59%	45%	19%
Day 6	48%		45%	17%
Day 14	58%	72%		26%
Day 28	55%	58%	57%	

Overlap % = Latest timepoint & earliest timepoint / ∑ Latest timepoint

Fig S5. Identical secondary TCRα chain in persisting clonotypes. Representative persisting gluten-specific TCR clonotypes that have identical secondary productive TCRα chains are shown. The number of circles represents the number of cells and each line represents the TCRα and TCRβ sequences used in the cell. The *TRAV/TRBV*, CDR3α/CDR3β (nucleotide) and *TRAJ/TRBJ* usage in the respective TCRα and TCRβ sequences are shown.

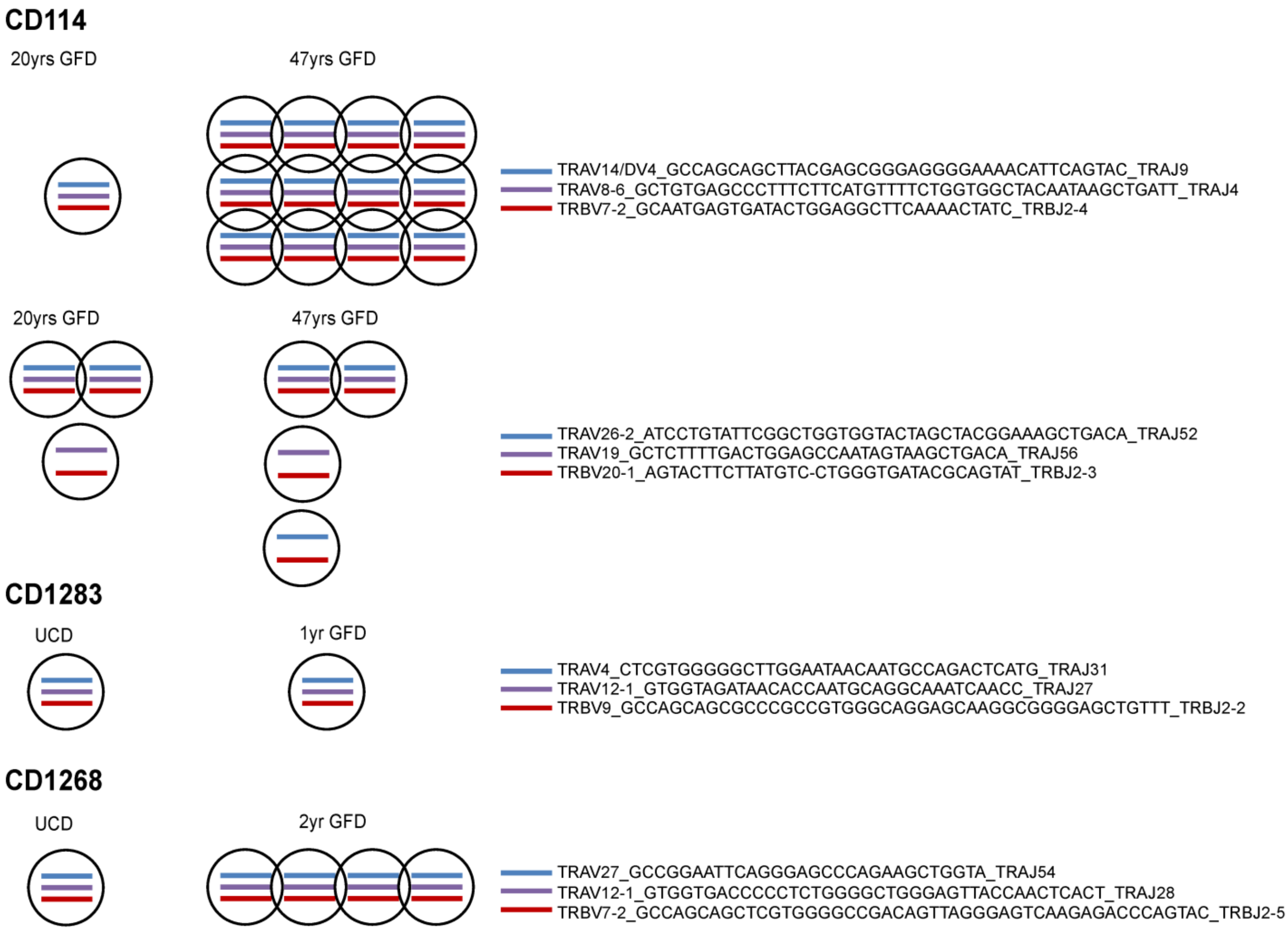


Fig. S6. Expanded T-cell clonotypes persist in gut tissue and blood over decades. Panel A shows sharing of TCRαβ clonotypes from in vitro expanded T-cell lines (TCL) from one single biopsy specimen and blood/gut samples of CD patients obtained 16-20 years apart. The overlap is depicted in area-proportional Venn diagrams and degree of overlap is calculated by dividing the number of shared clonotypes by the total number of clonotypes in the most recent samples. Panel B shows the fraction (%) of cells belonging to the shared clonotypes in the most recent samples. The total number of cells is depicted in the center of the pie charts.

