SUPPLEMENTARY APPENDIX

Somatic mutations and T-cell clonality in patients with immunodeficiency

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Supplementary information

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Supplementary Methods

Patients

We recruited 8 patients with late-onset CVID and 9 patients with other types of delayed-onset immunodeficiency or severe autoimmunity from the Helsinki University Hospital infectious disease clinic (Table 1). CVID patients were included in a previously described CVID cohort.[1] As healthy controls, we used blood donor buffy coat samples from the Red Cross Blood Service (Supplementary Table S1). This study was approved by local Ethics Committee, and the principles of Helsinki Declaration were followed. All patients signed informed consent.

Clinical manifestations of five patient cases have been previously described: patient 17 with biallelic germline mutation in *ADA2* gene (*CECR1*, p.Arg169Gln/p.Arg169Gln) and ADA2 deficiency,[2] patients 9-11 as germline gain-of-function mutations in *STAT3*,[3] and patient 12 as a case with compound immunodeficiency and 11q terminal deletion arr11q24.2q25 (126,074,297-134,927,114) x 1 (Jacobsen syndrome).[4]

Sample preparation

Peripheral-blood EDTA samples were obtained from all patients. For patient 9, only archived bone-marrow mononuclear cells were available. Mononuclear cells were enriched from peripheral blood via Ficoll gradient centrifugation (Ficoll-Paque PLUS, GE Healthcare). CD4+ and CD8+ cells were purified via positive selection with magnetic beads (Miltenyi Biotech). Purity of sorted cells was controlled with flow cytometry with anti-CD45 (2D1, PerCP), anti-CD3 (SK7, FITC), anti-CD4 (SK3, APC), and anti-CD8 antibodies (SK1, PE-Cy7) (Beckton Dickinson). DNA was extracted with NucleSpin Tissue kit (Machery Nagel) according to manufacturer's instructions; however, the samples of patient 15 were extracted with Qiagen DNEasy Blood & Tissue kit (Qiagen). B-cell phenotypes were analyzed with flow cytometry in a clinical laboratory according to published guidelines.[5,6]

T-cell receptor beta locus sequencing

TCRB sequencing was performed from CD8+ and CD4+ cells with the human TCRB immunoSEQ kit (Adaptive Biotechnologies) according to manufacturer's instructions.[7,8] The TCRB sequencing procedures have been described previously.[8,9] Healthy controls' CD4+ and CD8+ cells were also sequenced (n=27), and results were compared with the results of 7 CVID patients (pt.1-7). Only productive TCR sequences were taken into account in the analyses. ImmnoSEQ Analyzer software

(Adaptive Biotechnologies) and R version 3.4.2 and RStudio (version 1.1.383) were used for data analyses. The clonality metric was calculated as one minus Shannon entropy normalized by the logarithm of the number of productive TCR sequences.

To search for public TCR sequences, such as public pathogen-specific TCRs, we queried our TCR sequencing dataset on public TCRs that were included in the manually curated McPAS database, which includes approximately 9500 human TCR sequences.[10] For pathogen- and cancer-associated TCRs, only antigen-specific TCRs were queried (labels "1" and "2" in the McPAS database), but for autoimmune TCRs, all autoimmune-associated TCRs were included in the analyses. The pathogen-specific public TCRs comprised of TCRs targeting CMV, EBV, influenza, HIV, yellow fever virus, *Mycobacterium tuberculosis*, Herpes simplex 2 virus, and hepatitis C virus.

Physico-chemical similarities between TCRs were analyzed with a generic string kernel (GSKernel) algorithm,[11] which is designed for analysis of small peptides. The unsupervised clustering analysis of the TCR similarities was done with graph-theory based PhenoGraph.[12] The results were visualized with t-Distributed Stochastic Neighbor Embedding (t-SNE).[13] To focus on the most biologically meaningful TCRs and to minimize the amount of noise, we included only a subset of TCRs for the analyses:

1. Convergent TCRs that have more than 5 different clones OR convergent TCRs that make up at least 1% of the repertoire ("highly convergent")
2. TCR clones that comprise at least 1% of all rearrangements (CD8+ cells) or 0.1% of all rearrangements (CD4+ cells) ("highly expanded")

Also, these "highly convergent" and "expanded" clones were compared for their TCR amino-acid properties yielded by the "peptides" R package, which yields scores on the Cruciani *et al* properties (Polarity, Hydrophobicity, H-bonding),[14] GRAVY hydrophobicity index, and net charge.

Somatic variant detection: Sequencing library preparation

To discover somatic variants that occur even at small variant allele frequencies, we designed a custom sequencing panel that comprised of the coding areas of 2533 genes, covering approximately 5.2 million base-pairs. The gene selection was based on the InnateDB database (http://www.innatedb.ca/),[15–17] but also other genes that were important in hematopoietic cells, adaptive immune responses, and autoimmunity were included (Supplementary Table S2). The target probes were designed with NimbleGen SeqCap EZ Developer system.

All immunodeficiency patient samples and 12/21 control samples were prepared for targeted sequencing with Kapa Hyper library preparation kit (Roche). Double-stranded genomic DNA (300-500ng) was fragmented with Covaris E220 evolution instrument (Covaris) to retrieve mean fragment size of 200 base-pairs. Sample libraries and enrichment were performed according to SeqCapEZ HyperCap Workflow User's Guide version 1.0 (Roche Nimblegen). SeqCap adapters and 9 cycles were used for pre-capture amplification. Four samples were multiplexed for capture using 1 ug of each library. Post-capture amplification included 10 cycles. Libraries were quantified with 2100 Bioanalyzer High Sensitivity Kit (Agilent Technologies).

For 9/21 control samples, ThruPLEX DNA-seq library preparation kit (Rubicon Genomics) was used. Double-stranded genomic DNA (100ng) was fragmented with Episonic Multi-Functional Bioprocessor 1100 (Epigenetik Group Inc.) to retrieve mean fragment size of 200 base-pairs. Sequencing libraries were prepared according to ThruPLEX DNA-seq library preparation kit protocol (Rubicon Genomics) with five amplification cycles. Libraries were quantified with LabChip GX (Caliper Life Sciences, Inc.). Eight samples (100ng DNA each) were pooled for hydridization and target capture, and targets were captured according to "Exome Capture of ThruPLEX Libraries with Roche NimbleGen SeqCap EZ Library" (Rubicon Genomics) and "NimbleGen SeqCap EZ Exome Library SR User's Guide" (Roche). Post-capture amplification was performed with 10 cycles. Quantification for sequencing was performed with 2100 Bioanalyzer High Sensitivity Kit (Agilent Technologies). All samples were sequenced with HiSeq2500 (Illumina) with HiSeq high output mode using v4 kits (Illumina), using 101-length paired-end reads.

Somatic variant detection: Sequencing data analysis

Genome variants were called using a previously established Genome Analysis Toolkit (GATK) protocol.[18] Briefly, sequencing data was pre-processed with the Trimmomatic software,[19] and aligned to the GRCh38 genome with BWA-MEM.[20] The Picard toolset was used to mark PCR duplicates. Base recalibration was then performed with GATK BaseRecalibrator.[21] GATK IndelRealigner was used for local realignment near indels, , and GATK CalculateContamination was used to estimate cross-sample contaminations. Somatic variants were identified using the MuTect2 toolset with default settings, using a panel of normals based on data from the 21 heathy control samples.[22] Finally, levels of 8-oxoguanine and deamination artifacts were estimated and variant calls resulting from sequencing artifacts filtered. Calling of variants relied on GATK version

3 tools and GATK resource files that were converted from GRCh37 to GRCh38 using CrossMap[23] and EnsEMBL chain files downloaded from EnsEMBL. GATK version 4 tools were used to estimate levels sequencing artifacts and cross-sample contamination.

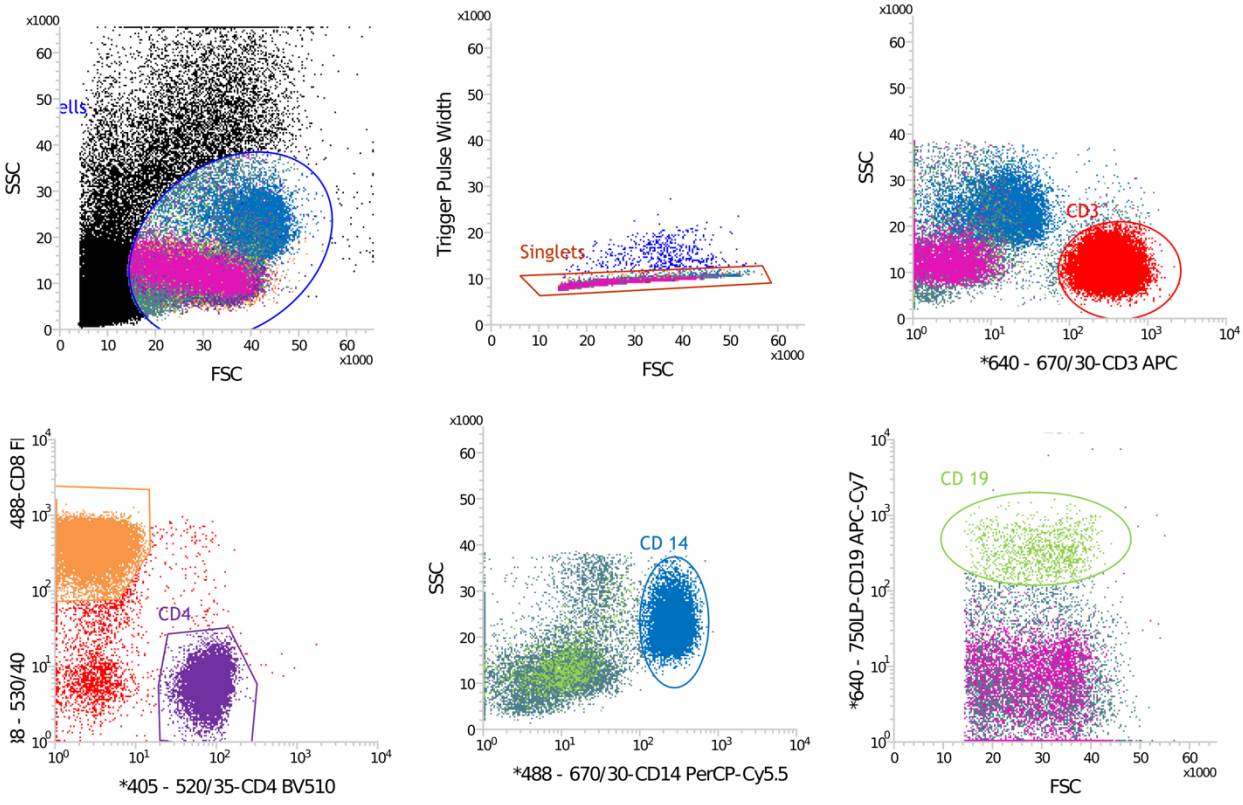
Filtering and annotation of variant calls was based on in-house scripts and Annovar.[24] Briefly, variant calls passing standard MuTect2 filters and with a quality of ≥40, read depth of ≥7, ≥1 forward and reverse strand read, and strand orientation bias (SOR) of ≤3 for single-nucleotide alterations or ≤11 for indel alterations were accepted. False-positive variant calls were then further filtered by removing calls with a variant allele frequency (VAF) of ≤1%, calls with a VAF of 1-2% and supported by ≤5 Catalogue of Somatic Mutations in Cancer (COSMIC) hematopoietic tissue samples, and calls that were associated with a population frequency >1% in gnomAD exome ALL, gnomAD exome FIN, gnomAD exome NFE, esp6500, or 1000g collections. Intronic and inframe variant calls were also removed. For all downstream analyses except mutational signature analyses, only nonsynonymous and splice-site mutations were included. Finally, nonsynonymous and splice-site variants were inspected visually with Integrative Genomics Viewer (IGV) to ensure high quality of variants.

Somatic variants specific for CD4+ and CD+ fractions were identified by performing a tumor-normal MuTect2 analysis between datasets in both directions. This procedure eliminates germline-derived variants. Variants that originate from hematopoietic progenitors (clonal hematopoiesis) and occurring in both CD4+ and CD8+ cells were in turn identified using MuTect2 tumor-only strategy and by searching for somatic calls mutually present in both fractions. To avoid false findings among these "clonal hematopoiesis -associated" variant calls, only variant calls associated with known clonal hematopoiesis -associated genes[25–27] and with a VAF of ≥2% in at least one fraction were accepted. Variants were also quality checked using IGV and indel calls were not allowed to be within 5 base-pairs of a homopolymer or repeat region.

Signaling pathways were annotated using the Reactome public database,[28] and gene functions were annotated using Gene Ontology (GO) Consortium database "biological process" terms (Supplementary Table S3).[29,30] Mutational signatures were identified from both non-coding mutations and mutations that alter protein amino-acid sequence with deconstructSigs with default parameters and cancer profiles downloaded from the COSMIC web site in 09/2017.[31,32] The variant filtering criteria for signature analyses were 2% VAF, at least 7 supporting reads, and variant calls in both reverse and forward strands.

Flow-cytometry-mediated cell sorting

We performed cell sorting to extract multiple, pure cell fractions from four patient samples (patients 2, 13, 16, 17). Patients' mononuclear cells were stained with the following antibodies: CD3-APC (SK7), CD8-FITC (SK1), CD4-BV510 (SK3), CD19-APC-Cy7 (SJ25C1), CD56-AF700 (B159), CD16-PE (Leu11c), CD14-PerCP-Cy5.5 (M5E2). They were sorted into CD3+CD4+, CD3+CD8+, $CD3^{neg}CD19+$, $CD3^{neg}CD14+$ and CD56+CD16+ cell fractions by FACS Influx (Beckton Dickinson). DNA was extracted by Qiagen DNEasy Blood & Tissue kit (Qiagen) according to manufacturer's instructions. DNA samples were prepared for Amplicon sequencing as described below. However, the yield of the fraction containing NK cells was so small that NK cells were not sequenced. The gating strategy is shown in the figure below. The purity of sorted fractions was controlled and was nearly 100%.



Populations:

Populations	Even…	% Total	% Parent
All Events	100,000	100.00%	####
Cells	59,543	59.54%	59.54%
Singlets	59,041	59.04%	99.16%
CD3	36,202	36.20%	61.32%
CD8	23,557	23.56%	65.07%
CD4	10,661	10.66%	29.45%
NOT(CD3)	22,839	22.84%	38.68%
CD 14	10,337	10.34%	45.26%
NOT(CD 14)	12,502	12.50%	54.74%
CD 19	1,173	1.17%	9.38%
CD16 CD56	5,144	5.14%	41.15%

Amplicon sequencing: confirmation of mutations with a multiplex panel

To gain higher confidence in the low VAF somatic mutations we performed a validation experiment by designing primers to cover genomic loci of 41 positions (Supplementary Table S9). Of these positions, 17 positions were negative controls. These 17 positions did not include any variants in the immunogene panel sequencing in our patient samples but had COSMIC identifiers. All positions were covered by amplicon primers that were multiplexed into a single reaction; the primers were designed by Paragon Genomics (Hayward, CA, USA) as a CleanPlex Custom NGS panel. Thus, all 41 positions were sequenced from all samples. Library preparation was performed according to manufacturer's instructions and the samples were sequenced with MiSeq PE150 v2 flow cell.

The sequencing data analysis pipeline has been described in detail previously.[33] Final variant refining included the following steps:

1. Discarding all variants with a frequency ratio less than 0.9
2. The variant must be first identified in the immunogene panel, as described in previous sections. Alternatively, it could be a control variant instead.
3. The variant should be supported by 10 or more reads. The VAFs of screened variants ranged from 0.017-0.13 in immunopanel data. Thus, a coverage of over 200-300 would be required to call variants in the positions with high confidence. Three amplicons had insufficient coverage (20-252x, Supplementary Table S9; *TET2* Q591fs, *DNMT3A* D531N, *JAK2* V617F) and were judged to be low confidence.

Additional Amplicon sequencing for *STAT5B* and *KRAS* mutations

In addition to the multiplexed Amplicon panel sequencing, we performed single amplicon sequencing for three mutations: *STAT5B* N418K, *STAT5B* T628S and *KRAS* T58I. Samples for *STAT5B* sequencing were prepared by flow-cytometry-mediated cell sorting. PBMNCs were stained with CD3 (APC, SK7), CD4 (PerCP, SK3), CD8 (Pe-Cy7, SK1), CD14 (Pacific Blue, MHCD1428) antibodies and a Vbeta antibody corresponding to the largest CD8+ clone in the patient (IO Test Vbeta Mark Kit, Beckman Coultier, PE and FITC fluorochromes). Cells were sorted with FACSAria II (Beckton Dickinson) into CD3+CD4+, CD3+CD8+Vbeta+, CD3+CD8+Vbeta^{neg}, CD3^{neg}CD14+ and CD3^{neg}CD14^{neg} cell fractions with nearly 100% purity. Afterwards, DNA extraction followed with the NucleSpin Tissue kit (Machery Nagel) according to manufacturer's instructions.

Short amplicons were designed to cover the mutation of interest. Amplicons were amplified with a two-step PCR protocol. The first PCR was performed in a volume of 20µl containing ≤10ng of sample DNA, 10µl of 2× Phusion High-Fidelity PCR Master Mix (Thermo Fisher Scientific, Waltham, MA, USA) and 0.25µM of each locus-specific primer. *KRAS* locus-specific primers were prone to forming primer dimers so 10µl of water was added to the ready PCR reaction to increase the volume to 30µl and the products were purified once with Agencourt AMPure XP beads (Beckman Coulter, Brea, CA, USA).

The second PCR was performed using the amplified product from step 1 and index primers. DNA Engine Tetrad 2 (Bio-Rad Laboratories) or G-Storm GS4 (Somerton) thermal cyclers were used to cycle both PCR steps. 27 cycles were used for the first PCR and 8 for the second (Index PCR). The amplified samples were pooled and the pool was purified with Agencourt AMPure XP beads twice using 0.8x volume of beads compared to the sample pool volume. Agilent 2100 Bioanalyzer (Agilent Genomics, Santa Clara, CA, USA) was used to quantify amplification performance and yield of the purified sample pools. Sample pools were sequenced with Illumina MiSeq System using Illumina MiSeq Reagent Kit v3 600 cycles kit (Illumina, San Diego, CA, USA).

RNA sequencing

To study if genes with somatic mutations are expressed in CD4+ or CD8+ cells, we utilized RNA sequencing from healthy controls' CD4+ cells (n=3) and CD8+ cells (n=5). RNA was extracted with miRNeasy kit including DNAse I digestion (Qiagen) or NucloSpin RNA II kit (Machery-Nagel) according to manufacturer's instructions. Total RNA (1-3ug) of cells was depleted from ribosomal RNA (Ribo-Zero, Epicentre). Ribodepleted and purified RNA (Nucleospin cleanup XS, Machery-Nagel) was converted to ds cDNA with the SuperScript Double-Stranded cDNA Synthesis Kit (Life Technologies), in all but two CD4+ samples, in which the NEBNext mRNA Library Prep Master Mix Set for Illumina was used. Random hexamers (New England BioLabs) were used to prime the first strand synthesis reaction and SPRI beads (Agencourt AMPure XP, Beckman Coulter) for cDNA purification. Illumina-compatible Nextera Technology (Illumina) was used for preparation of RNA sequencing libraries, but instead of DNA, ds cDNA (60ng) was used as a template. Following the tagmentation reaction, fragmented cDNA was purified with SPRI beads. To add Illumina-specific bridge-PCR sites and enrich the library, limited-cycle PCR (5 cycles) was done according to instructions of Nextera system with minor modifications. For barcoded libraries, 50 X Nextera Adaptor 2 was replaced with Nextera Bar Codes kit adapters (Illumina) in the PCR setup. SPRI beads were employed to purify the PCR products. Library quality was evaluated with

Agilent Bioanalyzer (Agilent Technologies). Libraries were sequenced with Illumina HiSeq2000 or Illumina Genome Analyzer II to produce 100 base-pair paired-end reads.

RNA sequencing data was processed and aligned as has been previously described.[18] Reads were first trimmed with Trimmomatic and then mapped to the human GRCh38 reference (EnsEMNL 82) using STAR with the default 2-pass per-sample mapping settings.[34] Reads sorting and duplicate marking was performed with the Picard toolkit. FastQC and RNA-SeQC were used for quality control analysis. Mapped reads were assigned to gene features (EnsEMBL v82) using FeatureCounts.[35] Multi-mapping reads and assignment of a read to more than one overlapping feature were allowed. Read counts were normalized with the Trimmed Mean of M-values (TMM) method with edgeR with default parameters,[36] and transformed to $\log_2$ values for graphing.

Statistical analyses

Variant calling procedures are described in the "Somatic variant detection" -section. Statistical analyses were performed using GraphPad Prism v.6 (GraphPad Software) and R version 3.4.2 (www.r-project.org). Data were inspected for normality both graphically and with Shapiro-Wilk tests, but due to small sample size and/or data skewing, mostly nonparametric statistical tests were employed. Statistical tests included Spearman correlation, t-test, Mann-Whitney test, Kruskall-Wallis test, and Dunn's multiple comparisons tests. Benjamini-Hochberg correction for multiple testing was used when analyzing V-family and J-gene usage.

Supplementary Tables.

Supplementary Table S1. Healthy controls used in the study.

Sample	Disease	Sex	Age	TCRB sequencing?	Immunogene panel sequencing?
HC1	HC	F	58	yes	yes
HC2	HC	M	58	yes	yes
HC13	HC	F	66	yes	yes
HC7	HC	M	48	yes	yes
HC8	HC	F	57	yes	yes
HC9	HC	F	56	yes	yes
HC10	HC	F	47	yes	yes
HC11	HC	M	48	yes	yes
HC12	HC	F	21	yes	yes
HC4	HC	F	44	yes	yes
HC5	HC	M	55	yes	yes
HC6	HC	M	52	yes	yes
HC3	HC	F	65	yes	yes
HC14	HC	F	63	yes	yes
HC15	HC	M	63	yes	yes
HC16	HC	F	65	yes	yes
HC17	HC	M	64	yes	yes
HC18	HC	F	65	yes	yes
HC19	HC	M	64	yes	yes
HC20	HC	F	63	yes	yes
HC21	HC	M	64	no	yes
HC22	HC	M	61	yes	no
HC23	HC	F	50	yes	no
HC27	HC	M	60	yes	no
HC28	HC	M	43	yes	no
HC26	HC	M	70	yes	no
HC24	HC	F	50	yes	no
HC25	HC	F	62	yes	no

Healthy controls used in TCRB and immunogene panel sequencing. Both CD4+ and CD8+ cells were sequenced. The median age for controls in TCRB sequencing was 58 (interquartile range 50-64), and the mean 56.2 (95% confidence interval 52.2-60.3) The median age for controls immunogene panel was 58 (interquartile range 50-64) and the mean 56.5 (95% confidence interval 51.6-61.3).

Supplementary Table S2. Genes sequenced in the immunogene panel.

Gene ID	Ensembl ID	Gene ID	Ensembl ID	Gene ID	Ensembl ID	Gene ID	Ensembl ID
A2M	ENSG00000175899	FOXO3	ENSG00000118689	OSM	ENSG00000099985	VPREB1	ENSG00000169575
A2ML1	ENSG00000166535	FOXP1	ENSG00000114861	OSMR	ENSG00000145623	VPREB3	ENSG00000128218
AAMP	ENSG00000127837	FOXP3	ENSG00000049768	OTUB1	ENSG00000167770	VPS13B	ENSG00000132549
ABCA1	ENSG00000165029	FPR1	ENSG00000171051	OTUB2	ENSG00000089723	VPS33B	ENSG00000184056
ABCA13	ENSG00000179869	FPR2	ENSG00000171049	OTUD5	ENSG00000068308	VPS45	ENSG00000136631
ABCB1	ENSG00000085563	FPR3	ENSG00000187474	OTUD7B	ENSG00000264522	VSIG1	ENSG00000101842
ABCB7	ENSG00000131269	FREM1	ENSG00000164946	OXNAD1	ENSG00000154814	VSTM2B	ENSG00000187135
ABCF1	ENSG00000204574	FRK	ENSG00000111816	P2RX7	ENSG00000089041	VTRNA2-1	ENSG00000270123
ABCG1	ENSG00000160179	FSCN1	ENSG00000075618	P2RY10	ENSG00000078589	VWF	ENSG00000110799
ABCG5	ENSG00000138075	FSTL1	ENSG00000163430	P2RY14	ENSG00000174944	WAS	ENSG00000015285
ABCG8	ENSG00000143921	FUT3	ENSG00000171124	P2RY8	ENSG00000182162	WASF1	ENSG00000112290
ABL1	ENSG00000097007	FXR1	ENSG00000114416	P4HTM	ENSG00000178467	WASF3	ENSG00000132970
ACAP1	ENSG00000072818	FYB	ENSG00000082074	PACSIN1	ENSG00000124507	WASL	ENSG00000106299
ACD	ENSG00000102977	FYN	ENSG00000010810	PADI4	ENSG00000159339	WDFY1	ENSG00000085449
ACE	ENSG00000159640	FZD1	ENSG00000157240	PAFAH1B1	ENSG00000007168	WDFY3-AS2	ENSG00000180769
ACE2	ENSG00000130234	FZD4	ENSG00000174804	PAFAH1B2	ENSG00000168092	WDFY4	ENSG00000128815
ACHE	ENSG00000087085	G3BP1	ENSG00000145907	PAFAH1B3	ENSG00000079462	WDR34	ENSG00000119333
ACOXL	ENSG00000153093	G6PC	ENSG00000131482	PAFAH2	ENSG00000158006	WDR62	ENSG00000075702
ACP5	ENSG00000102575	G6PC3	ENSG00000141349	PAK1	ENSG00000149269	WFDC12	ENSG00000168703
ACTB	ENSG00000075624	G6PD	ENSG00000160211	PAK2	ENSG00000180370	WHSC1	ENSG00000109685
ACTN1	ENSG00000072110	GAB1	ENSG00000109458	PAPD5	ENSG00000121274	WIPF1	ENSG00000115935
ACVRL1	ENSG00000139567	GAB2	ENSG00000033327	PARD3	ENSG00000148498	WNT2B	ENSG00000134245
ADA	ENSG00000196839	GABARAP	ENSG00000170296	PARK2	ENSG00000185345	WNT3A	ENSG00000154342
ADAM10	ENSG00000137845	GADD45A	ENSG00000116717	PARP1	ENSG00000143799	WNT9B	ENSG00000158955
ADAM17	ENSG00000151694	GADD45B	ENSG00000099860	PAX2	ENSG00000075891	WRAP53	ENSG00000141499
ADAM8	ENSG00000151651	GADD45G	ENSG00000130222	PAX5	ENSG00000196092	WT1	ENSG00000184937
ADAMTS14	ENSG00000138316	GALC	ENSG00000054983	PCBP1	ENSG00000169564	WWOX	ENSG00000186153
ADAR	ENSG00000160710	GALNS	ENSG00000141012	PCBP2	ENSG00000197111	XBP1	ENSG00000100219
ADCY1	ENSG00000164742	GAS2L3	ENSG00000139354	PDCD1	ENSG00000188389	XCL1	ENSG00000143184
ADCY2	ENSG00000078295	GAS6	ENSG00000183087	PDCD1	ENSG00000276977	XCL2	ENSG00000143185
ADCY3	ENSG00000138031	GATA1	ENSG00000102145	PDCD1LG2	ENSG00000197646	XCR1	ENSG00000173578
ADCY4	ENSG00000129467	GATA2	ENSG00000179348	PDE3B	ENSG00000152270	XDH	ENSG00000158125
ADCY5	ENSG00000173175	GATA3	ENSG00000107485	PDGFA	ENSG00000197461	XIAP	ENSG00000101966
ADCY6	ENSG00000174233	GATA4	ENSG00000136574	PDGFB	ENSG00000100311	XPO1	ENSG00000082898
ADCY7	ENSG00000121281	GATA6	ENSG00000141448	PDGFRA	ENSG00000134853	XRCC2	ENSG00000196584
ADCY8	ENSG00000155897	GBA	ENSG00000177628	PDGFRB	ENSG00000113721	XRCC5	ENSG00000079246
ADCY9	ENSG00000162104	GBA	ENSG00000262446	PDK1	ENSG00000152256	XRCC6	ENSG00000196419
ADIPOQ	ENSG00000181092	GBP1	ENSG00000117228	PDPK1	ENSG00000140992	YARS2	ENSG00000139131
ADRB2	ENSG00000169252	GBP2	ENSG00000162645	PDS5B	ENSG00000083642	YBX1	ENSG00000065978
ADRBK1	ENSG00000173020	GBP3	ENSG00000117226	PDSS2	ENSG00000164494	YJEFN3	ENSG00000250067
ADRBK2	ENSG00000100077	GBP4	ENSG00000162654	PEG3	ENSG00000198300	YWHAE	ENSG00000108953
AEBP1	ENSG00000106624	GBP5	ENSG00000154451	PELI1	ENSG00000197329	YWHAZ	ENSG00000164924
AEBP2	ENSG00000139154	GBP6	ENSG00000183347	PELI2	ENSG00000139946	YY1	ENSG00000100811
AFF3	ENSG00000144218	GBP7	ENSG00000213512	PELI3	ENSG00000174516	ZAP70	ENSG00000115085
AGBL2	ENSG00000165923	GFI1	ENSG00000162676	PF4	ENSG00000163737	ZBP1	ENSG00000124256
AGER	ENSG00000204305	GFI1B	ENSG00000165702	PF4V1	ENSG00000109272	ZBTB16	ENSG00000109906
AGFG1	ENSG00000173744	GH1	ENSG00000259384	PFKL	ENSG00000141959	ZBTB24	ENSG00000112365
AHI1	ENSG00000135541	GH2	ENSG00000136487	PFKM	ENSG00000152556	ZC2HC1A	ENSG00000104427
AHR	ENSG00000106546	GHR	ENSG00000112964	PGK1	ENSG00000102144	ZFP36L1	ENSG00000185650
AHSG	ENSG00000145192	GJA1	ENSG00000152661	PGLYRP1	ENSG00000008438	ZMIZ1	ENSG00000108175
AICDA	ENSG00000111732	GLI1	ENSG00000111087	PGLYRP2	ENSG00000161031	ORAI1	ENSG00000276045
AIM2	ENSG00000163568	GLIS2	ENSG00000126603	PGLYRP3	ENSG00000159527	VMP1	ENSG00000062716
AIMP1	ENSG00000164022	GLRX	ENSG00000173221	PGLYRP4	ENSG00000163218	FER	ENSG00000151422
AIRE	ENSG00000160224	GLRX5	ENSG00000182512	PGM3	ENSG00000013375	FERMT3	ENSG00000149781
AK1	ENSG00000106992	GNA12	ENSG00000146535	PHF6	ENSG00000156531	FFAR2	ENSG00000126262
AK2	ENSG00000004455	GNA13	ENSG00000120063	PHGDH	ENSG00000092621	FGA	ENSG00000171560
AKAP10	ENSG00000108599	GNAI1	ENSG00000127955	PIAS1	ENSG00000033800	FGB	ENSG00000171564
AKNA	ENSG00000106948	GNAI2	ENSG00000114353	PIAS2	ENSG00000078043	FGF1	ENSG00000113578
AKT1	ENSG00000142208	GNAI3	ENSG00000065135	PIAS3	ENSG00000131788	FGF10	ENSG00000070193
AKT1S1	ENSG00000204673	GNAS	ENSG00000087460	PIAS4	ENSG00000105229	FGF11	ENSG00000161958
AKT2	ENSG00000105221	GNB1	ENSG00000078369	PIEZO1	ENSG00000103335	FGF12	ENSG00000114279
AKT3	ENSG00000117020	GNB2	ENSG00000172354	PIGA	ENSG00000165195	FGF13	ENSG00000129682
ALAS2	ENSG00000158578	GNB2L1	ENSG00000204628	PIK3AP1	ENSG00000155629	FGF14	ENSG00000102466
ALCAM	ENSG00000170017	GNB3	ENSG00000111664	PIK3C3	ENSG00000078142	FGF16	ENSG00000196468
ALDOA	ENSG00000149925	GNB4	ENSG00000114450	PIK3CA	ENSG00000121879	FGF17	ENSG00000158815
ALK	ENSG00000171094	GNB5	ENSG00000069966	PIK3CB	ENSG00000051382	FGF18	ENSG00000156427
AMFR	ENSG00000159461	GNG10	ENSG00000242616	PIK3CD	ENSG00000171608	FGF19	ENSG00000162344
ANGPT1	ENSG00000154188	GNG11	ENSG00000127920	PIK3CG	ENSG00000105851	FGF2	ENSG00000138685
ANK1	ENSG00000029534	GNG12	ENSG00000172380	PIK3R1	ENSG00000145675	FGF20	ENSG00000078579
ANKRD17	ENSG00000132466	GNG13	ENSG00000127588	PIK3R2	ENSG00000105647	FGF21	ENSG00000105550
ANKRD26	ENSG00000107890	GNG2	ENSG00000186469	PIK3R3	ENSG00000117461	FGF22	ENSG00000070388
ANKRD30A	ENSG00000148513	GNG3	ENSG00000162188	PIK3R5	ENSG00000141506	FGF23	ENSG00000118972
ANKRD55	ENSG00000164512	GNG4	ENSG00000168243	PILRA	ENSG00000085514	FGF3	ENSG00000186895
ANO6	ENSG00000177119	GNG5	ENSG00000174021	PIM1	ENSG00000137193	FGF4	ENSG00000075388
ANP32B	ENSG00000136938	GNG7	ENSG00000176533	PIN1	ENSG00000127445	FGF5	ENSG00000138675
ANPEP	ENSG00000166825	GNG8	ENSG00000167414	PITPNM2	ENSG00000090975	FGF6	ENSG00000111241
ANXA1	ENSG00000135046	GNGT1	ENSG00000127928	PKLR	ENSG00000143627	FGF7	ENSG00000140285
ANXA2	ENSG00000182718	GNGT2	ENSG00000167083	PKN1	ENSG00000123143	FGF8	ENSG00000107831
ANXA3	ENSG00000138772	GNLY	ENSG00000115523	PLA2G4A	ENSG00000116711	FGF9	ENSG00000102678
ANXA4	ENSG00000196975	GNS	ENSG00000135677	PLA2G4B	ENSG00000243708	FGFBP1	ENSG00000137440
ANXA6	ENSG00000197043	GOPC	ENSG00000047932	PLA2G4C	ENSG00000105499	FGFR1	ENSG00000077782
AOC3	ENSG00000131471	GP1BA	ENSG00000185245	PLA2G4D	ENSG00000159337	FGFR2	ENSG00000066468
AP1S3	ENSG00000152056	GP1BB	ENSG00000203618	PLA2G4E	ENSG00000188089	FGFR3	ENSG00000068078
AP3B1	ENSG00000132842	GP2	ENSG00000169347	PLA2G4F	ENSG00000168907	FGFR4	ENSG00000160867
AP3D1	ENSG00000065000	GP5	ENSG00000178732	PLA2G7	ENSG00000146070	FGG	ENSG00000171557
AP4E1	ENSG00000081014	GP9	ENSG00000169704	PLA2R1	ENSG00000153246	FGR	ENSG00000000938
APCS	ENSG00000132703	GPI	ENSG00000105220	PLAA	ENSG00000137055	FIGF	ENSG00000165197
APOA1	ENSG00000118137	GPI	ENSG00000282019	PLAG1	ENSG00000181690	FLI1	ENSG00000151702
APOBEC3A	ENSG00000128383	GPR153	ENSG00000158292	PLAT	ENSG00000104368	FLNA	ENSG00000196924
APOBEC3B	ENSG00000179750	GPR183	ENSG00000169508	PLAU	ENSG00000122861	FLNB	ENSG00000136068