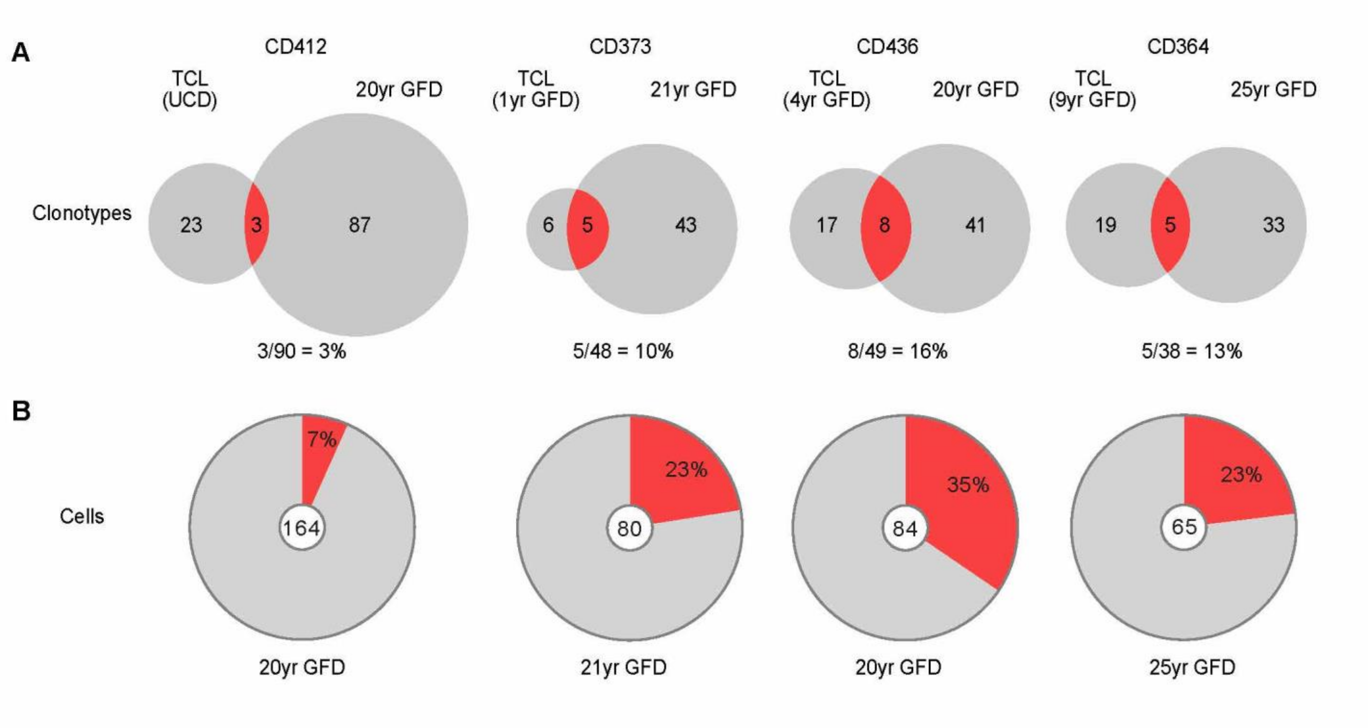


Table S1. Clinical features of patients included in the study

Patient ID[a]	HLA-DQ2/8	Year of birth	Year of diagnosis	Gluten status[b]	Marsh Score[c]	IgA-TG2[d]	IgG-DGP[e]	# Tetr+ T cells in gut[f]	# Tetr+ T cells in blood[g]	Sequencing library[h]
CD1228 (m)	2.5	1982	2013	UCD	3c	8.7	11	13400	-	bulkLib2
CD1308 (m)	2.5	1973	2015	UCD	3a	5.3	29	10300	16.9	bulkLib2
CD1317 (m)	2.5	1969	2015	UCD	3c	78.8	>100	9000	27.7	bulkLib2
CD1375 (m)	2.5	1975	2016	UCD	3a	41.7	14	24700	70.9	scLib3
				4w GFD	-	9.1	9	-	21.8	scLib4
				10w GFD	-	5.1	6.9	-	9.6	
CD1374 (f)	8	1992	2016	UCD	3c	32	54	5100	2.5	scLib4
				4w GFD	-	17.6	39	-	1.4	
				10w GFD	-	10.0	25	-	0.9	
CD1368 (m)	2.5	1972	2015	UCD	3c	18	>100	7200	8.4	scLib4
				10w GFD	-	3.8	>100	-	9.8	
				16w GFD	-	2.8	90.8	-	10.4	
				1yr GFD	2	<1	17	3400	4.7	scLib6
CD1237 (m)	2.5	1961	2013	UCD	3b	3.1	16	9400	8.5	scLib2
				1yr GFD	0	<1	<5	2400	0.5	
CD1283 (f)	2.5	1966	2014	UCD	3b	27.3	>100	-	12.7	scLib4
				1yr GFD	3a	4.0	39	4800	6.7	
				2yr GFD	3a-b	1.3	17	2300	3.3	scLib6
CD1268 (m)	2.5	1991	2014	UCD	3b-c	14.0	>100	-	34.0	scLib4
				1yr GFD	3a-b	<1	16	3800	71.7	
				2yr GFD	1-2	1.2	10	2900	10.7	scLib6
CD442 (m)	2.5	1958	2000	Baseline	3	2.3	8	22200	46.8	scLib2/3, bulkLib3
				Day 6	-	2.2	9	-	260.6	scLib3, bulkLib3
				Day 14	3	3.1	10	22800	183.2	
CD1300 (f)	2.5	1954	1987	Baseline	0	<1	<5	13800	12.1	scLib1/2, bulkLib3
				Day 6	-	<1	<5	-	881.4	scLib1, bulkLib2/3
				Day 14	3	<1	<5	31100	71.0	scLib1/2, bulkLib2/3
				Day 28	-	<1	<5	-	-	scLib6
CD1299 (f)	2.5	1993	2005	Baseline	0	<1	<5	6000	5.0	scLib1/2
				Day 6	-	<1	<5	-	55.9	scLib2
				Day 14	1	<1	<5	10800	23.1	
CD1340 (m)	2.5	1955	2008	Baseline	0	<1	<5	8200	2.2	scLib3
				Day 6	-	<1	<5	-	169.4	
				Day 14	1	<1	21	39900	23.4	
CD1339 (f)	2.5	1954	2009	Baseline	1	<1	5	3000	3.3	scLib3
				Day 6	-	<1	8	-	22.9	
				Day 14	1	<1	7	8000	23.2	
CD1295 (f)	2.5	1972	2003	Baseline	0	<1	<5	9200	49.5	scLib2
				Day 6	-	<1	<5	-	-	
				Day 14	3	<1	<5	17800	91.4	
CD1342 (f)	2.5	1988	2005	Baseline	0	<1	<5	1000	1.6	scLib3
				Day 6	-	2.4	<5	-	21.0	
				Day 14	1	2.3	5	5000	18.4	
CD114 (m)	2.5	1965	1969	19.5yr GFD	-	-	-	-	28.0	bulkLib4
				20yr GFD	-	-	-	-	50.8	scLib4/5, bulkLib4
				47yr GFD	0	<1	<5	5500	11.7	
CD412 (f)	2.5	1961	1996	UCD	-	-	-	TCL	72.0	scLib4/5, bulkLib4
				20yr GFD	0	<1	<5	3600	88.2	
CD373 (f)	2.5	1967	1995	1yr GFD	-	-	-	TCL	-	scLib4
				2yr GFD	-	-	-	-	4.3	
				21yr GFD	1	<1	<5	6800	13.2	scLib4/5
CD364 (f)	2.5	1950	1991	3yr GFD	-	-	-	-	2.4	scLib4
				9yr GFD	-	-	-	TCL	-	
				25yr GFD	0	<1	<5	12200	7.4	scLib4/5
CD436 (f)	2.5	1953	1996	4yr GFD	-	-	-	-	25.8	scLib4
				20yr GFD	0	<1	<5	2800	21.1	scLib4/5

[a] m – male, f – female
[b] Gluten status indicates time on a gluten-free diet; untreated celiac disease (UCD) (implicating a gluten-containing diet) or weeks (w) or years (yr) on a gluten-free diet. Gluten status also indicate stage of gluten challenge (Baseline, Day 6, Day 14, Day 28)
[c] Celiac disease is diagnosed based on histological appearance in the small intestinal mucosa, which can be graded according to the Marsh score into normal mucosa (Marsh 0), increased intraepithelial lymphocyte number (Marsh 1), hyperplastic lesion and crypt hyperplasia (Marsh 2) and variable degree of villous atrophy (Marsh 3a-c). In some cases, patchy lesions give variations in the histological assessment of different biopsy specimens.
[d] Titer of IgA anti-transglutaminase 2 (IgA-TG2) at celiac disease diagnosis. Undetectable titers are shown as <1.
[e] Titer of IgG anti-deamidated gliadin peptide (IgG-DGP) at celiac disease diagnosis. Undetectable titers are shown as <5.
[f] Number of HLA-DQ:gluten tetramer-binding $CD4^+$ T cells per million $CD4^+$ T cells in gut biopsy. TCL: T-cell line cultured in vitro from one single duodenal biopsy.
[g] Number of HLA-DQ:gluten tetramer-binding effector-memory gut-homing $CD4^+$ T cells per million $CD4^+$ T cells in blood.
[h] T cells were sorted at various time points and prepared and included in multiple TCR sequencing libraries. scLib: single-cell sequencing TCR library, bulkLib: bulk TCR sequencing library

Table S2. List of CDR3 amino acid sequences of public TCR sequences.