APOBEC3G	ENSG00000239713	GPR33	ENSG00000214943	PLAUR	ENSG00000011422	FLNC	ENSG00000128591
APOH	ENSG00000091583	GPR52	ENSG00000203737	PLCB1	ENSG00000182621	FLT3	ENSG00000122025
APOL1	ENSG00000100342	GPRASP1	ENSG00000198932	PLCB2	ENSG00000137841	FLT4	ENSG00000037280
AQP3	ENSG00000165272	GPRC5A	ENSG00000013588	PLCB3	ENSG00000149782	FOS	ENSG00000170345
ARAF	ENSG00000078061	GPSM1	ENSG00000160360	PLCB4	ENSG00000101333	FOXA2	ENSG00000125798
ARAP1	ENSG00000186635	GRB2	ENSG00000177885	PLCG1	ENSG00000124181	FOXK2	ENSG00000141568
ARF6	ENSG00000165527	GRHL2	ENSG00000083307	PLCG2	ENSG00000197943	FOXN1	ENSG00000109101
ARG1	ENSG00000118520	GRK1	ENSG00000185974	PLCL2	ENSG00000154822	FOXO1	ENSG00000150907
ARHGAP15	ENSG00000075884	GRK4	ENSG00000125388	PLEC	ENSG00000178209	NLRX1	ENSG00000160703
ARHGAP8/PRR5-ARHGAP8	ENSG00000248405	GRK5	ENSG00000198873	PLEK	ENSG00000115956	NMI	ENSG00000123609
ARID3A	ENSG00000116017	GRK6	ENSG00000198055	PLEKHG5	ENSG00000171680	NOD1	ENSG00000106100
ARID5B	ENSG00000150347	GRK7	ENSG00000114124	PLG	ENSG00000122194	NOD2	ENSG00000167207
ARL5B	ENSG00000165997	GRN	ENSG00000030582	PLK1	ENSG00000166851	NOL3	ENSG00000140939
ARRB1	ENSG00000137486	GSK3A	ENSG00000105723	PLK3	ENSG00000173846	NOP10	ENSG00000182117
ARRB2	ENSG00000141480	GSK3B	ENSG00000082701	PLSCR1	ENSG00000188313	NOP9	ENSG00000196943
ASCC3	ENSG00000112249	GSR	ENSG00000104687	PLTP	ENSG00000100979	NOS2	ENSG00000007171
ASXL1	ENSG00000171456	GSS	ENSG00000100983	PLXDC1	ENSG00000161381	NOTCH1	ENSG00000148400
ATF2	ENSG00000115966	GSTP1	ENSG00000084207	PLXNA4	ENSG00000221866	NOTCH2	ENSG00000134250
ATF3	ENSG00000162772	GUSB	ENSG00000169919	PLXNC1	ENSG00000136040	NOX1	ENSG00000007952
ATF4	ENSG00000128272	GYPA	ENSG00000170180	PMAIP1	ENSG00000141682	NOX4	ENSG00000086991
ATG12	ENSG00000145782	GYPB	ENSG00000250361	PML	ENSG00000140464	NOXA1	ENSG00000188747
ATG16L1	ENSG00000085978	GYPC	ENSG00000136732	PMS2	ENSG00000122512	NPC1	ENSG00000141458
ATG5	ENSG00000057663	GYPE	ENSG00000197465	PNP	ENSG00000198805	NPC2	ENSG00000119655
ATG7	ENSG00000197548	GZMA	ENSG00000145649	POLE	ENSG00000177084	NPEPPS	ENSG00000141279
ATG9A	ENSG00000198925	GZMB	ENSG00000100453	POLR1C	ENSG00000171453	NPM1	ENSG00000181163
ATM	ENSG00000149311	GZMK	ENSG00000113088	POLR1D	ENSG00000186184	NPTN	ENSG00000156642
ATP11A-AS1	ENSG00000232684	GZMM	ENSG00000197540	POLR2E	ENSG00000099817	NR1H3	ENSG00000025434
ATP6V0D2	ENSG00000147614	HAMP	ENSG00000105697	POLR2F	ENSG00000100142	NR1H4	ENSG00000012504
ATP7B	ENSG00000123191	HAVCR2	ENSG00000135077	POLR2H	ENSG00000163882	NR3C1	ENSG00000113580
ATRIP	ENSG00000164053	HAX1	ENSG00000143575	POLR2K	ENSG00000147669	NR4A1	ENSG00000123358
ATRX	ENSG00000085224	HBA1	ENSG00000206172	POLR2L	ENSG00000177700	NR4A3	ENSG00000119508
AVP	ENSG00000101200	HBA2	ENSG00000188536	POLR3A	ENSG00000148606	NR5A2	ENSG00000116833
AXL	ENSG00000167601	HBB	ENSG00000244734	POLR3B	ENSG00000013503	NRAS	ENSG00000213281
AZI2	ENSG00000163512	HCK	ENSG00000101336	POLR3C	ENSG00000186141	NRIP1	ENSG00000180530
B2M	ENSG00000166710	HCST	ENSG00000126264	POLR3D	ENSG00000168495	NT5C3A	ENSG00000122643
B2M	ENSG00000273686	HDAC1	ENSG00000116478	POLR3E	ENSG00000058600	NT5E	ENSG00000135318
B3GNT2	ENSG00000170340	HDAC11	ENSG00000163517	POLR3F	ENSG00000132664	NTF3	ENSG00000185652
BACH2	ENSG00000112182	HDAC2	ENSG00000196591	POLR3G	ENSG00000113356	NTF4	ENSG00000225950
BANK1	ENSG00000153064	HELLS	ENSG00000119969	POLR3GL	ENSG00000121851	NTN1	ENSG00000065320
BATF	ENSG00000156127	HERC5	ENSG00000138646	POLR3H	ENSG00000100413	NTRK1	ENSG00000198400
BAX	ENSG00000087088	HFE	ENSG00000010704	POLR3K	ENSG00000161980	NTRK2	ENSG00000148053
BCAM	ENSG00000187244	HFE2	ENSG00000168509	POMC	ENSG00000115138	NUDCD3	ENSG00000015676
BCAP31	ENSG00000185825	HGF	ENSG00000019991	POT1	ENSG00000128513	NUMB	ENSG00000133961
BCAR1	ENSG00000050820	HGSNAT	ENSG00000165102	POU2AF1	ENSG00000110777	NUMBL	ENSG00000105245
BCL10	ENSG00000142867	HHEX	ENSG00000152804	POU2F2	ENSG00000028277	NUP153	ENSG00000124789
BCL11B	ENSG00000127152	HIF1A	ENSG00000100644	PPARG	ENSG00000132170	NUP214	ENSG00000126883
BCL2	ENSG00000171791	HIF1AN	ENSG00000166135	PPARGC1A	ENSG00000109819	NXN	ENSG00000167693
BCL2A1	ENSG00000140379	HIF3A	ENSG00000124440	PPARGC1B	ENSG00000155846	OAS1	ENSG00000089127
BCL2L1	ENSG00000171552	HIST1H1B	ENSG00000184357	PPBP	ENSG00000163736	OAS2	ENSG00000111335
BCL2L11	ENSG00000153094	HIST1H1C	ENSG00000187837	PPIA	ENSG00000196262	OAS3	ENSG00000111331
BCL3	ENSG00000069399	HIST1H1D	ENSG00000124575	PPIL4	ENSG00000131013	OASL	ENSG00000135114
BCL6	ENSG00000113916	HIST1H1E	ENSG00000168298	PPM1A	ENSG00000100614	OLFM4	ENSG00000102837
BCOR	ENSG00000183337	HIST1H3B	ENSG00000274267	PPM1B	ENSG00000138032	OPTN	ENSG00000123240
BCORL1	ENSG00000085185	HK1	ENSG00000156515	PPM1D	ENSG00000170836	OR1D5	ENSG00000262628
BDKRB1	ENSG00000100739	HMGB1	ENSG00000189403	PPP1CA	ENSG00000172531	TYK2	ENSG00000105397
BDKRB2	ENSG00000168398	HMGB2	ENSG00000164104	PPP1CC	ENSG00000186298	TYRO3	ENSG00000092445
BDNF	ENSG00000176697	HMGB3	ENSG00000029993	PPP3CA	ENSG00000138814	TYROBP	ENSG00000011600
BECN1	ENSG00000126581	HMGN2	ENSG00000198830	PPP3CB	ENSG00000107758	TYW1	ENSG00000198874
BEND5	ENSG00000162373	HMMR	ENSG00000072571	PPP3CC	ENSG00000120910	U2AF1	ENSG00000160201
BEX2	ENSG00000133134	HMOX1	ENSG00000100292	PPP3R1	ENSG00000221823	U2AF2	ENSG00000063244
BEX4	ENSG00000102409	HNRNPL	ENSG00000104824	PPP3R2	ENSG00000188386	UBASH3A	ENSG00000160185
BEX5	ENSG00000184515	HOOK1	ENSG00000134709	PPP4C	ENSG00000149923	UBC	ENSG00000150991
BGN	ENSG00000182492	HOXA11	ENSG00000005073	PPP5C	ENSG00000011485	UBD	ENSG00000213886
BID	ENSG00000015475	HOXA9	ENSG00000078399	PPP5D1	ENSG00000230510	UBE2N	ENSG00000177889
BIRC2	ENSG00000110330	HOXC5	ENSG00000172789	PRDM1	ENSG00000057657	UBQLN1	ENSG00000135018
BIRC3	ENSG00000023445	HP	ENSG00000257017	PRDX5	ENSG00000126432	UBR5	ENSG00000104517
BIRC5	ENSG00000089685	HPS3	ENSG00000163755	PRDX6	ENSG00000117592	UCHL1	ENSG00000154277
BLK	ENSG00000136573	HRAS	ENSG00000174775	PREX1	ENSG00000124126	UCP2	ENSG00000175567
BLM	ENSG00000197299	HRG	ENSG00000113905	PRF1	ENSG00000180644	ULBP1	ENSG00000111981
BLNK	ENSG00000095585	HRH2	ENSG00000113749	PRG2	ENSG00000186652	ULBP2	ENSG00000131015
BLOC1S6	ENSG00000104164	HRH4	ENSG00000134489	PRKAA1	ENSG00000132356	ULBP3	ENSG00000131019
BMP2	ENSG00000125845	HSF1	ENSG00000185122	PRKAA2	ENSG00000162409	ULK1	ENSG00000177169
BMX	ENSG00000102010	HSP90AA1	ENSG00000080824	PRKACA	ENSG00000072062	ULK2	ENSG00000083290
BOP1	ENSG00000261236	HSP90AB1	ENSG00000096384	PRKACB	ENSG00000142875	ULK3	ENSG00000140474
BPI	ENSG00000101425	HSP90B1	ENSG00000166598	PRKACG	ENSG00000165059	UMODL1	ENSG00000177398
BRAF	ENSG00000157764	HSPA14	ENSG00000187522	PRKCA	ENSG00000154229	UNC119	ENSG00000109103
BRCC3	ENSG00000185515	HSPA1A	ENSG00000204389	PRKCB	ENSG00000166501	UNC13D	ENSG00000092929
BSG	ENSG00000172270	HSPA1B	ENSG00000204388	PRKCD	ENSG00000163932	UNC5CL	ENSG00000124602
BST1	ENSG00000109743	HSPA1L	ENSG00000204390	PRKCE	ENSG00000171132	UNC93B1	ENSG00000110057
BST2	ENSG00000130303	HSPA2	ENSG00000126803	PRKCG	ENSG00000126583	UNG	ENSG00000076248
BTBD11	ENSG00000151136	HSPA4	ENSG00000170606	PRKCH	ENSG00000027075	USB1	ENSG00000103005
BTG1	ENSG00000133639	HSPA6	ENSG00000173110	PRKCQ	ENSG00000065675	USP18	ENSG00000184979
BTG2	ENSG00000159388	HSPA8	ENSG00000109971	PRKCZ	ENSG00000067606	USP2	ENSG00000036672
BTK	ENSG00000010671	HSPB1	ENSG00000106211	PRKDC	ENSG00000253729	USP4	ENSG00000114316
BTLA	ENSG00000186265	HSPBP1	ENSG00000133265	PRKRA	ENSG00000180228	USP44	ENSG00000136014
BTN3A1	ENSG00000026950	HSPD1	ENSG00000144381	PRKX	ENSG00000183943	USP7	ENSG00000187555
BTN3A2	ENSG00000186470	HTN3	ENSG00000205649	PRL	ENSG00000172179	VASP	ENSG00000125753
BTN3A3	ENSG00000111801	HYAL1	ENSG00000114378	PRLR	ENSG00000113494	VAV1	ENSG00000141968
C10orf55	ENSG00000222047	HYOU1	ENSG00000149428	PRMT1	ENSG00000126457	VAV2	ENSG00000160293
C15orf41	ENSG00000186073	ICAM1	ENSG00000090339	PRNP	ENSG00000171867	VAV3	ENSG00000134215
C1orf106	ENSG00000163362	ICAM2	ENSG00000108622	PROC	ENSG00000115718	VCAM1	ENSG00000162692
C1QA	ENSG00000173372	ICAM3	ENSG00000076662	PROCR	ENSG00000101000	VCAN	ENSG00000038427
C1QB	ENSG00000173369	ICAM4	ENSG00000105371	PROM1	ENSG00000007062	VDR	ENSG00000111424

C1QBP	ENSG00000108561	ICOS	ENSG00000163600	PROS1	ENSG00000184500	VEGFA	ENSG00000112715
C1QC	ENSG00000159189	ICOSLG	ENSG00000160223	PRPF40B	ENSG00000110844	VEGFB	ENSG00000173511
C1QL1	ENSG00000131094	ID3	ENSG00000117318	PRPF8	ENSG00000174231	VEGFC	ENSG00000150630
C1QL2	ENSG00000144119	IDH1	ENSG00000138413	PRRC2A	ENSG00000204469	VENTX	ENSG00000151650
C1QL3	ENSG00000165985	IDH2	ENSG00000182054	PRSS16	ENSG00000112812	VHL	ENSG00000134086
C1QL4	ENSG00000186897	IDO1	ENSG00000131203	PRSS23	ENSG00000150687	VLDLR	ENSG00000147852
C1QTNF2	ENSG00000145861	IDS	ENSG00000010404	PRTN3	ENSG00000196415	F3	ENSG00000117525
C1QTNF3	ENSG00000082196	IDUA	ENSG00000127415	PRTN3	ENSG00000277804	F5	ENSG00000198734
C1QTNF4	ENSG00000172247	IFI16	ENSG00000163565	PSAP	ENSG00000197746	F7	ENSG00000057593
C1QTNF5	ENSG00000223953	IFI27	ENSG00000165949	PSG1	ENSG00000231924	F8	ENSG00000185010
C1QTNF6	ENSG00000133466	IFI30	ENSG00000216490	PSIP1	ENSG00000164985	F9	ENSG00000101981
C1QTNF7	ENSG00000163145	IFI35	ENSG00000068079	PSMA7	ENSG00000101182	FADD	ENSG00000168040
C1R	ENSG00000159403	IFI44	ENSG00000137965	PSMB10	ENSG00000205220	FADS1	ENSG00000149485
C1RL	ENSG00000139178	IFI44L	ENSG00000137959	PSMB5	ENSG00000100804	FADS2	ENSG00000134824
C1S	ENSG00000182326	IFI6	ENSG00000126709	PSMB6	ENSG00000142507	FADS3	ENSG00000221968
C2	ENSG00000166278	IFIH1	ENSG00000115267	PSMB7	ENSG00000136930	FAM172BP	ENSG00000175841
C3	ENSG00000125730	IFIT1	ENSG00000185745	PSMB8	ENSG00000204264	FAM46C	ENSG00000183508
C3AR1	ENSG00000171860	IFIT1B	ENSG00000204010	PSMB9	ENSG00000240065	FAM53B	ENSG00000258539
C4A	ENSG00000244731	IFIT2	ENSG00000119922	PSME1	ENSG00000092010	FAM84B	ENSG00000168672
C4B	ENSG00000224389	IFIT3	ENSG00000119917	PSME2	ENSG00000100911	FANCA	ENSG00000187741
C4BPA	ENSG00000123838	IFITM1	ENSG00000185885	PSME3	ENSG00000131467	FANCB	ENSG00000181544
C4BPB	ENSG00000123843	IFITM2	ENSG00000185201	PSMF1	ENSG00000125818	FANCC	ENSG00000158169
C5	ENSG00000106804	IFITM3	ENSG00000142089	PSMG1	ENSG00000183527	FANCD2	ENSG00000144554
C5AR1	ENSG00000197405	IFITM5	ENSG00000206013	PSTPIP1	ENSG00000140368	FANCE	ENSG00000112039
C5orf30	ENSG00000181751	IFNA1	ENSG00000197919	PTAFR	ENSG00000169403	FANCF	ENSG00000183161
C6	ENSG00000039537	IFNA10	ENSG00000186803	PTCH1	ENSG00000185920	FANCI	ENSG00000140525
C7	ENSG00000112936	IFNA13	ENSG00000233816	PTEN	ENSG00000171862	FANCL	ENSG00000115392
C8A	ENSG00000157131	IFNA14	ENSG00000228083	PTGER4	ENSG00000171522	FANCM	ENSG00000187790
C8B	ENSG00000021852	IFNA16	ENSG00000147885	PTGES	ENSG00000148344	FAS	ENSG00000026103
C8G	ENSG00000176919	IFNA17	ENSG00000234829	PTGES2	ENSG00000148334	FASLG	ENSG00000117560
C9	ENSG00000113600	IFNA2	ENSG00000188379	PTGFRN	ENSG00000134247	FBXO11	ENSG00000138081
C9orf47	ENSG00000186354	IFNA21	ENSG00000137080	PTGS2	ENSG00000073756	FBXW5	ENSG00000159069
CAB39	ENSG00000135932	IFNA4	ENSG00000236637	PTK2	ENSG00000169398	FBXW7	ENSG00000109670
CAB39L	ENSG00000102547	IFNA5	ENSG00000147873	PTK2B	ENSG00000120899	FCAMR	ENSG00000162897
CACNA1A	ENSG00000141837	IFNA6	ENSG00000120235	PTMA	ENSG00000187514	FCAR	ENSG00000186431
CACNA1B	ENSG00000148408	IFNA7	ENSG00000214042	PTPN11	ENSG00000179295	FCER1A	ENSG00000179639
CACNA1C	ENSG00000151067	IFNA8	ENSG00000120242	PTPN2	ENSG00000175354	FCER1G	ENSG00000158869
CACNA1D	ENSG00000157388	IFNAR1	ENSG00000142166	PTPN22	ENSG00000134242	FCER2	ENSG00000104921
CACNA1E	ENSG00000198216	IFNAR2	ENSG00000159110	PTPN5	ENSG00000110786	FCGR1A	ENSG00000150337
CACNA1F	ENSG00000102001	IFNB1	ENSG00000171855	PTPN6	ENSG00000111679	FCGR2A	ENSG00000143226
CACNA1G	ENSG00000006283	IFNE	ENSG00000184995	PTPN7	ENSG00000143851	FCGR2B	ENSG00000072694
CACNA1H	ENSG00000196557	IFNG	ENSG00000111537	PTPRC	ENSG00000081237	FCGR2C	ENSG00000244682
CACNA1I	ENSG00000100346	IFNGR1	ENSG00000027697	PTPRCAP	ENSG00000213402	FCGR3A	ENSG00000203747
CACNA1S	ENSG00000081248	IFNGR2	ENSG00000159128	PTPRE	ENSG00000132334	FCGR3B	ENSG00000162747
CACNA2D1	ENSG00000153956	IFNK	ENSG00000147896	PTPRJ	ENSG00000149177	FCGRT	ENSG00000104870
CACNA2D2	ENSG00000007402	IFNW1	ENSG00000177047	PTPRR	ENSG00000153233	FCN1	ENSG00000085265
CACNA2D3	ENSG00000157445	IGF1	ENSG00000017427	PTPRU	ENSG00000060656	FCN2	ENSG00000160339
CACNA2D4	ENSG00000151062	IGF1R	ENSG00000140443	PTX3	ENSG00000163661	FCN3	ENSG00000142748
CACNB1	ENSG00000067191	IGF2R	ENSG00000197081	PURA	ENSG00000185129	FCRL1	ENSG00000163534
CACNB2	ENSG00000165995	IGHA1	ENSG00000211895	PUS1	ENSG00000177192	FCRL3	ENSG00000160856
CACNB3	ENSG00000167535	IGHA2	ENSG00000211890	PVR	ENSG00000073008	FCRL5	ENSG00000143297
CACNB4	ENSG00000182389	IGHE	ENSG00000211891	PVRL1	ENSG00000110400	FCRLA	ENSG00000132185
CACNG1	ENSG00000108878	IGHG1	ENSG00000211896	PVRL2	ENSG00000130202	NDFIP1	ENSG00000131507
CACNG2	ENSG00000166862	IGHG2	ENSG00000211893	PVT1	ENSG00000249859	NDUFAF4P4	ENSG00000231378
CACNG3	ENSG00000006116	IGHG3	ENSG00000211897	PXK	ENSG00000168297	NDUFS3	ENSG00000213619
CACNG4	ENSG00000075461	IGHG4	ENSG00000211892	PXN	ENSG00000089159	NEU1	ENSG00000204386
CACNG5	ENSG00000075429	IGHM	ENSG00000211899	PXT1	ENSG00000179165	NF1	ENSG00000196712
CACNG6	ENSG00000130433	IGKC	ENSG00000211592	PYCARD	ENSG00000103490	NFAT5	ENSG00000102908
CACNG7	ENSG00000105605	IGLL1	ENSG00000128322	PYDC1	ENSG00000169900	NFATC1	ENSG00000131196
CACNG8	ENSG00000142408	IGSF8	ENSG00000162729	PYHIN1	ENSG00000163564	NFATC2	ENSG00000101096
CALCA	ENSG00000110680	IKBKAP	ENSG00000070061	RAB11A	ENSG00000103769	NFATC3	ENSG00000072736
CALCOCO2	ENSG00000136436	IKBKB	ENSG00000104365	RAB27A	ENSG00000069974	NFATC4	ENSG00000100968
CALM1	ENSG00000198668	IKBKE	ENSG00000263528	RAB8A	ENSG00000167461	NFE2L2	ENSG00000116044
CAMK1	ENSG00000134072	IKBKG	ENSG00000269335	RAC1	ENSG00000136238	NFIL3	ENSG00000165030
CAMK2A	ENSG00000070808	IKZF1	ENSG00000185811	RAC2	ENSG00000128340	NFKB1	ENSG00000109320
CAMK2B	ENSG00000058404	IKZF2	ENSG00000030419	RAC3	ENSG00000169750	NFKB2	ENSG00000077150
CAMK2D	ENSG00000145349	IKZF3	ENSG00000161405	RAD21	ENSG00000164754	NFKBIA	ENSG00000100906
CAMK2G	ENSG00000148660	IL10	ENSG00000136634	RAD23A	ENSG00000179262	NFKBIB	ENSG00000104825
CAMK4	ENSG00000152495	IL10RA	ENSG00000110324	RAD50	ENSG00000113522	NFKBIE	ENSG00000146232
CAMKK2	ENSG00000110931	IL10RB	ENSG00000243646	RAD51B	ENSG00000182185	NFKBIL1	ENSG00000204498
CAMLG	ENSG00000164615	IL11	ENSG00000095752	RAET1E	ENSG00000164520	NFKBIZ	ENSG00000144802
CAMP	ENSG00000164047	IL11RA	ENSG00000137070	RAET1G	ENSG00000203722	NFRKB	ENSG00000170322
CANX	ENSG00000127022	IL12A	ENSG00000168811	RAET1L	ENSG00000155918	NGF	ENSG00000134259
CAPN1	ENSG00000014216	IL12B	ENSG00000113302	RAF1	ENSG00000132155	NHEJ1	ENSG00000187736
CAPN2	ENSG00000162909	IL12RB1	ENSG00000096996	RAG1	ENSG00000166349	NHP2	ENSG00000145912
CAPRIN1	ENSG00000135387	IL12RB2	ENSG00000081985	RAG2	ENSG00000175097	NKIRAS1	ENSG00000197885
CARD11	ENSG00000198286	IL13	ENSG00000169194	RANBP9	ENSG00000010017	NKIRAS2	ENSG00000168256
CARD14	ENSG00000141527	IL13RA1	ENSG00000131724	RAP1A	ENSG00000116473	NKX2-3	ENSG00000119919
CARD16	ENSG00000204397	IL13RA2	ENSG00000123496	RAP1B	ENSG00000127314	NKX2-5	ENSG00000183072
CARD18	ENSG00000255501	IL15	ENSG00000164136	RAPGEF2	ENSG00000109756	NKX3-1	ENSG00000167034
CARD6	ENSG00000132357	IL15RA	ENSG00000134470	RARRES2	ENSG00000106538	NLK	ENSG00000087095
CARD8	ENSG00000105483	IL16	ENSG00000172349	RASA1	ENSG00000145715	NLRC3	ENSG00000167984
CARD9	ENSG00000187796	IL17A	ENSG00000112115	RASA2	ENSG00000155903	NLRC4	ENSG00000091106
CASKIN1	ENSG00000167971	IL17B	ENSG00000127743	RASGEF1B	ENSG00000138670	NLRC5	ENSG00000140853
CASP1	ENSG00000137752	IL17C	ENSG00000124391	RASGRF1	ENSG00000058335	NLRP1	ENSG00000091592
CASP10	ENSG00000003400	IL17D	ENSG00000172458	RASGRF2	ENSG00000113319	NLRP10	ENSG00000182261
CASP12	ENSG00000204403	IL17F	ENSG00000112116	RASGRP1	ENSG00000172575	NLRP11	ENSG00000179873
CASP2	ENSG00000106144	IL17RA	ENSG00000177663	RASGRP2	ENSG00000068831	NLRP12	ENSG00000142405
CASP3	ENSG00000164305	IL17RB	ENSG00000056736	RASGRP3	ENSG00000152689	NLRP13	ENSG00000173572
CASP4	ENSG00000196954	IL17RC	ENSG00000163702	RASGRP4	ENSG00000171777	NLRP14	ENSG00000158077
CASP5	ENSG00000137757	IL17RD	ENSG00000144730	RB1	ENSG00000139687	NLRP2	ENSG00000022556
CASP6	ENSG00000138794	IL17RE	ENSG00000163701	RBBP4	ENSG00000162521	NLRP3	ENSG00000162711
CASP7	ENSG00000165806	IL18	ENSG00000150782	RBBP7	ENSG00000102054	NLRP4	ENSG00000160505