AV_CDR3α_AJ	Number of patients	Total number of sequences	Number of sequences																
			CD1375	CD1368	CD1237	CD1268	CD1283	CD114	CD412	CD373	CD364	CD436	CD1300	CD442	CD1299	CD1340	CD1339	CD1295	CD1342
AV4_LVGDDTGFQKLV_AJ8	13	25	4		2	3	1		1	1	1	2	2	1	3			3	1
AV26-1_IAFNDYKLS_AJ20	9	28			5		4	1	3				4		8	1		1	1
AV8-1_AVNARNAGNMLT_AJ39	7	29	1	2		6		5	8				5				2		
AV4_LVGEGDSNYQLI_AJ33	5	11				2		6	1			1	1						
AV4_LVGGSGGYNKLI_AJ4	5	21				3			4						2	1			11
AV12-3_AMSAGTGNQFY_AJ49	4	7						1			1			3		2			
AV14/DV4_AMREGRYSSASKII_AJ3	3	6	4					1	1										
AV19_ALSEAFGAGGTSYGKLT_AJ52	4	8	1			2								2	3				
AV4_LVGGAGGYNKLI_AJ4	5	11		1	6						1	2						1	
AV8-3_AVGAAEYGNKLV_AJ47	4	14									2		7			2		3	
AV41_AVESGSNYQLI_AJ33	4	13	8			1							3			1			
AV12-3_AMSELPGGSNYKLT_AJ53	4	18		9				1					7						1
AV26-1_IVLNARLM_AJ31	4	7							1				2				2	2	
AV26-1_IVYGGSQGNLI_AJ42	3	10			1												8		1
AV26-1_IVFNDYKLS_AJ20	3	3	1	1												1			
AV19_ALSGAGANSKLT_AJ56	3	4							1						1	2			
AV26-1_IAYNDYKLS_AJ20	3	5							1									1	3
AV26-1_IVRVVGDDKII_AJ30	4	6		1		1					1							3	
AV4_LVGDGDGGATNKLI_AJ32	4	5	1				2	1							1				
AV35_AGNYGGATNKLI_AJ32	5	13	4	3					1	1							4		
AV12-3_AMTDYGNNRLA_AJ7	4	5			1	1								1			2		
AV41_AVEGGSNYKLT_AJ53	4	21					2					1				2	16		
AV12-2_AVSNRDDKII_AJ30	4	7			1			3	1									2	
AV19_ALSEAGANSKLT_AJ56	3	8			1								1			6			
AV9-2_ALSEGNFNKFY_AJ21	3	7										1	5					1	
AV12-2_AVPNRDDKII_AJ30	3	4				1			2				1						
AV12-1_VVTLMDTGRRALT_AJ5	3	13	11		1								1						
AV26-1_IDPGSSNTGKLI_AJ37	2	4	3												1				
AV35_AGFNTDKLI_AJ34	2	2						1			1								
AV26-1_IPNYGGSQGNLI_AJ42	2	2		1											1				
AV4_LVGGDNQGGKLI_AJ23	2	2		1										1					
AV19_ALSEGGNQGGKLI_AJ23	3	3	1							1						1			
AV1-2_AVTTSNTGKLI_AJ37	3	6				3									2	1			
AV26-1_IVYNDYKLS_AJ20	3	4		1			1	2											
AV35_AGPYNTDKLI_AJ34	3	3		1					1							1			
AV13-2_AETNAGGTSYGKLT_AJ52	3	3					1		1						1				
AV26-1_IGNYGGSQGNLI_AJ42	3	7							4		1					2			
AV12-3_AMIEAAGNKLT_AJ17	3	3												1		1			1
AV35_AGDSNYQLI_AJ33	3	10						1						1	8				
AV1-2_AVLTDSWGKLQ_AJ24	2	8						1					7						
AV26-1_ISFNDYKLS_AJ20	2	9											4					5	
AV13-2_AEGDAGGTSYGKLT_AJ52	2	4	2										2						
AV12-3_AMIQAAGNKLT_AJ17	2	2											1					1	
AV8-3_AVGAVEYGNKLV_AJ47	2	2											1		1				
AV8-3_AVGVSEYGNKLV_AJ47	2	7		1									6						
AV19_ALSEGGFGNVLH_AJ35	2	4	3										1						
AV35_AGQLGGATNKLI_AJ32	2	9					5						4						
AV8-3_AVGLTDSWGKLQ_AJ24	2	3									1		2						
AV4_LVGVMEYGNKLV_AJ47	2	2	1										1						
AV29/DV5_AASEETSGSRLT_AJ58	2	2					1						1						
AV12-3_AMSEIPGGSNYKLT_AJ53	2	3					2						1						
AV35_AGNDYKLS_AJ20	2	4											2					2	
AV38-1_AFTVYTGANSKLT_AJ56	2	4											1		3				