CASP8	ENSG00000064012	IL18BP	ENSG00000137496	RBCK1	ENSG00000125826	NLRP5	ENSG00000171487
CASP9	ENSG00000132906	IL18R1	ENSG00000115604	RBM11	ENSG00000185272	NLRP6	ENSG00000174885
CAV1	ENSG00000105974	IL18RAP	ENSG00000115607	RBM8A	ENSG00000265241	NLRP7	ENSG00000167634
CBL	ENSG00000110395	IL19	ENSG00000142224	RBPJ	ENSG00000168214	NLRP8	ENSG00000179709
CBLB	ENSG00000114423	IL1A	ENSG00000115008	RCAN1	ENSG00000159200	NLRP9	ENSG00000185792
CBLC	ENSG00000142273	IL1B	ENSG00000125538	RCAN3	ENSG00000117602	TRIM24	ENSG00000122779
CCBE1	ENSG00000183287	IL1F10	ENSG00000136697	RCOR1	ENSG00000089902	TRIM25	ENSG00000121060
CCDC88A	ENSG00000115355	IL1R1	ENSG00000115594	RECQL4	ENSG00000160957	TRIM26	ENSG00000234127
CCL1	ENSG00000108702	IL1R2	ENSG00000115590	REG3G	ENSG00000143954	TRIM27	ENSG00000204713
CCL11	ENSG00000172156	IL1RAP	ENSG00000196083	REG4	ENSG00000134193	TRIM28	ENSG00000130726
CCL13	ENSG00000181374	IL1RAPL1	ENSG00000169306	REL	ENSG00000162924	TRIM32	ENSG00000119401
CCL14	ENSG00000276409	IL1RAPL2	ENSG00000189108	RELA	ENSG00000173039	TRIM36	ENSG00000152503
CCL15	ENSG00000275718	IL1RL1	ENSG00000115602	RELB	ENSG00000104856	TRIM37	ENSG00000108395
CCL15-CCL14	ENSG00000275688	IL1RL2	ENSG00000115598	REST	ENSG00000084093	TRIM38	ENSG00000112343
CCL16	ENSG00000275152	IL1RN	ENSG00000136689	RETNLB	ENSG00000163515	TRIM42	ENSG00000155890
CCL17	ENSG00000102970	IL2	ENSG00000109471	RFTN1	ENSG00000131378	TRIM45	ENSG00000134253
CCL18	ENSG00000275385	IL20	ENSG00000162891	RFX1	ENSG00000132005	TRIM47	ENSG00000132481
CCL19	ENSG00000172724	IL20RA	ENSG00000016402	RFX5	ENSG00000143390	TRIM49	ENSG00000168930
CCL2	ENSG00000108691	IL20RB	ENSG00000174564	RFXANK	ENSG00000064490	TRIM5	ENSG00000132256
CCL20	ENSG00000115009	IL21	ENSG00000138684	RFXAP	ENSG00000133111	TRIM50	ENSG00000146755
CCL21	ENSG00000137077	IL21R	ENSG00000103522	RGMB	ENSG00000174136	TRIM55	ENSG00000147573
CCL22	ENSG00000102962	IL21R-AS1	ENSG00000259954	RGS1	ENSG00000090104	TRIM56	ENSG00000169871
CCL23	ENSG00000274736	IL22	ENSG00000127318	RGS14	ENSG00000169220	TRIM58	ENSG00000162722
CCL24	ENSG00000106178	IL22RA1	ENSG00000142677	RGS2	ENSG00000116741	TRIM6	ENSG00000121236
CCL25	ENSG00000131142	IL22RA2	ENSG00000164485	RHAG	ENSG00000112077	TRIM60	ENSG00000176979
CCL26	ENSG00000006606	IL23A	ENSG00000110944	RHBDF2	ENSG00000129667	TRIM61	ENSG00000183439
CCL27	ENSG00000213927	IL23R	ENSG00000162594	RHCE	ENSG00000188672	TRIM62	ENSG00000116525
CCL28	ENSG00000151882	IL24	ENSG00000162892	RHD	ENSG00000187010	TRIM63	ENSG00000158022
CCL3	ENSG00000277632	IL25	ENSG00000166090	RHEB	ENSG00000106615	TRIM65	ENSG00000141569
CCL3L1	ENSG00000277796	IL26	ENSG00000111536	RHOA	ENSG00000067560	TRIM66	ENSG00000166436
CCL3L3	ENSG00000276085	IL27	ENSG00000197272	RHOG	ENSG00000177105	TRIM67	ENSG00000119283
CCL4	ENSG00000275302	IL27RA	ENSG00000104998	RHOH	ENSG00000168421	TRIM7	ENSG00000146054
CCL4L2	ENSG00000276070	IL2RA	ENSG00000134460	RICTOR	ENSG00000164327	TRIM71	ENSG00000206557
CCL5	ENSG00000271503	IL2RB	ENSG00000100385	RIPK1	ENSG00000137275	TRIM8	ENSG00000171206
CCL7	ENSG00000108688	IL2RG	ENSG00000147168	RIPK2	ENSG00000104312	TRIM9	ENSG00000100505
CCL8	ENSG00000108700	IL3	ENSG00000164399	RIPK3	ENSG00000129465	TRIP6	ENSG00000087077
CCNA2	ENSG00000145386	IL31	ENSG00000204671	RIT1	ENSG00000143622	TRNT1	ENSG00000072756
CCND1	ENSG00000110092	IL31RA	ENSG00000164509	RLTPR	ENSG00000159753	TRPM2	ENSG00000142185
CCND2	ENSG00000118971	IL32	ENSG00000008517	RMI2	ENSG00000175643	TRPV2	ENSG00000187688
CCND3	ENSG00000112576	IL33	ENSG00000137033	RMRP	ENSG00000277027	TSC1	ENSG00000165699
CCNE1	ENSG00000105173	IL36A	ENSG00000136694	RNASE7	ENSG00000165799	TSC2	ENSG00000103197
CCNT1	ENSG00000129315	IL36G	ENSG00000136688	RNASEH2A	ENSG00000104889	TSC22D3	ENSG00000157514
CCR1	ENSG00000163823	IL36RN	ENSG00000136695	RNASEH2B	ENSG00000136104	TSFM	ENSG00000123297
CCR10	ENSG00000184451	IL37	ENSG00000125571	RNASEH2C	ENSG00000172922	TSLP	ENSG00000145777
CCR2	ENSG00000121807	IL3RA	ENSG00000185291	RNASEL	ENSG00000135828	TSPYL2	ENSG00000184205
CCR3	ENSG00000183625	IL4	ENSG00000113520	RNF125	ENSG00000101695	TSR2	ENSG00000158526
CCR4	ENSG00000183813	IL4I1	ENSG00000104951	RNF135	ENSG00000181481	TTC37	ENSG00000198677
CCR5	ENSG00000160791	IL4R	ENSG00000077238	RNF168	ENSG00000163961	TTC7A	ENSG00000068724
CCR6	ENSG00000112486	IL5	ENSG00000113525	RNF31	ENSG00000092098	TUBB1	ENSG00000101162
CCR7	ENSG00000126353	IL5RA	ENSG00000091181	RNF41	ENSG00000181852	TUFM	ENSG00000178952
CCR8	ENSG00000179934	IL6	ENSG00000136244	RNF5	ENSG00000204308	TXNDC11	ENSG00000153066
CCR9	ENSG00000173585	IL6R	ENSG00000160712	ROCK1	ENSG00000067900	TXNIP	ENSG00000265972
CCRL2	ENSG00000121797	IL6ST	ENSG00000134352	ROCK2	ENSG00000134318	ELAVL1	ENSG00000066044
CCRN4L	ENSG00000151014	IL7	ENSG00000104432	ROR1	ENSG00000185483	ELF1	ENSG00000120690
CD101	ENSG00000134256	IL7R	ENSG00000168685	RORA	ENSG00000069667	ELF2	ENSG00000109381
CD109	ENSG00000156535	IL9	ENSG00000145839	RORC	ENSG00000143365	ELF4	ENSG00000102034
CD14	ENSG00000170458	IL9R	ENSG00000124334	RPA1	ENSG00000132383	ELK1	ENSG00000126767
CD151	ENSG00000177697	ILF2	ENSG00000143621	RPL10	ENSG00000147403	ELK4	ENSG00000158711
CD160	ENSG00000117281	ILF3	ENSG00000129351	RPL11	ENSG00000142676	ELMO1	ENSG00000155849
CD163	ENSG00000177575	IMPDH2	ENSG00000178035	RPL15	ENSG00000174748	ELMOD2	ENSG00000179387
CD164	ENSG00000135535	ING4	ENSG00000111653	RPL19	ENSG00000108298	ELP2	ENSG00000134759
CD164L2	ENSG00000174950	INHBA	ENSG00000122641	RPL35A	ENSG00000182899	ENC1	ENSG00000171617
CD180	ENSG00000134061	INO80	ENSG00000128908	RPL5	ENSG00000122406	ENG	ENSG00000106991
CD19	ENSG00000177455	INPP5D	ENSG00000168918	RPS10	ENSG00000124614	ENTPD1	ENSG00000138185
CD1A	ENSG00000158477	INS	ENSG00000254647	RPS15	ENSG00000115268	EOMES	ENSG00000163508
CD1B	ENSG00000158485	INSIG1	ENSG00000186480	RPS15AP6	ENSG00000233072	EP300	ENSG00000100393
CD1C	ENSG00000158481	INSR	ENSG00000171105	RPS16	ENSG00000105193	EPAS1	ENSG00000116016
CD1D	ENSG00000158473	INTS12	ENSG00000138785	RPS17	ENSG00000182774	EPB42	ENSG00000166947
CD1E	ENSG00000158488	IP6K1	ENSG00000176095	RPS19	ENSG00000105372	EPO	ENSG00000130427
CD2	ENSG00000116824	IQCB1	ENSG00000173226	RPS2	ENSG00000140988	EPOR	ENSG00000187266
CD200	ENSG00000091972	IQGAP1	ENSG00000140575	RPS24	ENSG00000138326	EPS15L1	ENSG00000127527
CD200R1	ENSG00000163606	IRAK1	ENSG00000184216	RPS26	ENSG00000197728	EPS8	ENSG00000151491
CD200R1L	ENSG00000206531	IRAK1BP1	ENSG00000146243	RPS28	ENSG00000233927	EPX	ENSG00000121053
CD207	ENSG00000116031	IRAK2	ENSG00000134070	RPS29	ENSG00000213741	ERAP1	ENSG00000164307
CD209	ENSG00000090659	IRAK3	ENSG00000090376	RPS6	ENSG00000137154	ERBB2IP	ENSG00000112851
CD22	ENSG00000012124	IRAK4	ENSG00000198001	RPS6KA1	ENSG00000117676	ERCC6L2	ENSG00000182150
CD226	ENSG00000150637	IRF1	ENSG00000125347	RPS6KA2	ENSG00000071242	ERGIC2	ENSG00000087502
CD244	ENSG00000122223	IRF2	ENSG00000168310	RPS6KA3	ENSG00000177189	ERLIN1	ENSG00000107566
CD247	ENSG00000198821	IRF2BP1	ENSG00000170604	RPS6KA4	ENSG00000162302	ERN1	ENSG00000178607
CD248	ENSG00000174807	IRF3	ENSG00000126456	RPS6KA5	ENSG00000100784	ETNK1	ENSG00000139163
CD27	ENSG00000139193	IRF4	ENSG00000137265	RPS6KA6	ENSG00000072133	ETS1	ENSG00000134954
CD274	ENSG00000120217	IRF5	ENSG00000128604	RPS6KB1	ENSG00000108443	ETS2	ENSG00000157557
CD276	ENSG00000103855	IRF6	ENSG00000117595	RPS6KB2	ENSG00000175634	ETV6	ENSG00000139083
CD28	ENSG00000178562	IRF7	ENSG00000185507	RPS7	ENSG00000171863	ETV7	ENSG00000010030
CD2AP	ENSG00000198087	IRF8	ENSG00000140968	RPSA	ENSG00000168028	EVI5	ENSG00000067208
CD2BP2	ENSG00000169217	IRF9	ENSG00000213928	RPTOR	ENSG00000141564	EZH1	ENSG00000108799
CD300A	ENSG00000167851	IRGM	ENSG00000237693	RRAGA	ENSG00000155876	EZH2	ENSG00000106462
CD300C	ENSG00000167850	IRS1	ENSG00000169047	RRAGB	ENSG00000083750	EZR	ENSG00000092820
CD300E	ENSG00000186407	ISG15	ENSG00000187608	RRAGC	ENSG00000116954	F10	ENSG00000126218
CD300LB	ENSG00000178789	ISG20	ENSG00000172183	RRAGD	ENSG00000025039	F11	ENSG00000088926
CD300LF	ENSG00000186074	ISL2	ENSG00000159556	RRAS	ENSG00000126458	F12	ENSG00000131187
CD300LG	ENSG00000161649	ITCH	ENSG00000078747	RRAS2	ENSG00000133818	F13A1	ENSG00000124491
CD302	ENSG00000241399	ITFG1	ENSG00000129636	RSAD2	ENSG00000134321	F13B	ENSG00000143278