AV8-4/8-2_ASLSNFGNEKLT_AJ48	2	3											1					2	
AV12-3_AMSEGTGNQFY_AJ49	2	2											1	1					
AV9-2_ALSDQTGANNLF_AJ36	2	2						1					1						
AV29/DV5_AASAGETSGSRLT_AJ58	2	8															7		1
AV12-2_ASQDTGRRALT_AJ5	2	13															1		12
AV19_ALSEGGNAGNMLT_AJ39	2	2						1										1	
AV16_ALSDSNYQLI_AJ33	2	3			2													1	
AV35_AGVYNNNDMR_AJ43	2	3					2											1	
AV26-1_IVYNARLM_AJ31	2	3						2										1	
AV17_ATEGNTGFQKLV_AJ8	2	2		1														1	
AV6_ALPSGYALN_AJ41	2	2							1									1	
AV2_AVEDLRAGSYQLT_AJ28	2	2			1													1	
AV8-3_AVGVDRGSTLGRLY_AJ18	2	7	6											1					
AV4_LVGGDSSYKLI_AJ12	2	2	1	1															
AV12-2_AVFPGGATNKLI_AJ32	2	3	1																2
AV14/DV4_AMREEGSQGNLI_AJ42	2	2	1												1				
AV19_ALSGGGANSKLT_AJ56	2	2	1											1					
AV4_LVGDENTGTASKLT_AJ44	2	11				10									1				
AV29/DV5_AATNTNAGKST_AJ27	2	2				1			1										
AV6_ALSTDSWGKLQ_AJ24	2	3			2	1													
AV16_ALNSGGYQKVT_AJ13	2	15		2				13											
AV29/DV5_AASALTSGTYKYI_AJ40	2	3		2								1							
AV39_AVDPGYALN_AJ41	2	2		1						1									
AV29/DV5_AASEQSGGSNYKLT_AJ53	2	3		2															1
AV12-3_AMLEAAGNKLT_AJ17	2	24								1		23							
AV9-2_ALAEYNFNKFY_AJ21	2	2						1				1							
AV41_AVETSGSRLT_AJ58	2	2					1					1							
AV35_AGQVGSSNTGKLI_AJ37	2	2										1			1				
AV9-2_ALSDPTGTASKLT_AJ44	3	5					2					1		2					
AV12-3_AMRDYGQNFV_AJ26	2	12					3								9				
AV1-2_AVRAVVSGGYNKLI_AJ4	2	18					1							17					
AV35_AGDSGGGADGLT_AJ45	2	3							2					1					
AV4_LVGTLTGGGNKLT_AJ10	2	9							8		1								
AV9-2_ALSDQDTGRRALT_AJ5	2	32								1				31					
AV9-2_ALSDGSGAGSYQLT_AJ28	2	11						9		2									
AV22_AVELQGAQKLV_AJ54	2	3						1	2										
AV29/DV5_AASVATDSWGKLQ_AJ24	2	2							1		1								
AV2_AVEVYNFNKFY_AJ21	2	3						1	2										
AV8-3_AVATDRGSTLGRLY_AJ18	2	3													1	2			
AV19_ALSEGSNAGNMLT_AJ39	2	4						1							3				
AV29/DV5_AASADAGGTSYGKLT_AJ52	2	2													1	1			
AV12-1_VVNSASSASKII_AJ3	2	6			5											1			
AV8-3_AVGLDRGSTLGRLY_AJ18	2	2						1								1			
AV26-1_IVTGNQFY_AJ49	2	4						1									3		
AV8-1_AVNRNTGFQKLV_AJ8	2	6												1			5		
AV4_LVGQNFGNEKLT_AJ48	2	8								2	6								
AV12-3_AMKDYGQNFV_AJ26	2	8									6								2
AV12-3_AMSEAAGNKLT_AJ17	2	4	3								1								
AV17_ATDDKGGSEKLV_AJ57	2	3												1					2
AV12-3_AMSASSGGGADGLT_AJ45	2	7						6											1
AV4_LVDNAGNMLT_AJ39	2	4						1						3					
AV1-2_AVRAVFSGGYNKLI_AJ4	2	4						3						1					
AV26-1_IVHNARLM_AJ31	2	2							1			1							
AV26-1_IVYNNDMR_AJ43	2	2					1					1							
AV26-1_IVTDGQKLL_AJ16	2	5										1				4			
AV21_AVTGTYKYI_AJ40	2	2									1					1			
AV1-2_AVTSSNTGKLI_AJ37	2	2						1			1								
AV8-3_AVGTDRGSTLGRLY_AJ18	2	3		2						1									
Total number of sequences			**58**	**33**	**28**	**35**	**29**	**67**	**49**	**11**	**26**	**38**	**76**	**70**	**52**	**34**	**50**	**34**	**40**

Same TCRα

Shared with one TCRβ

Shared with two TCRβ

Shared with three TCRβ

BV_CDR3β_BJ	Number of patients	Total number of sequences	CD1375	CD1368	CD1237	CD1268	CD1283	CD114	CD412	CD373	CD364	CD436	CD1300	CD442	CD1299	CD1340	CD1339	CD1295	CD1342
			Number of sequences																
BV7-2_ASSLRSTDTQY_BJ2-3	15	25	1	1	1	1	1	2	1	1	1	1	4			1	4	4	1
BV7-2_ASSIRSTDTQY_BJ2-3	13	29		3	3	2		3	2	3	1	1	4	1			2	3	1
BV7-2_ASSVRSTDTQY_BJ2-3	11	33		1	1		1	4	5	1		1	1		1		16		1
BV7-3_ASSIRSTDTQY_BJ2-3	8	15	4	1	1		1		1		1		5					1	
BV7-2_ASSFRSTDTQY_BJ2-3	10	30		3	1		4	1	3	1		1			9		4		3
BV7-2_ASSLRAGGADTQY_BJ2-3	6	9	1						1		1	2						3	1
BV7-2_ASSLRFTDTQY_BJ2-3	7	11		2			2		2			1					2	1	1
BV7-2_ASSIRATDTQY_BJ2-3	5	8		4			1					1	1		1				
BV15_ATSRAGGGGEKLF_BJ1-4	3	7	4						2									1	
BV7-2_ASSLVGWETQY_BJ2-5	4	4			1		1	1	1										
BV20-1_SASRQVNTEAF_BJ1-1	4	4				1	1	1									1		
BV7-2_ASSIRHTDTQY_BJ2-3	5	5			1				1					1			1	1	
BV5-1_ASSFDGETQY_BJ2-5	3	12				6		1					5						
BV29-1_SVGGSGANVLT_BJ2-6	4	10				1							3			1			5
BV7-3_ASSFRSTDTQY_BJ2-3	5	10				1			1				1				6		1
BV7-3_ASSIRATDTQY_BJ2-3	4	13	7			3							2			1			
BV11-2_ASSSTAQETQY_BJ2-5	3	7				2			4						1				
BV7-2_ASSLRYTDTQY_BJ2-3	4	5		1							1				1			2	
BV9_ASSVGGGAGDTQY_BJ2-3	4	9			3						1	4						1	
BV4-3/4-2_ASSQGSGGNEQF_BJ2-1	4	5	1				2	1							1				
BV4-3/4-2_ASSQGLAGRQETQY_BJ2-5	4	6		2		1						2				1			
BV7-2_ASSLRATDTQY_BJ2-3	4	6			1				2	1							2		
BV7-2_ASSLRHTDTQY_BJ2-3	3	12										2	8					2	
BV7-3_ASSQGQDTEAF_BJ1-1	3	3		1									1						1
BV19_ASSIRTGGSEQY_BJ2-7	3	12											3	1	8				
BV7-6_ASSFGSYNEQF_BJ2-1	3	3		1									1	1					
BV29-1_SVGAVSTDTQY_BJ2-3	3	5									1		3			1			
BV30_AWSVTGWDTGELF_BJ2-2	3	4									2		1		1				
BV5-1_ASSLGGGAGDTQY_BJ2-3	3	3											1			1			1
BV7-2_ASSFRYTDTQY_BJ2-3	2	2		1					1										
BV7-2_ASSYRSTDTQY_BJ2-3	2	2	1															1	
BV7-3_ASSLRATDTQY_BJ2-3	2	2					1											1	
BV7-2_ASSLRAGGGDTQY_BJ2-3	2	4		3														1	
BV7-2_ASSFRHTDTQY_BJ2-3	2	2			1				1										
BV7-2_ASSIRYTDTQY_BJ2-3	2	3		2								1							
BV7-2_ASSIRFTDTQY_BJ2-3	3	36								2					33			1	
BV7-3_ASSLRSTDTQY_BJ2-3	3	3						1							1			1	
BV7-2_ASSVRFTDTQY_BJ2-3	3	11				1		2	8										
BV7-6_ASSLAGFDSPLH_BJ1-6	3	8		3						4									1
BV20-1_SARVWNTEAF_BJ1-1	3	5		2				1	2										
BV5-6/5-5_ASSFGVTGELF_BJ2-2	3	3		1			1	1											
BV7-6_ASSLASAGGTDTQY_BJ2-3	3	3		1					1							1			
BV29-1_SGGQGETQY_BJ2-5	3	3		1											1	1			
BV29-1_SVGAGGTGELF_BJ2-2	3	20					2										15		3
BV5-1_ASSLGQPSTDTQY_BJ2-3	2	2	1										1						
BV5-6/5-5_ASSFGPSNQPQH_BJ1-5	2	10											9			1			
BV18_ASSPAGWDTEAF_BJ1-1	2	2					1						1						
BV12-3/12-4_ASRLTLGTDTQY_BJ2-3	2	2		1									1						
BV29-1_SAGQGGTGELF_BJ2-2	2	4							1				3						
BV4-1_ASSLSDSDQPQH_BJ1-5	2	2											1		1				