CD320	ENSG00000167775	ITGA1	ENSG00000213949	RTEL1	ENSG00000258366	F2	ENSG00000180210
CD33	ENSG00000105383	ITGA2	ENSG00000164171	RTKN2	ENSG00000182010	F2R	ENSG00000181104
CD34	ENSG00000174059	ITGA2B	ENSG00000005961	RUNX1	ENSG00000159216	F2RL1	ENSG00000164251
CD36	ENSG00000135218	ITGA3	ENSG00000005884	RUNX3	ENSG00000020633	F2RL2	ENSG00000164220
CD37	ENSG00000104894	ITGA4	ENSG00000115232	RUSC1	ENSG00000160753	F2RL3	ENSG00000127533
CD38	ENSG00000004468	ITGA5	ENSG00000161638	RXRA	ENSG00000186350	MRAS	ENSG00000158186
CD3D	ENSG00000167286	ITGA6	ENSG00000091409	S100A10	ENSG00000197747	MRC1	ENSG00000260314
CD3E	ENSG00000198851	ITGAD	ENSG00000156886	S100A12	ENSG00000163221	MRC2	ENSG00000011028
CD3EAP	ENSG00000117877	ITGAE	ENSG00000083457	S100A8	ENSG00000143546	MRE11A	ENSG00000020922
CD3G	ENSG00000160654	ITGAL	ENSG00000005844	S100A9	ENSG00000163220	MRGPRX2	ENSG00000183695
CD4	ENSG00000010610	ITGAM	ENSG00000169896	S1PR1	ENSG00000170989	MS4A1	ENSG00000156738
CD40	ENSG00000101017	ITGAV	ENSG00000138448	SAA1	ENSG00000173432	MS4A3	ENSG00000149516
CD40LG	ENSG00000102245	ITGAX	ENSG00000140678	SAA2	ENSG00000134339	MS4A5	ENSG00000166930
CD44	ENSG00000026508	ITGB1	ENSG00000150093	SAMD12	ENSG00000177570	MSH6	ENSG00000116062
CD46	ENSG00000117335	ITGB2	ENSG00000160255	SAMHD1	ENSG00000101347	MSR1	ENSG00000038945
CD47	ENSG00000196776	ITGB3	ENSG00000259207	SAMSN1	ENSG00000155307	MST1	ENSG00000173531
CD48	ENSG00000117091	ITGB4	ENSG00000132470	SARM1	ENSG00000004139	MST1R	ENSG00000164078
CD5	ENSG00000110448	ITK	ENSG00000113263	SATB2	ENSG00000119042	MTA1	ENSG00000182979
CD52	ENSG00000169442	ITPR1	ENSG00000150995	SBDS	ENSG00000126524	MTHFD1	ENSG00000100714
CD53	ENSG00000143119	ITPR3	ENSG00000096433	SBF2	ENSG00000133812	MTOR	ENSG00000198793
CD55	ENSG00000196352	JAGN1	ENSG00000171135	SBK1	ENSG00000188322	MUC1	ENSG00000185499
CD58	ENSG00000116815	JAK1	ENSG00000162434	SCAF11	ENSG00000139218	MUL1	ENSG00000090432
CD59	ENSG00000085063	JAK2	ENSG00000096968	SCAMP5	ENSG00000198794	MVK	ENSG00000110921
CD5L	ENSG00000073754	JAK3	ENSG00000105639	SCARB1	ENSG00000073060	MX1	ENSG00000157601
CD6	ENSG00000013725	JAM3	ENSG00000166086	SCARB2	ENSG00000138760	MX2	ENSG00000183486
CD63	ENSG00000135404	JARID2	ENSG00000008083	SCARF1	ENSG00000074660	MXRA5	ENSG00000101825
CD68	ENSG00000129226	JAZF1	ENSG00000153814	SCGB3A1	ENSG00000161055	MYC	ENSG00000136997
CD69	ENSG00000110848	JMJD7-PLA2G4B	ENSG00000168970	SCML1	ENSG00000047634	MYD88	ENSG00000172936
CD7	ENSG00000173762	JUN	ENSG00000177606	SCN5A	ENSG00000183873	MYH9	ENSG00000100345
CD70	ENSG00000125726	JUND	ENSG00000130522	SDC1	ENSG00000115884	MYLK	ENSG00000065534
CD72	ENSG00000137101	KAT2B	ENSG00000114166	SDC3	ENSG00000162512	MYO18A	ENSG00000196535
CD74	ENSG00000019582	KAZALD1	ENSG00000107821	SDC4	ENSG00000124145	MYO5A	ENSG00000197535
CD79A	ENSG00000105369	KCNJ8	ENSG00000121361	SDF2	ENSG00000132581	MYSM1	ENSG00000162601
CD79B	ENSG00000007312	KCNMA1	ENSG00000156113	SDF2L1	ENSG00000128228	NAGLU	ENSG00000108784
CD80	ENSG00000121594	KDM4A	ENSG00000066135	SDK2	ENSG00000069188	NAIP	ENSG00000249437
CD81	ENSG00000110651	KDM6A	ENSG00000147050	SDR42E1	ENSG00000184860	NAMPT	ENSG00000105835
CD82	ENSG00000085117	KDR	ENSG00000128052	SEC23B	ENSG00000101310	NBAS	ENSG00000151779
CD83	ENSG00000112149	KEAP1	ENSG00000079999	SELE	ENSG00000007908	NBEA	ENSG00000172915
CD84	ENSG00000066294	KEL	ENSG00000197993	SELL	ENSG00000188404	NBEAL2	ENSG00000160796
CD86	ENSG00000114013	KHSRP	ENSG00000088247	SELP	ENSG00000174175	NBN	ENSG00000104320
CD8A	ENSG00000153563	KIAA0226	ENSG00000145016	SELPLG	ENSG00000110876	NCAM1	ENSG00000149294
CD8B	ENSG00000172116	KIF21B	ENSG00000116852	SEMA3A	ENSG00000075213	NCF1	ENSG00000158517
CD9	ENSG00000010278	KIF23	ENSG00000137807	SEMA4D	ENSG00000187764	NCF2	ENSG00000116701
CD93	ENSG00000125810	KIR2DL1	ENSG00000125498	SEMA7A	ENSG00000138623	NCF4	ENSG00000100365
CD96	ENSG00000153283	KIR2DL3	ENSG00000243772	SENP2	ENSG00000163904	NCK1	ENSG00000158092
CD99	ENSG00000002586	KIR2DL4	ENSG00000189013	SERPINA1	ENSG00000197249	NCK2	ENSG00000071051
CD99L2	ENSG00000102181	KIR2DP1	ENSG00000242473	SERPINA5	ENSG00000188488	NCKAP1L	ENSG00000123338
CDAN1	ENSG00000140326	KIR2DS4	ENSG00000221957	SERPINB2	ENSG00000197632	NCOR2	ENSG00000196498
CDC25B	ENSG00000101224	KIR3DL1	ENSG00000167633	SERPINB9	ENSG00000170542	NCR1	ENSG00000189430
CDC42	ENSG00000070831	KIR3DL2	ENSG00000240403	SERPINC1	ENSG00000117601	NCR2	ENSG00000096264
CDCA7	ENSG00000144354	KIR3DX1	ENSG00000104970	SERPIND1	ENSG00000099937	NCR3	ENSG00000204475
CDH23	ENSG00000107736	KIT	ENSG00000157404	SERPINE1	ENSG00000106366	TNIP3	ENSG00000050730
CDH3	ENSG00000062038	KITLG	ENSG00000049130	SERPINF2	ENSG00000167711	TNK1	ENSG00000174292
CDH5	ENSG00000179776	KLF1	ENSG00000105610	SERPING1	ENSG00000149131	TOLLIP	ENSG00000078902
CDK2	ENSG00000123374	KLF4	ENSG00000136826	SETBP1	ENSG00000152217	TOM1	ENSG00000100284
CDK4	ENSG00000135446	KLHL6	ENSG00000172578	SF3A1	ENSG00000099995	TOMM70A	ENSG00000154174
CDK6	ENSG00000105810	KLK1	ENSG00000167748	SF3B1	ENSG00000115524	TONSL	ENSG00000160949
CDK9	ENSG00000136807	KLKB1	ENSG00000164344	SFRP4	ENSG00000106483	TP53	ENSG00000141510
CDKN1A	ENSG00000124762	KLRB1	ENSG00000111796	SFRP5	ENSG00000120057	TP63	ENSG00000073282
CDKN2A	ENSG00000147889	KLRC1	ENSG00000134545	SFTPA1	ENSG00000122852	TP73	ENSG00000078900
CDKN2B	ENSG00000147883	KLRC2	ENSG00000205809	SFTPA2	ENSG00000185303	TPD52	ENSG00000076554
CEACAM1	ENSG00000079385	KLRC3	ENSG00000205810	SFTPD	ENSG00000133661	TPH1	ENSG00000129167
CEACAM3	ENSG00000170956	KLRD1	ENSG00000134539	SGK1	ENSG00000118515	TPI1	ENSG00000111669
CEACAM5	ENSG00000105388	KLRK1	ENSG00000213809	SGSH	ENSG00000181523	TPO	ENSG00000115705
CEACAM6	ENSG00000086548	KMT2D	ENSG00000167548	SH2B3	ENSG00000111252	TPP2	ENSG00000134900
CEACAM8	ENSG00000124469	KNG1	ENSG00000113889	SH2D1A	ENSG00000183918	TPSB2	ENSG00000197253
CEBPA	ENSG00000245848	KPNA1	ENSG00000114030	SH2D1B	ENSG00000198574	TPST1	ENSG00000169902
CEBPB	ENSG00000172216	KRAS	ENSG00000133703	SH3BP2	ENSG00000087266	TRABD2A	ENSG00000186854
CEBPD	ENSG00000221869	KREMEN2	ENSG00000131650	SHANK1	ENSG00000161681	TRAC	ENSG00000277734
CEBPE	ENSG00000092067	KRT16	ENSG00000186832	SHARPIN	ENSG00000179526	TRADD	ENSG00000102871
CECR1	ENSG00000093072	KY	ENSG00000174611	SHC1	ENSG00000160691	TRAF1	ENSG00000056558
CENPO	ENSG00000138092	L1CAM	ENSG00000198910	SHC2	ENSG00000129946	TRAF2	ENSG00000127191
CEP57	ENSG00000166037	LACC1	ENSG00000179630	SHC3	ENSG00000148082	TRAF3	ENSG00000131323
CFB	ENSG00000243649	LAG3	ENSG00000089692	SHC4	ENSG00000185634	TRAF3IP1	ENSG00000204104
CFD	ENSG00000197766	LAIR1	ENSG00000167613	SIAH1	ENSG00000196470	TRAF3IP2	ENSG00000056972
CFH	ENSG00000000971	LAIR2	ENSG00000167618	SIAH2	ENSG00000181788	TRAF4	ENSG00000076604
CFHR1	ENSG00000244414	LAMB4	ENSG00000091128	SIGIRR	ENSG00000185187	TRAF5	ENSG00000082512
CFHR2	ENSG00000080910	LAMP1	ENSG00000185896	SIGLEC1	ENSG00000088827	TRAF6	ENSG00000175104
CFHR2	ENSG00000276911	LAMP2	ENSG00000005893	SIGLEC10	ENSG00000142512	TRAF7	ENSG00000131653
CFHR3	ENSG00000116785	LAMP3	ENSG00000078081	SIGLEC11	ENSG00000161640	TRAFD1	ENSG00000135148
CFHR4	ENSG00000134365	LAMTOR2	ENSG00000116586	SIGLEC15	ENSG00000197046	TRAIP	ENSG00000183763
CFHR5	ENSG00000134389	LAMTOR3	ENSG00000109270	SIGLEC5	ENSG00000105501	TRAT1	ENSG00000163519
CFI	ENSG00000205403	LAP3	ENSG00000002549	SIGLEC6	ENSG00000105492	TRAV30	ENSG00000259092
CFLAR	ENSG00000003402	LAT	ENSG00000213658	SIGLEC7	ENSG00000168995	TRDJ1	ENSG00000211825
CFP	ENSG00000126759	LAX1	ENSG00000122188	SIGLEC8	ENSG00000105366	TREH	ENSG00000118094
CFTR	ENSG00000001626	LBH	ENSG00000213626	SIGLEC9	ENSG00000129450	TREM1	ENSG00000124731
CHAT	ENSG00000070748	LBP	ENSG00000129988	SIKE1	ENSG00000052723	TREM2	ENSG00000095970
CHD2	ENSG00000173575	LCAT	ENSG00000213398	SIRPA	ENSG00000198053	TREML2	ENSG00000112195
CHD7	ENSG00000171316	LCK	ENSG00000182866	SIRT1	ENSG00000096717	TREX1	ENSG00000213689
CHEK1	ENSG00000149554	LCN2	ENSG00000148346	SIVA1	ENSG00000184990	TRIB2	ENSG00000071575
CHGA	ENSG00000100604	LCP1	ENSG00000136167	SKIV2L	ENSG00000204351	TRIB3	ENSG00000101255
CHL1	ENSG00000134121	LCP2	ENSG00000043462	SLA	ENSG00000155926	TRIM13	ENSG00000204977
CHUK	ENSG00000213341	LEAP2	ENSG00000164406	SLAMF1	ENSG00000117090	TRIM14	ENSG00000106785

CIITA	ENSG00000179583	LEF1	ENSG00000138795	SLAMF6	ENSG00000162739	TRIM15	ENSG00000204610
CISH	ENSG00000114737	LEP	ENSG00000174697	SLAMF7	ENSG00000026751	TRIM21	ENSG00000132109
CKLF	ENSG00000217555	LEPR	ENSG00000116678	SLAMF8	ENSG00000158714	TRIM22	ENSG00000132274
CLCF1	ENSG00000175505	LGALS1	ENSG00000100097	SLAMF9	ENSG00000162723	TRIM23	ENSG00000113595
CLEC10A	ENSG00000132514	LGALS2	ENSG00000100079	SLC11A1	ENSG00000018280	DNMT3B	ENSG00000088305
CLEC12A	ENSG00000172322	LGALS3	ENSG00000131981	SLC15A4	ENSG00000139370	DOCK2	ENSG00000134516
CLEC16A	ENSG00000038532	LGALS3BP	ENSG00000108679	SLC19A2	ENSG00000117479	DOCK4	ENSG00000128512
CLEC1B	ENSG00000165682	LGALS4	ENSG00000171747	SLC1A4	ENSG00000115902	DOCK8	ENSG00000107099
CLEC4A	ENSG00000111729	LGALS8	ENSG00000116977	SLC22A3	ENSG00000146477	DOK3	ENSG00000146094
CLEC4C	ENSG00000198178	LGALS9	ENSG00000168961	SLC25A38	ENSG00000144659	DPP4	ENSG00000197635
CLEC4D	ENSG00000166527	LGMN	ENSG00000100600	SLC29A3	ENSG00000198246	DPY19L2	ENSG00000177990
CLEC4E	ENSG00000166523	LGR4	ENSG00000205213	SLC2A4RG	ENSG00000125520	DRD2	ENSG00000149295
CLEC4M	ENSG00000104938	LIF	ENSG00000128342	SLC35C1	ENSG00000181830	DTNBP1	ENSG00000047579
CLEC5A	ENSG00000258227	LIFR	ENSG00000113594	SLC37A4	ENSG00000137700	DUOX1	ENSG00000137857
CLEC6A	ENSG00000205846	LIG1	ENSG00000105486	SLC3A2	ENSG00000168003	DUOX2	ENSG00000140279
CLEC7A	ENSG00000172243	LIG4	ENSG00000174405	SLC40A1	ENSG00000138449	DUSP1	ENSG00000120129
CLEC9A	ENSG00000197992	LILRA1	ENSG00000104974	SLC44A1	ENSG00000070214	DUSP10	ENSG00000143507
CLECL1	ENSG00000184293	LILRA2	ENSG00000239998	SLC44A2	ENSG00000129353	DUSP16	ENSG00000111266
CLIP1	ENSG00000130779	LILRA3	ENSG00000273884	SLC46A1	ENSG00000076351	DUSP2	ENSG00000158050
CLIP2	ENSG00000106665	LILRA4	ENSG00000239961	SLC4A1	ENSG00000004939	DUSP3	ENSG00000108861
CLNK	ENSG00000109684	LILRA5	ENSG00000187116	SLC6A12	ENSG00000111181	DUSP4	ENSG00000120875
CLPB	ENSG00000162129	LILRA6	ENSG00000244482	SLC7A11	ENSG00000151012	DUSP5	ENSG00000138166
CLTC	ENSG00000141367	LILRB1	ENSG00000104972	SLC7A5	ENSG00000103257	DUSP6	ENSG00000139318
CLU	ENSG00000120885	LILRB2	ENSG00000131042	SLC9A8	ENSG00000197818	DUSP7	ENSG00000164086
CMA1	ENSG00000092009	LILRB3	ENSG00000204577	SLX4	ENSG00000188827	DUSP8	ENSG00000184545
CMKLR1	ENSG00000174600	LILRB4	ENSG00000186818	SMAD3	ENSG00000166949	DUSP9	ENSG00000130829
CMTM1	ENSG00000089505	LILRB5	ENSG00000105609	SMAD4	ENSG00000141646	E2F1	ENSG00000101412
CMTM2	ENSG00000140932	LIPA	ENSG00000107798	SMAD6	ENSG00000137834	EBF1	ENSG00000164330
CMTM3	ENSG00000140931	LITAF	ENSG00000189067	SMAD7	ENSG00000101665	EBF2	ENSG00000221818
CMTM4	ENSG00000183723	LPCAT2	ENSG00000087253	SMARCA2	ENSG00000080503	EBI3	ENSG00000105246
CMTM5	ENSG00000166091	LPIN2	ENSG00000101577	SMARCA4	ENSG00000127616	ECSIT	ENSG00000130159
CMTM6	ENSG00000091317	LPO	ENSG00000167419	SMARCAL1	ENSG00000138375	EDIL3	ENSG00000164176
CMTM7	ENSG00000153551	LRBA	ENSG00000198589	SMARCE1	ENSG00000073584	EDN1	ENSG00000078401
CMTM8	ENSG00000170293	LRG1	ENSG00000171236	SMC1A	ENSG00000072501	EED	ENSG00000074266
CNKSR2	ENSG00000149970	LRP1	ENSG00000123384	SMC3	ENSG00000108055	EGF	ENSG00000138798
CNN3	ENSG00000117519	LRRC8A	ENSG00000136802	SMPD1	ENSG00000166311	EGFR	ENSG00000146648
CNOT3	ENSG00000088038	LRRFIP1	ENSG00000124831	SNAP23	ENSG00000092531	EGLN1	ENSG00000135766
CNOT4	ENSG00000080802	LRRFIP2	ENSG00000093167	SNCA	ENSG00000145335	EGLN2	ENSG00000269858
CNOT8	ENSG00000155508	LRRK2	ENSG00000188906	SNX27	ENSG00000143376	EGLN3	ENSG00000129521
CNPY3	ENSG00000137161	LSP1	ENSG00000130592	SOAT2	ENSG00000167780	EGR1	ENSG00000120738
CNRIP1	ENSG00000119865	LST1	ENSG00000204482	SOCS1	ENSG00000185338	EHMT2	ENSG00000204371
CNTF	ENSG00000242689	LTA	ENSG00000226979	SOCS2	ENSG00000120833	EIF2AK2	ENSG00000055332
CNTFR	ENSG00000122756	LTA4H	ENSG00000111144	SOCS3	ENSG00000184557	EIF4B	ENSG00000063046
CNTLN	ENSG00000044459	LTB	ENSG00000227507	SOCS4	ENSG00000180008	EIF4E	ENSG00000151247
COCH	ENSG00000100473	LTB4R	ENSG00000213903	SOCS5	ENSG00000171150	EIF4E1B	ENSG00000175766
COG6	ENSG00000133103	LTB4R2	ENSG00000213906	SOCS6	ENSG00000170677	EIF4E2	ENSG00000135930
COL6A1	ENSG00000142156	LTBR	ENSG00000111321	SOCS7	ENSG00000274211	EIF4EBP1	ENSG00000187840
COLEC11	ENSG00000118004	LTF	ENSG00000012223	SOD1	ENSG00000142168	EIF4EBP2	ENSG00000148730
COLEC12	ENSG00000158270	LUC7L2	ENSG00000269955	SOD3	ENSG00000109610	ELANE	ENSG00000197561
COPA	ENSG00000122218	LUM	ENSG00000139329	SOS1	ENSG00000115904	ELANE	ENSG00000277571
COPS5	ENSG00000121022	LY6E	ENSG00000160932	SOS2	ENSG00000100485	MIR499A	ENSG00000207635
COPS8	ENSG00000198612	LY6E	ENSG00000278032	SP110	ENSG00000135899	MIR517A	ENSG00000207734
CORO1A	ENSG00000102879	LY75	ENSG00000054219	SP140	ENSG00000079263	MIR517C	ENSG00000207838
CORO2A	ENSG00000106789	LY86	ENSG00000112799	SPAG11A	ENSG00000178287	MIR548AN	ENSG00000263515
COX4I2	ENSG00000131055	LY9	ENSG00000122224	SPAG7	ENSG00000091640	MIR548G	ENSG00000221369
COX5B	ENSG00000135940	LY96	ENSG00000154589	SPHK1	ENSG00000176170	MIRLET7B	ENSG00000207875
CPB2	ENSG00000080618	LYG2	ENSG00000185674	SPI1	ENSG00000066336	MIRLET7C	ENSG00000199030
CR1	ENSG00000203710	LYN	ENSG00000254087	SPINK2	ENSG00000128040	MKL1	ENSG00000196588
CR1L	ENSG00000197721	LYNX1	ENSG00000180155	SPINK5	ENSG00000133710	MKNK1	ENSG00000079277
CR2	ENSG00000117322	LYST	ENSG00000143669	SPN	ENSG00000197471	MKNK2	ENSG00000099875
CRADD	ENSG00000169372	LYZ	ENSG00000090382	SPON2	ENSG00000159674	MLPH	ENSG00000115648
CREB1	ENSG00000118260	MAD1L1	ENSG00000002822	SPP1	ENSG00000118785	MLST8	ENSG00000167965
CREBBP	ENSG00000005339	MAF	ENSG00000178573	SPRED1	ENSG00000166068	MME	ENSG00000196549
CRIP2	ENSG00000182809	MAFB	ENSG00000204103	SPRED2	ENSG00000198369	MMEL1	ENSG00000142606
CRK	ENSG00000167193	MAGT1	ENSG00000102158	SPRED3	ENSG00000188766	MMP1	ENSG00000196611
CRKL	ENSG00000099942	MAL	ENSG00000172005	SPRY1	ENSG00000164056	MMP10	ENSG00000166670
CRLF1	ENSG00000006016	MALT1	ENSG00000172175	SPRY2	ENSG00000136158	MMP11	ENSG00000099953
CRLF2	ENSG00000205755	MANBA	ENSG00000109323	SPRY4	ENSG00000187678	MMP11	ENSG00000275365
CRLF3	ENSG00000176390	MAP1LC3C	ENSG00000197769	SPTA1	ENSG00000163554	MMP12	ENSG00000262406
CRP	ENSG00000132693	MAP2K1	ENSG00000169032	SPTB	ENSG00000070182	MMP13	ENSG00000137745
CRYAB	ENSG00000109846	MAP2K2	ENSG00000126934	SQSTM1	ENSG00000161011	MMP14	ENSG00000157227
CSF1	ENSG00000184371	MAP2K3	ENSG00000034152	SRC	ENSG00000197122	MMP15	ENSG00000102996
CSF1R	ENSG00000182578	MAP2K4	ENSG00000065559	SREBF1	ENSG00000072310	MMP16	ENSG00000156103
CSF2	ENSG00000164400	MAP2K5	ENSG00000137764	SREBF2	ENSG00000198911	MMP17	ENSG00000198598
CSF2RA	ENSG00000198223	MAP2K6	ENSG00000108984	SRF	ENSG00000112658	MMP19	ENSG00000123342
CSF2RB	ENSG00000100368	MAP2K7	ENSG00000076984	SRP72	ENSG00000174780	MMP2	ENSG00000087245
CSF3	ENSG00000108342	MAP3K1	ENSG00000095015	SRSF2	ENSG00000161547	MMP20	ENSG00000137674
CSF3R	ENSG00000119535	MAP3K11	ENSG00000173327	SRXN1	ENSG00000271303	MMP21	ENSG00000154485
CSH1	ENSG00000136488	MAP3K12	ENSG00000139625	ST6GAL1	ENSG00000073849	MMP23A	ENSG00000215914
CSH2	ENSG00000213218	MAP3K13	ENSG00000073803	ST6GALNAC1	ENSG00000070526	MMP23B	ENSG00000189409
CSK	ENSG00000103653	MAP3K14	ENSG00000006062	STAB1	ENSG00000010327	MMP24	ENSG00000125966
CSMD1	ENSG00000183117	MAP3K2	ENSG00000169967	STAG1	ENSG00000118007	MMP25	ENSG00000008516
CSN2	ENSG00000135222	MAP3K3	ENSG00000198909	STAG2	ENSG00000101972	MMP26	ENSG00000167346
CST7	ENSG00000077984	MAP3K4	ENSG00000085511	STAM	ENSG00000136738	MMP27	ENSG00000137675
CTC1	ENSG00000178971	MAP3K5	ENSG00000197442	STAM2	ENSG00000115145	MMP28	ENSG00000271447
CTCF	ENSG00000102974	MAP3K6	ENSG00000142733	STAP2	ENSG00000178078	MMP3	ENSG00000149968
CTF1	ENSG00000150281	MAP3K7	ENSG00000135341	STAT1	ENSG00000115415	MMP7	ENSG00000137673
CTLA4	ENSG00000163599	MAP3K8	ENSG00000107968	STAT2	ENSG00000170581	MMP8	ENSG00000118113
CTNNAL1	ENSG00000119326	MAP4K1	ENSG00000104814	STAT3	ENSG00000168610	MMP9	ENSG00000100985
CTNNB1	ENSG00000168036	MAP4K2	ENSG00000168067	STAT4	ENSG00000138378	MOGS	ENSG00000115275
CTNND1	ENSG00000198561	MAP4K3	ENSG00000011566	STAT5A	ENSG00000126561	MOS	ENSG00000172680
CTPS1	ENSG00000171793	MAP4K4	ENSG00000071054	STAT5B	ENSG00000173757	MOV10	ENSG00000155363
CTSB	ENSG00000164733	MAP9	ENSG00000164114	STAT6	ENSG00000166888	MPL	ENSG00000117400