BV5-1_ASSLVAWDTEAF_BJ1-1	2	10					5						5						
BV7-2_ASSLRVGDTQY_BJ2-3	2	2											1	1					
BV5-1_ASSLGIALSSYNEQF_BJ2-1	2	2											1		1				
BV7-2_ASSIRDTDTQY_BJ2-3	2	5			4								1						
BV7-2_ASSIRVTDTQY_BJ2-3	2	2											1	1					
BV29-1_SVGLVSTDTQY_BJ2-3	2	2						1					1						
BV5-1_ASSLGVALSSYNEQF_BJ2-1	2	2					1						1						
BV6-1_ASFLGPVFPGGYT_BJ1-2	2	3											1					2	
BV7-3_ASSLRHTDTQY_BJ2-3	2	6				1												5	
BV19_ASSIFSLAGASYNEQF_BJ2-1	2	3	2															1	
BV20-1_SASPGEEKLF_BJ1-4	2	2												1				1	
BV7-7_ASSLLAGGDTQY_BJ2-3	2	2													1			1	
BV7-2_ASSLRWTDTQY_BJ2-3	3	3							1			1						1	
BV20-1_SARRQADQPQH_BJ1-5	3	12	8								1				3				
BV5-1_ASSWGMNTEAF_BJ1-1	2	2	1												1				
BV5-1_ASSFDAETQY_BJ2-5	2	3	1	2															
BV6-5_ASSGRTGRYTEAF_BJ1-1	2	2	1		1														
BV5-6/5-5_ASSLKEGYGYT_BJ1-2	2	2	1								1								
BV5-6/5-5_ASSLGRSYGYT_BJ1-2	2	2				1			1										
BV29-1_SVGQVSTDTQY_BJ2-3	2	5				4										1			
BV7-2_ASSIRTGDGNTQY_BJ2-3	2	2				1						1							
BV7-6_ASSLGTWDTGELF_BJ2-2	2	3		2													1		
BV7-3_ASSIRGTDTQY_BJ2-3	2	2		1			1												
BV7-3_ASSLNWDTEAF_BJ1-1	3	7		5							1								1
BV20-1_SLFGGGSTDTQY_BJ2-3	2	7		1							6								
BV4-3/4-2_ASSQRQGGNTIY_BJ1-3	2	2		1										1					
BV5-6/5-5_ASSLVNMNTEAF_BJ1-1	2	3		1										2					
BV9_ASSLGGGAGDTQY_BJ2-3	2	20								1		19							
BV20-1_SATLQGDYGYT_BJ1-2	2	2			1							1							
BV29-1_SVGAGGSGELF_BJ2-2	2	3										1				2			
BV7-6_ASSYGSYNEQF_BJ2-1	2	2					1							1					
BV19_ASSIGTSGETQY_BJ2-5	2	4					1									3			
BV5-6 /5-5_ASSRRQGYGYT_BJ1-2	2	2					1			1									
BV7-2_ASSLRGWETQY_BJ2-5	2	2					1							1					
BV29-1_SVEDQSGEKLF_BJ1-4	2	10							9		1								
BV29-1_SVAESSNSPLH_BJ1-6	2	3						1	2										
BV7-3_ASSVRATDTQY_BJ2-3	2	4			1				3										
BV10-3_AISASGTEAF_BJ1-1	2	2							1		1								
BV24-1_ATSDFQGNYGYT_BJ1-2	2	11						9	2										
BV5-5_ASSLAQGGDTQY_BJ2-3	2	4												2		2			
BV5-6/5-5_ASSLRQLYEQY_BJ2-7	2	2								1						1			
BV29-1_SGFLGETQY_BJ2-5	2	3			2												1		
BV24-1_ATSDSQGLYGYT_BJ1-2	2	3						2									1		
BV5-1_ASSLGGPNTGELF_BJ2-2	2	2												1			1		
BV20-1_SAESGYNEQF_BJ2-1	2	2												1			1		
BV7-2_ASSIRGTDTQY_BJ2-3	2	7								2	5								
BV7-8_ASSFDSNSPLH_BJ1-6	2	8									6								2
BV28_ASSRLQDHEQY_BJ2-7	2	2						1											1
BV7-3_ASSVRSTDTQY_BJ2-3	2	4						3							1				
BV5-6/5-5_ASSLSGLTEAF_BJ1-1	2	3			2			1											
BV29-1_SVGTVSTDTQY_BJ2-3	2	2			1									1					
BV7-2_ASSLAFLAGEETQY_BJ2-5	2	2												1	1				
BV20-1_SASAGTFTDTQY_BJ2-3	2	2							1		1								
BV5-6/5-5_ASSFTNTGELF_BJ2-2	2	2					1			1									
Total number of sequences			**34**	**48**	**26**	**26**	**31**	**37**	**60**	**19**	**32**	**40**	**72**	**18**	**67**	**18**	**58**	**35**	**24**