CTSC	ENSG00000109861	MAPK1	ENSG00000100030	STIM1	ENSG00000167323	MPO	ENSG00000005381
CTSD	ENSG00000117984	MAPK10	ENSG00000109339	STK11	ENSG00000118046	MPZL3	ENSG00000160588
CTSF	ENSG00000174080	MAPK11	ENSG00000185386	STK3	ENSG00000104375	MR1	ENSG00000153029
CTSG	ENSG00000100448	MAPK12	ENSG00000188130	STK4	ENSG00000101109	TLR3	ENSG00000164342
CTSH	ENSG00000103811	MAPK13	ENSG00000156711	STMN1	ENSG00000117632	TLR4	ENSG00000136869
CTSK	ENSG00000143387	MAPK14	ENSG00000112062	STRADA	ENSG00000266173	TLR5	ENSG00000187554
CTSL	ENSG00000135047	MAPK3	ENSG00000102882	STUB1	ENSG00000103266	TLR6	ENSG00000174130
CTSO	ENSG00000256043	MAPK6	ENSG00000069956	STX11	ENSG00000135604	TLR7	ENSG00000196664
CTSS	ENSG00000163131	MAPK7	ENSG00000166484	STXBP2	ENSG00000076944	TLR8	ENSG00000101916
CTSV	ENSG00000136943	MAPK8	ENSG00000107643	SUCNR1	ENSG00000198829	TLR9	ENSG00000239732
CTSW	ENSG00000172543	MAPK8IP1	ENSG00000121653	SUGT1	ENSG00000165416	TMC6	ENSG00000141524
CTSZ	ENSG00000101160	MAPK8IP2	ENSG00000008735	SUOX	ENSG00000139531	TMC8	ENSG00000167895
CUL7	ENSG00000044090	MAPK8IP3	ENSG00000138834	SUZ12	ENSG00000178691	TMED7	ENSG00000134970
CUX1	ENSG00000257923	MAPK9	ENSG00000050748	SWAP70	ENSG00000133789	TMEM126A	ENSG00000171202
CX3CL1	ENSG00000006210	MAPKAPK2	ENSG00000162889	SYDE2	ENSG00000097096	TMEM173	ENSG00000184584
CX3CR1	ENSG00000168329	MAPKAPK3	ENSG00000114738	SYK	ENSG00000165025	TMEM220	ENSG00000187824
CXCL1	ENSG00000163739	MAPKAPK5	ENSG00000089022	SYNGR1	ENSG00000100321	TMEM30A	ENSG00000112697
CXCL10	ENSG00000169245	MAPT	ENSG00000186868	SYP	ENSG00000102003	TMIGD2	ENSG00000167664
CXCL11	ENSG00000169248	MARCH5	ENSG00000198060	TAB1	ENSG00000100324	TNF	ENSG00000232810
CXCL12	ENSG00000107562	MARCO	ENSG00000019169	TAB2	ENSG00000055208	TNFAIP3	ENSG00000118503
CXCL13	ENSG00000156234	MASP1	ENSG00000127241	TAB3	ENSG00000157625	TNFAIP8L2	ENSG00000163154
CXCL14	ENSG00000145824	MASP2	ENSG00000009724	TACR1	ENSG00000115353	TNFRSF10A	ENSG00000104689
CXCL16	ENSG00000161921	MAVS	ENSG00000088888	TAGAP	ENSG00000164691	TNFRSF10B	ENSG00000120889
CXCL2	ENSG00000081041	MAX	ENSG00000125952	TAL1	ENSG00000162367	TNFRSF10C	ENSG00000173535
CXCL3	ENSG00000163734	MB21D1	ENSG00000164430	TANK	ENSG00000136560	TNFRSF10D	ENSG00000173530
CXCL5	ENSG00000163735	MBL2	ENSG00000165471	TAOK1	ENSG00000160551	TNFRSF11A	ENSG00000141655
CXCL6	ENSG00000124875	MBP	ENSG00000197971	TAOK2	ENSG00000149930	TNFRSF12A	ENSG00000006327
CXCL9	ENSG00000138755	MBTPS1	ENSG00000140943	TAOK3	ENSG00000135090	TNFRSF13B	ENSG00000240505
CXCR1	ENSG00000163464	MBTPS2	ENSG00000012174	TAP1	ENSG00000168394	TNFRSF13C	ENSG00000159958
CXCR2	ENSG00000180871	MCAM	ENSG00000076706	TAP2	ENSG00000204267	TNFRSF14	ENSG00000157873
CXCR3	ENSG00000186810	MCL1	ENSG00000143384	TAPBP	ENSG00000231925	TNFRSF17	ENSG00000048462
CXCR4	ENSG00000121966	MCM10	ENSG00000065328	TAX1BP1	ENSG00000106052	TNFRSF18	ENSG00000186891
CXCR5	ENSG00000160683	MCM4	ENSG00000104738	TAZ	ENSG00000102125	TNFRSF1A	ENSG00000067182
CXCR6	ENSG00000172215	MDC1	ENSG00000137337	TBK1	ENSG00000183735	TNFRSF1B	ENSG00000028137
CYBA	ENSG00000051523	MDM2	ENSG00000135679	TBKBP1	ENSG00000198933	TNFRSF25	ENSG00000215788
CYBB	ENSG00000165168	MECOM	ENSG00000085276	TBL1XR1	ENSG00000177565	TNFRSF4	ENSG00000186827
CYCS	ENSG00000172115	MED1	ENSG00000125686	TBX1	ENSG00000184058	TNFRSF8	ENSG00000120949
CYLD	ENSG00000083799	MED12	ENSG00000184634	TBX21	ENSG00000073861	TNFRSF9	ENSG00000049249
CYP24A1	ENSG00000019186	MEF2B	ENSG00000213999	TCEB1	ENSG00000154582	TNFSF10	ENSG00000121858
CYSLTR1	ENSG00000173198	MEF2C	ENSG00000081189	TCEB2	ENSG00000103363	TNFSF11	ENSG00000120659
CYTIP	ENSG00000115165	MEFV	ENSG00000103313	TCF3	ENSG00000071564	TNFSF12	ENSG00000239697
CYTL1	ENSG00000170891	MERTK	ENSG00000153208	TCF4	ENSG00000196628	TNFSF13	ENSG00000161955
DAB2IP	ENSG00000136848	MFF	ENSG00000168958	TCF7	ENSG00000081059	TNFSF13B	ENSG00000102524
DAG1	ENSG00000173402	MFGE8	ENSG00000140545	TCIRG1	ENSG00000110719	TNFSF14	ENSG00000125735
DAGLB	ENSG00000164535	MFI2	ENSG00000163975	TCL1A	ENSG00000100721	TNFSF15	ENSG00000181634
DAPK1-IT1	ENSG00000236709	MFN1	ENSG00000171109	TCL1B	ENSG00000213231	TNFSF4	ENSG00000117586
DAXX	ENSG00000204209	MFN2	ENSG00000116688	TCN2	ENSG00000185339	TNFSF8	ENSG00000106952
DCD	ENSG00000161634	MICA	ENSG00000204520	TDP2	ENSG00000111802	TNFSF9	ENSG00000125657
DCHS1	ENSG00000166341	MICB	ENSG00000204516	TEC	ENSG00000135605	TNIP1	ENSG00000145901
DCLRE1C	ENSG00000152457	MID1	ENSG00000101871	TECPR1	ENSG00000205356		
DCN	ENSG00000011465	MID2	ENSG00000080561	TEK	ENSG00000120156		
DDAH1	ENSG00000153904	MIF	ENSG00000240972	TENM3	ENSG00000218336		
DDI1	ENSG00000170967	MINOS1-NBL1/NBL1	ENSG00000158747	TERC	ENSG00000270141		
DDIT3	ENSG00000175197	MIR107	ENSG00000198997	TERF1	ENSG00000147601		
DDIT4	ENSG00000168209	MIR10A	ENSG00000274592	TERF2	ENSG00000132604		
DDR1	ENSG00000204580	MIR10B	ENSG00000207744	TERT	ENSG00000164362		
DDX1	ENSG00000079785	MIR1204	ENSG00000275264	TET1	ENSG00000138336		
DDX21	ENSG00000165732	MIR1208	ENSG00000221261	TET2	ENSG00000168769		
DDX3X	ENSG00000215301	MIR122	ENSG00000207778	TEX41	ENSG00000226674		
DDX41	ENSG00000183258	MIR124-1	ENSG00000275677	TFAP2A	ENSG00000137203		
DDX58	ENSG00000107201	MIR125B1	ENSG00000207971	TFPI	ENSG00000003436		
DEFA1	ENSG00000206047	MIR125B2	ENSG00000207863	TFR2	ENSG00000106327		
DEFA3	ENSG00000239839	MIR126	ENSG00000199161	TFRC	ENSG00000072274		
DEFA4	ENSG00000164821	MIR1275	ENSG00000221697	TGFB1	ENSG00000105329		
DEFA5	ENSG00000164816	MIR132	ENSG00000267200	TGFB2	ENSG00000092969		
DEFA6	ENSG00000164822	MIR133A1	ENSG00000276792	TGFB3	ENSG00000119699		
DEFB1	ENSG00000164825	MIR135B	ENSG00000199059	TGFBI	ENSG00000120708		
DEFB103A	ENSG00000176797	MIR141	ENSG00000207708	TGFBR1	ENSG00000106799		
DEFB103B	ENSG00000177243	MIR145	ENSG00000276365	TGFBR2	ENSG00000163513		
DEFB105A	ENSG00000186562	MIR146A	ENSG00000277727	TGFBR3	ENSG00000069702		
DEFB106A	ENSG00000186579	MIR149	ENSG00000207611	TGM2	ENSG00000198959		
DEFB119	ENSG00000180483	MIR15B	ENSG00000207779	THBD	ENSG00000178726		
DEFB123	ENSG00000180424	MIR16-1	ENSG00000208006	THBS1	ENSG00000137801		
DEFB4A	ENSG00000171711	MIR16-2	ENSG00000198987	THPO	ENSG00000090534		
DHCR24	ENSG00000116133	MIR181A2	ENSG00000207595	THRB	ENSG00000151090		
DHX36	ENSG00000174953	MIR187	ENSG00000207797	THY1	ENSG00000154096		
DHX58	ENSG00000108771	MIR200C	ENSG00000207713	TIAM1	ENSG00000156299		
DHX9	ENSG00000135829	MIR208B	ENSG00000215991	TICAM1	ENSG00000127666		
DICER1	ENSG00000100697	MIR21	ENSG00000199004	TICAM2	ENSG00000243414		
DIDO1	ENSG00000101191	MIR212	ENSG00000267195	TIMMDC1	ENSG00000113845		
DIS3	ENSG00000083520	MIR223	ENSG00000207939	TIMP1	ENSG00000102265		
DKC1	ENSG00000130826	MIR23A	ENSG00000207980	TINF2	ENSG00000092330		
DKKL1	ENSG00000104901	MIR23B	ENSG00000207563	TIRAP	ENSG00000150455		
DLG1	ENSG00000075711	MIR302B	ENSG00000274389	TKTL2	ENSG00000151005		
DLK1	ENSG00000185559	MIR3148	ENSG00000264788	TLN1	ENSG00000137076		
DMBT1	ENSG00000187908	MIR372	ENSG00000199095	TLR1	ENSG00000174125		
DNM1L	ENSG00000087470	MIR373	ENSG00000199143	TLR10	ENSG00000174123		
DNMT3A	ENSG00000119772	MIR497	ENSG00000273895	TLR2	ENSG00000137462		

Coding exons of listed genes were included in the custom sequencing panel. The table shows the genes and Ensembl Gene IDs for each sequenced gene.

Supplementary Table S3. GO terms for gene annotations.

Lymphocyte functions		Cell proliferation		Inflammation	
GO:0031295	GO:2001185	GO:0008283	GO:0042104	GO:0006925	
GO:0030217	GO:2000456	GO:0043616	GO:0042130	GO:0006954	
GO:0045058	GO:2000457	GO:0097325	GO:0003249	GO:1900225	
GO:0045066	GO:2000452	GO:1990705	GO:2000090	GO:1900227	
GO:0045065	GO:2000451	GO:0003263	GO:1905938	GO:1900226	
GO:0045062	GO:2000450	GO:0035988	GO:1905937	GO:1900016	
GO:0045061	GO:2000449	GO:0033687	GO:0060502	GO:1900015	
GO:0043029	GO:2000329	GO:0007405	GO:0060916	GO:1900017	
GO:0043316	GO:2000330	GO:0046651	GO:0035739	GO:0035492	
GO:0043379	GO:2000570	GO:0002941	GO:0035736	GO:0035491	
GO:0043368	GO:2000555	GO:0002158	GO:0035740	GO:0035490	
GO:0043383	GO:2000554	GO:0070661	GO:0060722	GO:0044546	
GO:0070489	GO:2000553	GO:0072574	GO:0033091	GO:0071646	
GO:0070231	GO:2000552	GO:0061517	GO:0033083	GO:0071647	
GO:0042093	GO:2000556	GO:0061516	GO:0033080	GO:0071648	
GO:0042098	GO:2000551	GO:0035172	GO:0033087	GO:0071642	
GO:0042110	GO:2000566	GO:0048144	GO:1902462	GO:0071640	
GO:0035709	GO:2000565	GO:0051450	GO:1902460	GO:0071641	
GO:0035704	GO:2000564	GO:0070341	GO:1902461	GO:0071607	
GO:0035683	GO:2000563	GO:0070343	GO:0032945	GO:0071608	
GO:0035685	GO:2000562	GO:0070342	GO:0032946	GO:0002861	
GO:0035684	GO:2000561	GO:0042100	GO:0032817	GO:0002862	
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GO:0120117	GO:0050862	GO:1990922	GO:0071338	GO:0002878	
GO:0002360	GO:0050860	GO:0021534	GO:0071336	GO:0002879	
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GO:0033292	GO:0032832	GO:0072137	GO:0072126	GO:0002526	
GO:0035398	GO:0002841	GO:0072135	GO:0072124	GO:0002527	
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GO:0002709	GO:0070240	GO:0046013	GO:0035741	GO:0001807	
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GO:0002711	GO:0070235	GO:0030889	GO:0060723	GO:0001805	
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GO:0002725	GO:0035399	GO:0070347	GO:0060664	GO:0001803	
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GO:0043375			GO:0090094	
GO:0070237			GO:0014843	
			GO:0072513	
			GO:0061913	
			GO:0061914	
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			GO:2000081	

Gene Ontology (GO) Consortium terms for biological processes were used to annotate the genes with mutations in patients and controls.

Supplementary Table S4. Immune cell subsets in the study patients.

ID	Disease	EUROClass	TCRg	IgG	IgM	IgA	CD3 (% of lymphocytes)	CD4/CD8 -ratio	NK cells (% of lymphocytes)
1	CVID	B+smB^{neg}CD21^{low}Tr^{norm}	neg	0.6	<0.10	<0.10	90	0.7	4
2	CVID	B+smB^{neg}CD21^{low}Tr^{norm}	ND	1.2	1.70	<0.10	86	1.4	10
3	CVID	B-	pos	1.1	0.14	<0.10	90	0.4	9
4	CVID	B+smB+CD21^{norm}	ND	5.50	1.07	0.36	66	2.5	26
5	CVID	B+smB+CD21^{low}	neg	0.60	0.10	0.10	88	1.5	7
6	CVID	B+smB+CD21^{norm}	ND	3.90	0.20	1.24	88	2.3	8
7	CVID	B+smB^{neg}CD21^{low}Tr^{norm}	ND	1.10	0.27	0.10	85	0.8	6
8	CVID	B-	ND	2.80	0.38	0.00	90	0.6	10
9	*STAT3* GOF	B+mB^{neg}CD21^{low}Tr^{norm}	ND	5.6	3.38	1.67	71	1.2	12
10	*STAT3* GOF	B+mB^{neg}CD21^{low}Tr^{norm}	pos	2.8	1.44	0.21	86	1.4	3-0.5
11	*STAT3* GOF	B+smB^{neg}CD21^{low}Tr^{norm}	ND	0.16	0.6	1.7	74	2.3	4-13
12	Jacobsen sdr	B+smB+CD21^{norm}	pos	3.6	0.81	0.51	87	0.5	9
13	Other	B+smB+CD21^{norm}	neg	2.8	0.92	1.32	70	5,1	23
14	Other	B+smB+CD21^{norm}	neg	8.1	1.01	0.38	72	3,8	12
15	Other	ND	ND	15.1	0.22	0.79	76	4.6	16
16	Good sdr	B-	pos	1.9	<0.10	<0.10	84	0.1	16
17	ADA2 def	B-	pos	0.8	0.24	0.16	99	0.4	<1%

Characteristics of different adaptive immune cells of the patients included in the study are shown. B cell phenotypes were characterized according to the EUROClass classification system.[5]
Abbreviations: ND, not determined; TCRg, T-cell receptor gamma chain rearrangement; pos, positive; neg, negative; sdr, syndrome; GOF, gain-of-function.

Supplementary Table S5. All somatic mutations identified in paired-sample analyses in CD4+ and CD8+ cells.

Pt. ID	Disease	Cells	HGVS	AA change	COSMIC	Gene	VAF	SIFT	Polyphen 2
1	CVID	CD8+	1:g.1804503C>G	NM_001282539:exon6:c.G346C:p.G116R		*GNB1*	0.07	D	D
1	CVID	CD8+	3:g.38580953G>A	NM_198056:exon17:c.C3206T:p.T1069M	COSM1422791,COSM1422790,COSM1422792	*SCN5A*	0.055	D	D
1	CVID	CD8+	10:g.13136832C>T	NM_001008212:exon15:c.C1700T:p.T567M		*OPTN*	0.037	D	D
1	CVID	CD8+	19:g.16404674G>A	NM_001258374:exon14:c.C1342T:p.R448C		*EPS15L1*	0.037	D	D
1	CVID	CD8+	5:g.38881704G>A	NM_001323505:exon4:c.G358A:p.D120N	COSM737822	*OSMR*	0.035	T	D
2	CVID	CD4+	4:g.105235713delC	NM_001127208:exon3:c.1771delC:p.Q591fs		*TET2*	0.056	NA	NA
2	CVID	CD4+	4:g.105243618G>T	NM_001127208:exon6:c.G3643T:p.E1215X	COSM3719016	*TET2*	0.053	NA	NA
2	CVID	CD4+	16:g.50699619G>T	NM_022162:exon2:c.G205T:p.E69X		*NOD2*	0.06	NA	NA
2	CVID	CD4+	4:g.105269703C>T	NM_001127208:exon9:c.C4138T:p.H1380Y	COSM87161	*TET2*	0.027	D	D
2	CVID	CD4+	16:g.66398469T>C	NM_001795:exon10:c.T1499C:p.I500T		*CDH5*	0.027	D	D
2	CVID	CD4+	17:g.42217380A>T	NM_012448:exon10:c.T1254A:p.N418K		*STAT5B*	0.036	D	D
2	CVID	CD4+	21:g.44426694C>T	NM_001320350:exon27:c.C3980T:p.T1327M	COSM242069	*TRPM2*	0.036	T	D
2	CVID	CD8+	11:g.89804202C>A	NM_020358:exon3:c.G268T:p.E90X		*TRIM49*	0.072	NA	NA
2	CVID	CD8+	20:g.62881301C>A	NM_033081:exon16:c.G4655T:p.S1552I		*DIDO1*	0.086	T	B
3	CVID	CD8+	7:g.100677602C>G	NM_005273:exon6:c.C372G:p.Y124X		*GNB2*	0.051	NA	NA
3	CVID	CD8+	11:g.75290010T>G	NM_004041:exon2:c.A50C:p.K17T		*ARRB1*	0.025	D	D
3	CVID	CD8+	17:g.63714087A>C	NM_001003787:exon5:c.T145G:p.S49A		*STRADA*	0.032	D	D
3	CVID	CD8+	1:g.153337250C>A	NM_020393:exon8:c.G874T:p.V292F		*PGLYRP4*	0.043	T	D
3	CVID	CD8+	10:g.49646579G>A	NM_020549:exon8:c.G1186A:p.V396M		*CHAT*	0.024	T	B
4	CVID	CD4+	9:g.5073770G>T	NM_001322195:exon13:c.G1849T:p.V617F	COSM12600	*JAK2*	0.017	D	D
7	CVID	CD8+	12:g.9090395G>A	NM_000014:exon20:c.C2557T:p.R853W		*A2M*	0.03	D	D
8	CVID	CD8+	11:g.119028330G>A	NM_001164278:exon4:c.C245T:p.S82F		*SLC37A4*	0.022	T	B
8	CVID	CD8+	16:g.66617335G>A	NM_178818:exon5:c.C647T:p.T216I		*CMTM4*	0.021	D	B
12	Jacobsen sdr	CD4+	5:g.83512294C>T	NM_004385:exon6:c.C940T:p.Q314X		*VCAN*	0.02	NA	NA
12	Jacobsen sdr	CD4+	22:g.36929726C>T	NM_000395:exon6:c.C637T:p.R213W		*CSF2RB*	0.026	D	D
12	Jacobsen sdr	CD4+	2:g.39336960T>C	NM_003618:exon6:c.A374G:p.Y125C		*MAP4K3*	0.042	.	D
12	Jacobsen sdr	CD4+	17:g.29098415C>G	NM_078471:exon24:c.G3811C:p.E1271Q		*MYO18A*	0.027	T	D
12	Jacobsen sdr	CD4+	19:g.47319962C>T	NM_001736:exon2:c.C185T:p.T62M	COSM400357	*C5AR1*	0.02	T	D
12	Jacobsen sdr	CD8+	2:g.9526225T>A	NM_003183:exon6:c.A639T:p.K213N		*ADAM17*	0.031	T	P
12	Jacobsen sdr	CD8+	2:g.47839497C>G	NM_001190274:exon3:c.G364C:p.A122P		*FBXO11*	0.037	T	P
12	Jacobsen sdr	CD8+	X:g.21432736G>A	NM_014927:exon3:c.G353A:p.R118Q		*CNKSR2*	0.03	T	D
13	Other	CD4+	17:g.42210194G>C	NM_012448:exon15:c.C1883G:p.T628S	COSM6022929	*STAT5B*	0.032	D	D
15	Other	CD8+	20:g.3706656C>A	NM_023068:exon2:c.G100T:p.G34W		*SIGLEC1*	0.028	D	D

15	Other	CD8+	22:g.25667739C>G	NM_005160:exon6:c.C442G:p.P148A		*GRK3*	0.034	P	P
16	Good sdr	CD4+	3:g.185624078C>T	NM_021627:exon15:c.C1607T:p.P536L		*SENP2*	0.035	D	P
16	Good sdr	CD8+	16:g.3243607delT	NM_000243:exon10:c.1880delA:p.E627fs		*MEFV*	0.242	NA	NA
16	Good sdr	CD8+	1:g.56692436C>T	NM_006252:exon4:c.C409T:p.H137Y		*PRKAA2*	0.032	D	D
16	Good sdr	CD8+	12:g.25227351G>A	NM_004985:exon3:c.C173T:p.T58I	COSM87288,COSM549051 3	*KRAS*	0.079	D	D
16	Good sdr	CD8+	15:g.41573360A>T	NM_006293:exon17:c.A2038T:p.I680F		*TYRO3*	0.079	D	D
16	Good sdr	CD8+	19:g.13298754G>A	NM_023035:exon19:c.C2891T:p.A964V		*CACNA1A*	0.07	T	P
16	Good sdr	CD8+	19:g.19535620G>A	NM_198537:exon6:c.G635A:p.R212H		*YJEFN3*	0.292	T	D
16	Good sdr	CD8+	19:g.47320366C>T	NM_001736:exon2:c.C589T:p.R197W	COSM4667798	*C5AR1*	0.13	T	P
17	ADA2 def	CD8+	11:g.18026604C>T	NM_004179:exon6:c.G689A:p.R230H		*TPH1*	0.029	D	D
17	ADA2 def	CD8+	5:g.138466921G>A	NM_001964:exon2:c.G472A:p.V158I		*EGR1*	0.023	D	P
17	ADA2 def	CD8+	12:g.107319038A>G	NM_001018072:exon1:c.A98G:p.N33S		*BTBD11*	0.03	T	B
HC1	Healthy	CD8+	9:g.35707732T>C	NM_006289:exon35:c.A4631G:p.K1544R		*TLN1*	0.021	T	P
HC3	Healthy	CD8+	15:g.41056702G>A	NM_017553:exon17:c.C1990T:p.R664C	COSM5383245,COSM5383244	*INO80*	0.068	D	D
HC10	Healthy	CD8+	11:g.27674144A>C	NM_001143810:exon2:c.T141G:p.C47W		*BDNF*	0.03	D	P
HC10	Healthy	CD8+	19:g.55912295G>C	NLRP13:NM_176810:exon5:c.C1522G:p.L508V		*NLRP13*	0.031	T	D
HC11	Healthy	CD8+	2:g.25240306A>G	NM_175629:exon19:c.T2318C:p.L773P	COSM1583115	*DNMT3A*	0.043	D	D
HC11	Healthy	CD8+	5:g.170270842C>G	NM_005565:exon7:c.G400C:p.E134Q		*LCP2*	0.045	T	P
HC11	Healthy	CD8+	9:g.130880097T>C	NM_007313:exon9:c.T1510C:p.S504P		*ABL1*	0.059	D	P
HC15	Healthy	CD8+	3:g.49302514A>G	NM_003363:exon10:c.T1157C:p.F386S		*USP4*	0.043	D	D
HC15	Healthy	CD8+	5:g.111072933G>A	NM_033035:exon2:c.216+1G>A		*TSLP*	0.049	NA	NA
HC16	Healthy	CD8+	3:g.184365148T>G	NM_001278698:exon3:c.T173G:p.L58W		*POLR2H*	0.032	D	D
HC16	Healthy	CD8+	4:g.38797118T>C	NM_003263:exon4:c.A1714G:p.M572V		*TLR1*	0.021	T	B
HC16	Healthy	CD8+	19:g.51501460G>A	NM_053003:exon1:c.C274T:p.R92X	COSM4766319	*SIGLEC12*	0.023	NA	NA
HC17	Healthy	CD4+	7:g.2002123T>A	NM_001013836:exon15:c.1360-2A>T		*MAD1L1*	0.044	NA	NA
HC17	Healthy	CD4+	19:g.51458037C>G	NM_014442:exon1:c.G351C:p.R117S		*SIGLEC8*	0.024	T	B
HC17	Healthy	CD8+	5:g.148827319T>G	NM_000024:exon1:c.T488G:p.L163R		*ADRB2*	0.057	D	D
HC17	Healthy	CD8+	15:g.74036026C>G	NM_033247:exon5:c.C1274G:p.A425G		*PML*	0.025	T	B
HC17	Healthy	CD8+	16:g.31266064A>T	NM_001145808:exon5:c.A344T:p.E115V		*ITGAM*	0.05	D	P
HC17	Healthy	CD8+	21:g.31251838C>G	NM_003253:exon6:c.G1315C:p.A439P		*TIAM1*	0.029	T	D
HC17	Healthy	CD8+	21:g.31266560T>A	NM_003253:exon5:c.A413T:p.D138V		*TIAM1*	0.047	D	P
HC18	Healthy	CD8+	7:g.84011182C>T	NM_006080:exon9:c.925+1G>A		*SEMA3A*	0.037	NA	NA
HC18	Healthy	CD8+	8:g.99192975A>G	NM_017890:exon17:c.A2433G:p.I811M		*VPS13B*	0.02	D	P
HC18	Healthy	CD8+	12:g.7499159G>A	NM_004244:exon4:c.C487T:p.R163C	COSM4670363,COSM4670362	*CD163*	0.034	D	B
HC18	Healthy	CD8+	14:g.68880046C>G	NM_001130004:exon18:c.G2196C:p.E732D		*ACTN1*	0.02	T	P
HC18	Healthy	CD8+	18:g.23556356T>C	NM_000271:exon8:c.A1213G:p.T405A		*NPC1*	0.028	T	B
HC20	Healthy	CD8+	7:g.48508005C>A	NM_152701:exon50:c.C13480A:p.L4494I		*ABCA13*	0.029	T	D

HC20	Healthy	CD8+	10:g.122576623C>T	NM_001320644:exon7:c.C508T:p.R170C	COSM3367939,COSM3367940,COSM3367938	*DMBT1*	0.042	T	D
HC20	Healthy	CD8+	11:g.129870009T>C	NM_006165:exon22:c.A3091G:p.I1031V		*NFRKB*	0.054	T	P
HC21	Healthy	CD4+	1:g.114716123C>T	NM_002524:exon2:c.G38A:p.G13D	COSM573	*NRAS*	0.018	D	B

All mutations discovered in healthy controls and immnodeficiency patients in CD4+ and CD8+ cells by paired-sample analyses by MuTect2. Abbreviations: Pt., patient; AA, amino acid; VAF, variant allele frequency; SIFT, SIFT prediction; PolyPhen2, Polyphen2 HDIV prediction; T, tolerated; D, deleterious (SIFT)/probably damaging (PolyPhen2); B, benign; P, possibly damaging; NA, not available (splice-site, frameshift, or nonsense variant).

Supplementary table S6. Somatic mutations in T cells do not occur in non-hematopoietic tissue samples.

Pt. ID	Disease	HGVS	AA change	Gene	VAF in CD8+	CD8+		CD4+		Skin	
						Variant reads	Normal reads	Variant reads	Normal reads	Variant reads	Normal reads
7	CVID	12:g.9090395G>A	NM_000014:exon20:c.C2557T:p.R853W	*A2M*	0.03	14	462	0	535	0	427
15	Other	20:g.3706656C>A	NM_023068:exon2:c.G100T:p.G34W	*SIGLEC1*	0.028	11	331	0	285	0	359
15	Other	22:g.25667739C>G	NM_005160:exon6:c.C442G:p.P148A	*GRK3*	0.034	25	692	0	740	0	765

Most of our data on somatic mutations has been called using paired-sample comparisons between CD4+ and CD8+ cells. However, from two patients, we had DNA available from non-hematopoietic tissues (patient 7: skin fibroblasts; patient 15: skin biopsy). These samples were sequenced with the same sequencing panel as CD4+ and CD8+ cells. The table shows the sequencing results from these patient samples. Somatic variants were called using a paired-sample strategy, CD4+ cells vs. CD8+ and *vice versa*, but also using the non-hematopoietic tissue sample as a control sample. Three different somatic variants were identified in these patients, but the variants were discovered to exist only in CD8+ cells, regardless of which germline control (CD4+ or non-hematopoietic tissue) was used. Only CD8+ cells harbored sequencing reads that supported the variant; these reads did not exist in CD4+ or in non-hematopoietic tissue samples.
Abbreviations: Pt., patient; AA, amino acid; VAF, variant allele frequency.

Supplementary Table S7. Mapped bases in sequenced samples.

ID	Disease	Sex	Age	Mapped bases CD4+	Mapped bases CD8+	Library
1	CVID	M	61	5 547 239 430	5 264 291 170	Kapa
2	CVID	M	67	5 605 211 973	4 424 304 170	Kapa
3	CVID	M	54	6 425 897 948	6 289 169 731	Kapa
4	CVID	M	70	7 913 485 919	8 249 467 672	Kapa
5	CVID	F	70	6 111 957 589	5 949 483 474	Kapa
6	CVID	F	67	8 409 971 358	7 793 689 636	Kapa
7	CVID	F	35	5 794 543 945	5 843 367 134	Kapa
8	CVID	M	37	5 843 723 928	5 172 024 026	Kapa
9	STAT3 GOF	F	17	5 893 167 691	5 986 103 640	Kapa
10	STAT3 GOF	F	15	6 686 032 805	6 307 531 709	Kapa
11	STAT3 GOF	F	22	6 283 989 638	5 740 280 375	Kapa
12	Jacobsen sdr	F	46	9 142 391 648	9 203 546 364	Kapa
13	Other	F	73	8 908 263 746	8 932 451 607	Kapa
14	Other	F	70	6 227 668 622	6 191 344 170	Kapa
15	Other	M	60	5 880 893 385	6 520 578 161	Kapa
16	Good sdr	M	70	5 799 566 210	6 230 264 907	Kapa
17	ADA2 deficiency	F	41	5 944 877 329	6 040 071 375	Kapa
HC1	HC	F	58	4 836 247 489	4 907 094 913	Kapa
HC10	HC	F	47	3 332 774 616	3 000 407 005	ThruPLEX
HC11	HC	M	48	3 006 395 425	3 839 564 953	ThruPLEX
HC12	HC	F	21	1 537 950 784	3 041 728 643	ThruPLEX
HC13	HC	F	66	5 178 847 798	4 906 517 851	Kapa
HC14	HC	F	63	3 915 254 480	4 303 882 913	Kapa
HC15	HC	M	63	4 255 679 405	4 062 759 031	Kapa
HC16	HC	F	65	5 326 558 097	5 534 346 901	Kapa
HC17	HC	M	64	5 485 499 484	5 668 209 736	Kapa
HC18	HC	F	65	4 360 042 314	4 283 227 672	Kapa
HC19	HC	M	64	4 324 897 537	4 645 201 325	Kapa
HC2	HC	M	58	4 840 430 099	4 898 833 343	Kapa
HC20	HC	F	63	4 651 864 808	4 815 541 862	Kapa
HC21	HC	M	64	4 688 775 892	4 567 660 361	Kapa
HC3	HC	F	65	5 001 034 164	5 223 776 490	Kapa
HC4	HC	F	44	3 377 389 646	2 296 486 796	ThruPLEX
HC5	HC	M	55	2 865 922 283	3 585 929 964	ThruPLEX
HC6	HC	M	52	3 163 636 155	4 482 310 699	ThruPLEX
HC7	HC	M	48	1 332 951 785	3 315 440 185	ThruPLEX
HC8	HC	F	57	3 012 854 365	3 367 018 062	ThruPLEX
HC9	HC	F	56	3 083 658 397	2 669 438 976	ThruPLEX

The numbers of mapped bases in immnunogene sequencing for healthy controls and immnunodeficiency patients. Abbreviations: HC, healthy control; GOF, gain-of-function; sdr,

syndrome; Library, sequencing library prepation kit; Kapa, Kapa Hyper library preparation kit (Roche); ThruPLEX, ThruPLEX DNA-seq Library Preparion Kit (Rubicon Genomics).

Supplementary Table S8. Clonal hematopoiesis variants occurring in both CD4+ and CD8+ cells.

Patient	AA change	Consequence	CD4+ (VAF)	CD8+ (VAF)	Targeted deep seq of sorted cells (VAF)				
					CD3+ CD4+	CD3+ CD8+	CD19+	CD14+	WB
13	*DNMT3A*:NM_022552:exon20:c.2388dupT:p.N797_L798delinsX	nonsense	0.043	0.038	0.046	0.030	0.027	0	0.037
2	*TET2*:NM_001127208:exon6:c.G3643T:p.E1215X	nonsense	0.053	0.027	0.039	0	0.040	0	0.010
2	*TET2*:NM_001127208:exon11:c.C4889G:p.S1630X	nonsense	0.041	0.032	0.037	0.023	0	0	0

We performed a sorting and sequencing experiment to investigate in which cell types the variants associated with clonal hematopoiesis existed. CD3+CD4+, CD3+CD8+, CD19+, CD14+ and whole-blood cells were sequenced with targeted deep Amplicon sequencing. The VAFs in each cell fraction are shown in the table. In addition to T-cell fractions, mutations were also found in CD19+ B cells, but not in CD14+ monocytes. Abbreviations: VAF, variant allele frequency; AA, amino acid; WB, whole blood.

Supplementary Table S9. The sequencing panel for mutation validations.

Gene name	Control position or somatic variant?	Chr	Position (GRCh38)	COSMIC identifier
GNB1	control	1	1815790	COSM211450
TET2	control	4	105276128	COSM41741
NOD2	control	16	50710787	COSM2834328
GNB2	control	7	100678546	COSM4687440
JAK2	control	9	5078360	COSM29300
A2M	control	12	9112203	COSM1177109
CSF2RB	control	22	36936577	COSM4411434
STAT5B	control	17	42202370	COSM1716827
SIGLEC1	control	20	3694821	COSM84704
KRAS	control	12	25245350	COSM521
C5AR1	control	19	47320786	COSM1751014
EGR1	control	5	138467408	COSM74487
DNMT3A	control	2	25234373	COSM52944
SIGLEC12	control	19	51499608	COSM116869
CD163	control	12	7486950	COSM298612
DMBT1	control	10	122643283	COSM1346480
NRAS	control	1	114713909	COSM580
GNB1	somatic variant	1	1804503	
TET2	somatic variant	4	105235713	
TET2	somatic variant	4	105243618	COSM3719016
NOD2	somatic variant	16	50699619	
TET2	somatic variant	4	105269703	COSM87161
STAT5B	somatic variant	17	42217380	
GNB2	somatic variant	7	100677602	
JAK2	somatic variant	9	5073770	COSM12600
A2M	somatic variant	12	9090395	
CSF2RB	somatic variant	22	36929726	
STAT5B	somatic variant	17	42210194	COSM6022929
SIGLEC1	somatic variant	20	3706656	
KRAS	somatic variant	12	25227351	COSM87288,COSM5490513
C5AR1	somatic variant	19	47320366	COSM4667798
EGR1	somatic variant	5	138466921	
DNMT3A	somatic variant	2	25240306	COSM1583115
SIGLEC12	somatic variant	19	51501460	COSM4766319
CD163	somatic variant	12	7499159	COSM4670363,COSM4670362
DMBT1	somatic variant	10	122576623	COSM3367939,COSM3367940,COSM3367938
NRAS	somatic variant	1	114716123	COSM573
DNMT3A	somatic variant	2	25239149	
TET2	somatic variant	4	105235712	

TET2	somatic variant	4	105275399	COSM5945066
DNMT3A	somatic variant	2	25244616	COSM1583077

A ParagonGenomics CleanPlex Custom Amplicon panel was designed to perform confirmative a sequencing experiment on the discovered somatic mutations. Positions covered by the multiplex panel are listed above. The panel included 24 mutation positions and 17 control positions. The individual with the *SIGLEC12* mutation (HC16) was not included in sequencing due to sample amount restraints, although the position was included in the panel.