Same TCRβ

Shared with one TCRα

Shared with two TCRα

Shared with three TCRα

Table S3. List of CDR3 nucleotide sequences of paired public TCR sequences.

Sequence ID	Donor ID	Time-point	Source	Sequencing library	CDR3α(nt)*	CDR3β(nt)*
AV4_LVGDGDGGATNKLI_AJ32 : BV4-2_ASSQGSGGNEQF_BJ2-1	CD1283	UCD	PBMC	lib4	ctcgtgggtgacggagatggtggtgctacaaacaagctcatc	gccagcagccaagggagcgggggcaatgagcagttc
	CD1283	2 yr GFD	PBMC	lib6	ctcgtgggtgacgggggatggtggtgctacaaacaagctcatc	gccagcagccaagggtccgggggcaatgagcagttc
	CD114	20 yr GFD	PBMC	lib5	ctcgtgggtgacgggggatggtggtgctacaaacaagctcatc	gccagcagccaaggctcgggcggaaatgagcagttc
	CD1299	Day 14	Gut	lib2	ctcgtgggtgacgggggatggtggtgctacaaacaagctcatc	gccagcagccaagggagtgggggcaatgagcagttc
	CD1375	4 wk GFD	PBMC	lib4	ctcgtgggtgacgggggatggtggtgctacaaacaagctcatc	gccagcagccaagggagcgggggcaatgagcagttc
AV12-3_AMSAGTGNQFY_AJ49: BV29-1_SVGAVSTDTQY_BJ2-3	CD1340	Day 14	PBMC	lib3	gcaatgagcgcagggaccggtaaccagttctat	agcgttgggggcggtgagcacagatacgcagtat
	CD1300	Day 14	PBMC	lib1	gcaatgagcgcggggaccggtaaccagttctat	agcgttgggggcagtaagcacagatacgcagtat
	CD1300	Day 6	PBMC	lib1	gcaatgagcgcggggaccggtaaccagttctat	agcgttgggggcagtaagcacagatacgcagtat
	CD364	25 yr GFD	Gut	lib4	gcaatgagcgcggggaccggtaaccagttctat	agcgttggagcggtgagcacagatacgcagtat
AV8-1_AVNARNAGNMLT_AJ39: BV5-1_ASSFDGETQY_BJ2-5	CD114	20 yr GFD	PBMC	lib4	gccgtgaatgcaaggaatgcaggcaacatgctcacc	gccagcagcttcgacggagagacccagtac
	CD1268	1 year GFD	Gut	lib4	gccgtgaatgcacgaaatgcaggcaacatgctcacc	gccagcagctttgacggagagacccagtac
	CD1268	1 year GFD	Gut	lib4	gccgtgaatgcacgaaatgcaggcaacatgctcacc	gccagcagctttgacggagagacccagtac
	CD1268	1 year GFD	PBMC	lib4	gccgtgaatgcacgaaatgcaggcaacatgctcacc	gccagcagctttgacggagagacccagtac
	CD1268	2 yr GFD	Gut	lib6	gccgtgaatgcacgaaatgcaggcaacatgctcacc	gccagcagctttgacggagagacccagtac
	CD1268	UCD	PBMC	lib4	gccgtgaatgcacgaaatgcaggcaacatgctcacc	gccagcagctttgacggagagacccagtac
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	CD114	47 yr GFD	PBMC	lib5	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	47 yr GFD	PBMC	lib5	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	20 yr GFD	PBMC	lib4	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	47 yr GFD	PBMC	lib4	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	47 yr GFD	PBMC	lib4	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	20 yr GFD	PBMC	lib4	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
	CD114	47 yr GFD	PBMC	lib4	gctctgagtgatggctctggggctgggagttaccaactcact	gccaccagtgatttccagggtaactatggctacacc
AV19_ALSEGGNQGGKLI_AJ23: BV5-5_ASSLRQLYEQY_BJ2-7	CD1340	Baseline	Gut	lib3	gctctgagtgagggaggtaaccagggaggaaagcttatc	gccagcagcttgcgacagctctacgagcagtac
	CD373	21 yr GFD	PBMC	lib4	gctctgagtgagggggggtaaccagggaggaaagcttatc	gccagcagcttgagacagctctacgagcagtac
AV12-3_AMIEAAGNKLT_AJ17: BV5-1_ASSLGGGAGDTQY_BJ2-3	CD1342	Baseline	Gut	lib3	gcaatgatcgaagctgcaggcaacaagctaact	gccagcagcttgggagggggggccggagatacgcagtat
	CD1340	Baseline	Gut	lib3	gcaatgattgaagctgcaggcaacaagctaact	gccagcagccttgggggggagcggggatacgcagtat
AV26-1_IVYGGSQGNLI_AJ42: BV7-3_ASSFRSTDTQY_BJ2-3	CD1339	Day 6	PBMC	lib3	atcgtctatggaggaagccaaggaaatctcatc	gccagcagcttccggagcacagatacgcagtat
	CD1339	Day 14	Gut	lib3	atcgtctatggaggaagccaaggaaatctcatc	gccagcagcttccggagcacagatacgcagtat
	CD1339	Day 14	Gut	lib3	atcgtctatggaggaagccaaggaaatctcatc	gccagcagcttccggagcacagatacgcagtat
	CD1339	Day 6	PBMC	lib3	atcgtctatggaggaagccaaggaaatctcatc	gccagcagcttccggagcacagatacgcagtat
	CD1339	Day 14	Gut	lib3	atcgtctatggaggaagccaaggaaatctcatc	gccagcagcttccggagcacagatacgcagtat
	CD1342	Day 14	Gut	lib3	atcgtttatggaggaagccaaggaaatctcatc	gccagcagcttccgtagcacagatacgcagtat
AV12-3_AMTDYGNNRLA_AJ7: BV5-1_ASSLGGPNTGELF_BJ2-2	CD442	Day 6	PBMC	lib3	gcaatgaccgactatgggaacaacagactcgct	gccagcagcttgggcggaccgaacaccggggagctgttt
	CD1339	Day 14	Gut	lib3	gcaatgaccgactatgggaacaacagactcgct	gccagcagcttgggagggccgaacaccggggagctgttt
AV26-1_IVTGNQFY_AJ49: BV7-2_ASSIRSTDTQY_BJ2-3	CD1339	Baseline	Gut	lib3	atcgtcaccggtaaccagttctat	gccagcagcatccggagcacagatacgcagtat
	CD114	47 yr GFD	PBMC	lib4	atcgtcaccggtaaccagttctat	gccagcagcatccggagcacagatacgcagtat
AV12-3_AMSEAAGNKLT_AJ17: BV9_ASSVGGGAGDTQY_BJ2-3	CD1237	UCD	PBMC	lib2	gcaatgagcgaagctgcaggcaacaagctaact	gccagcagcgtaggcgggggggccggagatacgcagtat
	CD1237	UCD	PBMC	lib2	gcaatgagcgaagctgcaggcaacaagctaact	gccagcagcgtaggcgggggggccggagatacgcagtat
	CD1237	UCD	PBMC	lib2	gcaatgagcgaagctgcaggcaacaagctaact	gccagcagcgtaggcgggggggccggagatacgcagtat
	CD364	25 yr GFD	PBMC	lib4	gcaatgagcgaggctgcaggcaacaagctaact	gccagcagcgtaggtgggggggctggagatacgcagtat
AV12-3_AMKDYGQNFV_AJ26: BV7-8_ASSFDSNSPLH_BJ1-6	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
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	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
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	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
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	CD364	9 yr GFD	Gut	lib5	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
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	CD364	25 yr GFD	Gut	lib4	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	25 yr GFD	Gut	lib4	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	25 yr GFD	Gut	lib4	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	25 yr GFD	Gut	lib4	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD364	25 yr GFD	Gut	lib4	gcaatgaaagactatggtcagaattttgtc	gccagcagcttcgacagcaattcacccctccac
	CD1342	Day 6	PBMC	lib3	gcaatgaaggactatggtcagaattttgtc	gccagcagcttcgacagtaattcacccctccac

AV26-1_IAYNDYKLS_AJ20: BV7-2_ASSFRSTDTQY_BJ2-3	CD1342	Day 6	PBMC	lib3	atcgcctataacgactacaagctcagc	gccagcagctttagaagcacagatacgcagtat
	CD1342	Day 6	PBMC	lib3	atcgcctataacgactacaagctcagc	gccagcagctttagaagcacagatacgcagtat
	CD1342	Day 6	PBMC	lib3	atcgcctataacgactacaagctcagc	gccagcagctttagaagcacagatacgcagtat
	CD114	20 yr GFD	PBMC	lib4	atcgcttataacgactacaagctcagc	gccagcagcttccggagcacagatacgcagtat

* The non-germline encoded nucleotides are underlined. Due to uncertainities in D-segment assignment, all the nucleotide that are non-germline encoded in V or J are underlined. The different nucleotides that encode same amino acids are shown in red.