Supplementary Table S10. Confirmatory Amplicon sequencing on selected variants.

Pt. ID	Disease	Cells	HGVS	AA change	Gene	VAF in immunopanel	VAF in amplicon sequencing
1	CVID	CD8+	1:g.1804503C>G	NM_001282539:exon6:c.G346C:p.G116R	*GNB1*	0.07	0.056
2	CVID	CD4+	17:g.42217380A>T	NM_012448:exon10:c.T1254A:p.N418K	*STAT5B*	0.036	0.060
2	CVID	CD4+	4:g.105243618G>T	NM_001127208:exon6:c.G3643T:p.E1215X	*TET2*	0.053	0.026
2	CVID	CD4+	16:g.50699619G>T	NM_022162:exon2:c.G205T:p.E69X	*NOD2*	0.06	0.064
2	CVID	CD4+	4:g.105269703C>T	NM_001127208:exon9:c.C4138T:p.H1380Y	*TET2*	0.027	0.020
3	CVID	CD8+	7:g.100677602C>G	NM_005273:exon6:c.C372G:p.Y124X	*GNB2*	0.051	0.038
7	CVID	CD8+	12:g.9090395G>A	NM_000014:exon20:c.C2557T:p.R853W	*A2M*	0.03	0.029
12	Jacobsen sdr	CD4+	22:g.36929726C>T	NM_000395:exon6:c.C637T:p.R213W	*CSF2RB*	0.026	0.015
13	Other	CD4+	17:g.42210194G>C	NM_012448:exon15:c.C1883G:p.T628S	*STAT5B*	0.032	0.035
15	Other	CD8+	20:g.3706656C>A	NM_023068:exon2:c.G100T:p.G34W	*SIGLEC1*	0.028	0.023
16	Good sdr	CD8+	12:g.25227351G>A	NM_004985:exon3:c.C173T:p.T58I	*KRAS*	0.079	0.073
16	Good sdr	CD8+	19:g.47320366C>T	NM_001736:exon2:c.C589T:p.R197W	*C5AR1*	0.13	0.101
17	ADA2 def	CD8+	5:g.138466921G>A	NM_001964:exon2:c.G472A:p.V158I	*EGR1*	0.023	0.031
HC11	Healthy	CD8+	2:g.25240306A>G	NM_175629:exon19:c.T2318C:p.L773P	*DNMT3A*	0.043	0.034
HC18	Healthy	CD8+	12:g.7499159G>A	NM_004244:exon4:c.C487T:p.R163C	*CD163*	0.034	0.031
HC20	Healthy	CD8+	10:g.122576623C>T	NM_001320644:exon7:c.C508T:p.R170C	*DMBT1*	0.042	0.036
HC21	Healthy	CD4+	1:g.114716123C>T	NM_002524:exon2:c.G38A:p.G13D	*NRAS*	0.018	0.023

Amplicon sequencing was performed to confirm a subset of somatic mutations. The table shows the mutations identified by paired-sample calling in immunogene panel sequencing. Mutations associated with clonal hematopoiesis are presented in Supplementary Table S8. The variant allele frequencies (VAFs), determined by both immnunogene panel and amplicon sequencing, are shown. Abbreviations: Pt., patient; AA, amino acid; VAF, variant allele frequency. All variants that were covered by sufficient sequencing depth were confirmed by an independent method, targeted deep amplicon sequencing.

Supplementary Table S11. Amino-acid properties of convergent and highly expanded TCRs.

		Peptide hydrophobicity	Charge	PP1 (~polarity)	PP2 (~hydrophobicity)	PP3 (~Hydrogen bonding)
CD8+ highly convergent	Difference between means	-0.0988	0.0329	0.0297	0.0073	-0.0064
	CI lower	-0.1339	-0.0352	0.0190	0.0015	-0.0133
	CI higher	-0.0637	0.1011	0.0405	0.0131	0.0006
	p-value	**3.696*10E-08**	0.3429	**6.321*10E-08**	**0.0137**	0.0731
CD8+ Highly expanded	Difference between means	-0.0681	-0.1623	0.0220	0.0030	-0.0201
	CI lower	-0.2150	-0.4666	-0.0254	-0.0219	-0.0520
	CI higher	0.0788	0.1420	0.0694	0.0278	0.0118
	p-value	0.3607	0.2934	0.3593	0.8131	0.2136
CD4+ Highly convergent	Difference between means	-0.0196	0.0306	-0.0005	-0.0021	0.0120
	CI lower	-0.1192	-0.1467	-0.0289	-0.0188	-0.0055
	CI higher	0.0801	0.2078	0.0279	0.0146	0.0295
	p-value	0.6993	0.7342	0.9703	0.8042	0.1789
CD4+ Highly expanded	Difference between means	0.0639	0.0765	-0.0101	-0.0045	0.0166
	CI lower	-0.0739	-0.1597	-0.0488	-0.0264	-0.0069
	CI higher	0.2017	0.3127	0.0287	0.0173	0.0402
	p-value	0.3613	0.5233	0.6083	0.6810	0.1652

The amino-acid properties (PP1, PP2, and PP3 by Cruciani *et al*)[14] were compared between selected TCR subsets between CVID patients and healthy controls by a Welch T-test. No multiple comparison adjustments were made. The table shows the test p-values, differences between means (CVID vs healthy), and 95% confidence intervals for the difference between means. "Highly convergent" and "highly expanded" TCR definitions are included in the Methods-section. CVID CD8+ convergent TCRs showed differential physico-chemical properties when compared to healthy controls' convergent TCRs, but no differences existed between CVID and controls in CD4+ cells, or "highly expanded" CD8+ TCRs. Abbreviations: HC, healthy control.

Supplementary Table S12. T-cell clone sizes and mutation VAFs.

Pt. ID	Disease	Cells	Gene	AA change	HGVS	max clone size	VAF
1	CVID	CD8+	*GNB1*	NM_001282539:exon6:c.G346C:p.G116R	1:g.1804503C>G	0.173069224	0.07
1	CVID	CD8+	*SCN5A*	NM_198056:exon17:c.C3206T:p.T1069M	3:g.38580953G>A	0.173069224	0.055
1	CVID	CD8+	*OPTN*	NM_001008212:exon15:c.C1700T:p.T567M	10:g.13136832C>T	0.173069224	0.037
1	CVID	CD8+	*EPS15L1*	NM_001258374:exon14:c.C1342T:p.R448C	19:g.16404674G>A	0.173069224	0.037
1	CVID	CD8+	*OSMR*	NM_001323505:exon4:c.G358A:p.D120N	5:g.38881704G>A	0.173069224	0.035
2	CVID	CD4+	*TET2*	NM_001127208:exon3:c.1771delC:p.Q591fs	4:g.105235713delC	0.004372718829553281	0.056
2	CVID	CD4+	*TET2*	NM_001127208:exon6:c.G3643T:p.E1215X	4:g.105243618G>T	0.004372718829553281	0.053
2	CVID	CD4+	*NOD2*	NM_022162:exon2:c.G205T:p.E69X	16:g.50699619G>T	0.004372718829553281	0.06
2	CVID	CD4+	*TET2*	NM_001127208:exon9:c.C4138T:p.H1380Y	4:g.105269703C>T	0.004372718829553281	0.027
2	CVID	CD4+	*CDH5*	NM_001795:exon10:c.T1499C:p.I500T	16:g.66398469T>C	0.004372718829553281	0.027
2	CVID	CD4+	*STAT5B*	NM_012448:exon10:c.T1254A:p.N418K	17:g.42217380A>T	0.004372718829553281	0.036
2	CVID	CD4+	*TRPM2*	NM_001320350:exon27:c.C3980T:p.T1327M	21:g.44426694C>T	0.004372718829553281	0.036
2	CVID	CD8+	*TRIM49*	NM_020358:exon3:c.G268T:p.E90X	11:g.89804202C>A	0.202465609	0.072
2	CVID	CD8+	*DIDO1*	NM_033081:exon16:c.G4655T:p.S1552I	20:g.62881301C>A	0.202465609	0.086
3	CVID	CD8+	*GNB2*	NM_005273:exon6:c.C372G:p.Y124X	7:g.100677602C>G	0.0646392182	0.051
3	CVID	CD8+	*ARRB1*	NM_004041:exon2:c.A50C:p.K17T	11:g.75290010T>G	0.0646392182	0.025
3	CVID	CD8+	*STRADA*	NM_001003787:exon5:c.T145G:p.S49A	17:g.63714087A>C	0.0646392182	0.032
3	CVID	CD8+	*PGLYRP4*	NM_020393:exon8:c.G874T:p.V292F	1:g.153337250C>A	0.0646392182	0.043
3	CVID	CD8+	*CHAT*	NM_020549:exon8:c.G1186A:p.V396M	10:g.49646579G>A	0.0646392182	0.024
4	CVID	CD4+	*JAK2*	NM_001322195:exon13:c.G1849T:p.V617F	9:g.5073770G>T	0.002205217535162855	0.017
7	CVID	CD8+	*A2M*	NM_000014:exon20:c.C2557T:p.R853W	12:g.9090395G>A	0.0647578761	0.03
8	CVID	CD8+	*SLC37A4*	NM_001164278:exon4:c.C245T:p.S82F	11:g.119028330G>A	NA	0.022
8	CVID	CD8+	*CMTM4*	NM_178818:exon5:c.C647T:p.T216I	16:g.66617335G>A	NA	0.021
12	Jacobsen syndrome	CD4+	*VCAN*	NM_004385:exon6:c.C940T:p.Q314X	5:g.83512294C>T	0.0717540607	0.02
12	Jacobsen syndrome	CD4+	*CSF2RB*	NM_000395:exon6:c.C637T:p.R213W	22:g.36929726C>T	0.0717540607	0.026
12	Jacobsen syndrome	CD4+	*MAP4K3*	NM_003618:exon6:c.A374G:p.Y125C	2:g.39336960T>C	0.0717540607	0.042
12	Jacobsen syndrome	CD4+	*MYO18A*	NM_078471:exon24:c.G3811C:p.E1271Q	17:g.29098415C>G	0.0717540607	0.027
12	Jacobsen syndrome	CD4+	*C5AR1*	NM_001736:exon2:c.C185T:p.T62M	19:g.47319962C>T	0.0717540607	0.02
12	Jacobsen syndrome	CD8+	*ADAM17*	NM_003183:exon6:c.A639T:p.K213N	2:g.9526225T>A	0.110719606	0.031
12	Jacobsen syndrome	CD8+	*FBXO11*	NM_001190274:exon3:c.G364C:p.A122P	2:g.47839497C>G	0.110719606	0.037
12	Jacobsen syndrome	CD8+	*CNKSR2*	NM_014927:exon3:c.G353A:p.R118Q	X:g.21432736G>A	0.110719606	0.03
13	Other	CD4+	*STAT5B*	NM_012448:exon15:c.C1883G:p.T628S	17:g.42210194G>C	8.97995840678191E-4	0.032
15	Other	CD8+	*SIGLEC1*	NM_023068:exon2:c.G100T:p.G34W	20:g.3706656C>A	0.0996980518	0.028
15	Other	CD8+	*GRK3*	NM_005160:exon6:c.C442G:p.P148A	22:g.25667739C>G	0.0996980518	0.034
16	Good syndrome	CD4+	*SENP2*	NM_021627:exon15:c.C1607T:p.P536L	3:g.185624078C>T	0.0307179019	0.035
16	Good syndrome	CD8+	*MEFV*	NM_000243:exon10:c.1880delA:p.E627fs	16:g.3243607delT	0.512191474	0.242
16	Good syndrome	CD8+	*PRKAA2*	NM_006252:exon4:c.C409T:p.H137Y	1:g.56692436C>T	0.512191474	0.032
16	Good syndrome	CD8+	*KRAS*	NM_004985:exon3:c.C173T:p.T58I	12:g.25227351G>A	0.512191474	0.079
16	Good syndrome	CD8+	*TYRO3*	NM_006293:exon17:c.A2038T:p.I680F	15:g.41573360A>T	0.512191474	0.079
16	Good syndrome	CD8+	*CACNA1A*	NM_023035:exon19:c.C2891T:p.A964V	19:g.13298754G>A	0.512191474	0.07
16	Good syndrome	CD8+	*YJEFN3*	NM_198537:exon6:c.G635A:p.R212H	19:g.19535620G>A	0.512191474	0.292

16	Good syndrome	CD8+	*C5AR1*	NM_001736:exon2:c.C589T:p.R197W	19:g.47320366C>T	0.512191474	0.13
17	ADA2 deficiency	CD8+	*TPH1*	NM_004179:exon6:c.G689A:p.R230H	11:g.18026604C>T	NA	0.029
17	ADA2 deficiency	CD8+	*EGR1*	NM_001964:exon2:c.G472A:p.V158I	5:g.138466921G>A	NA	0.023
17	ADA2 deficiency	CD8+	*BTBD11*	NM_001018072:exon1:c.A98G:p.N33S	12:g.107319038A>G	NA	0.03
HC1	Healthy	CD8+	*TLN1*	NM_006289:exon35:c.A4631G:p.K1544R	9:g.35707732T>C	0.118211403	0.021
HC3	Healthy	CD8+	*INO80*	NM_017553:exon17:c.C1990T:p.R664C	15:g.41056702G>A	0.24665913	0.068
HC10	Healthy	CD8+	*BDNF*	NM_001143810:exon2:c.T141G:p.C47W	11:g.27674144A>C	0.0707740486	0.03
HC10	Healthy	CD8+	*NLRP13*	NLRP13:NM_176810:exon5:c.C1522G:p.L508V	19:g.55912295G>C	0.0707740486	0.031
HC11	Healthy	CD8+	*DNMT3A*	NM_175629:exon19:c.T2318C:p.L773P	2:g.25240306A>G	0.110654257	0.043
HC11	Healthy	CD8+	*LCP2*	NM_005565:exon7:c.G400C:p.E134Q	5:g.170270842C>G	0.110654257	0.045
HC11	Healthy	CD8+	*ABL1*	NM_007313:exon9:c.T1510C:p.S504P	9:g.130880097T>C	0.110654257	0.059
HC15	Healthy	CD8+	*USP4*	NM_003363:exon10:c.T1157C:p.F386S	3:g.49302514A>G	0.065790467	0.043
HC15	Healthy	CD8+	*TSLP*	NM_033035:exon2:c.216+1G>A	5:g.111072933G>A	0.065790467	0.049
HC16	Healthy	CD8+	*POLR2H*	NM_001278698:exon3:c.T173G:p.L58W	3:g.184365148T>G	0.114472464	0.032
HC16	Healthy	CD8+	*TLR1*	NM_003263:exon4:c.A1714G:p.M572V	4:g.38797118T>C	0.114472464	0.021
HC16	Healthy	CD8+	*SIGLEC12*	NM_053003:exon1:c.C274T:p.R92X	19:g.51501460G>A	0.114472464	0.023
HC17	Healthy	CD4+	*MAD1L1*	NM_001013836:exon15:c.1360-2A>T	7:g.2002123T>A	0.185848787	0.044
HC17	Healthy	CD4+	*SIGLEC8*	NM_014442:exon1:c.G351C:p.R117S	19:g.51458037C>G	0.185848787	0.024
HC17	Healthy	CD8+	*ADRB2*	NM_000024:exon1:c.T488G:p.L163R	5:g.148827319T>G	0.0644821748	0.057
HC17	Healthy	CD8+	*PML*	NM_033247:exon5:c.C1274G:p.A425G	15:g.74036026C>G	0.0644821748	0.025
HC17	Healthy	CD8+	*ITGAM*	NM_001145808:exon5:c.A344T:p.E115V	16:g.31266064A>T	0.0644821748	0.05
HC17	Healthy	CD8+	*TIAM1*	NM_003253:exon6:c.G1315C:p.A439P	21:g.31251838C>G	0.0644821748	0.029
HC17	Healthy	CD8+	*TIAM1*	NM_003253:exon5:c.A413T:p.D138V	21:g.31266560T>A	0.0644821748	0.047
HC18	Healthy	CD8+	*SEMA3A*	NM_006080:exon9:c.925+1G>A	7:g.84011182C>T	0.136208773	0.037
HC18	Healthy	CD8+	*VPS13B*	NM_017890:exon17:c.A2433G:p.I811M	8:g.99192975A>G	0.136208773	0.02
HC18	Healthy	CD8+	*CD163*	NM_004244:exon4:c.C487T:p.R163C	12:g.7499159G>A	0.136208773	0.034
HC18	Healthy	CD8+	*ACTN1*	NM_001130004:exon18:c.G2196C:p.E732D	14:g.68880046C>G	0.136208773	0.02
HC18	Healthy	CD8+	*NPC1*	NM_000271:exon8:c.A1213G:p.T405A	18:g.23556356T>C	0.136208773	0.028
HC20	Healthy	CD8+	*ABCA13*	NM_152701:exon50:c.C13480A:p.L4494I	7:g.48508005C>A	0.0919760615	0.029
HC20	Healthy	CD8+	*DMBT1*	NM_001320644:exon7:c.C508T:p.R170C	10:g.122576623C>T	0.0919760615	0.042
HC20	Healthy	CD8+	*NFRKB*	NM_006165:exon22:c.A3091G:p.I1031V	11:g.129870009T>C	0.0919760615	0.054
HC21	Healthy	CD4+	*NRAS*	NM_002524:exon2:c.G38A:p.G13D	1:g.114716123C>T	8.011564664076844E-4	0.018

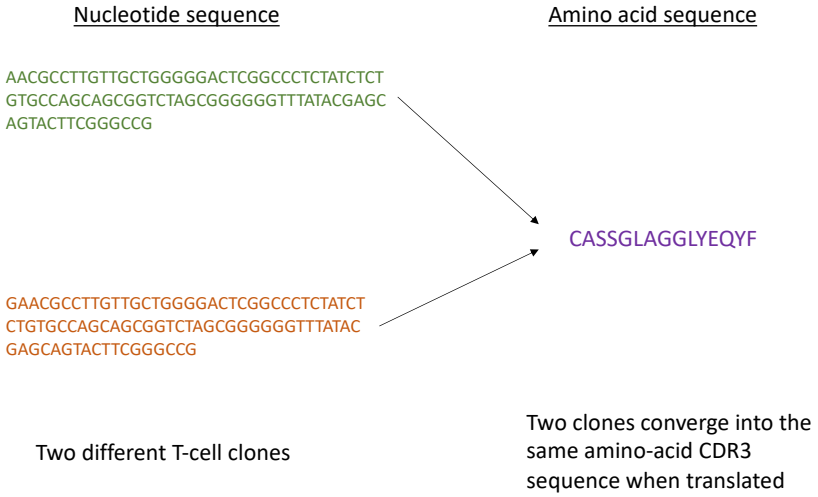
The table shows each mutation discovered in the paired-sample mutation analyses. The cell type harboring the mutation is shown (CD4+ or CD8+). Also, the "max clone size" -column shows the frequency of the largest T-cell clone of all of the sequenced cells (CD4+ or CD8+). The clone frequency shown always corresponds to the cell fraction in which the mutation was discovered.

Supplementary Table S13. *STAT5B* and *KRAS* mutations in sorted T cells.

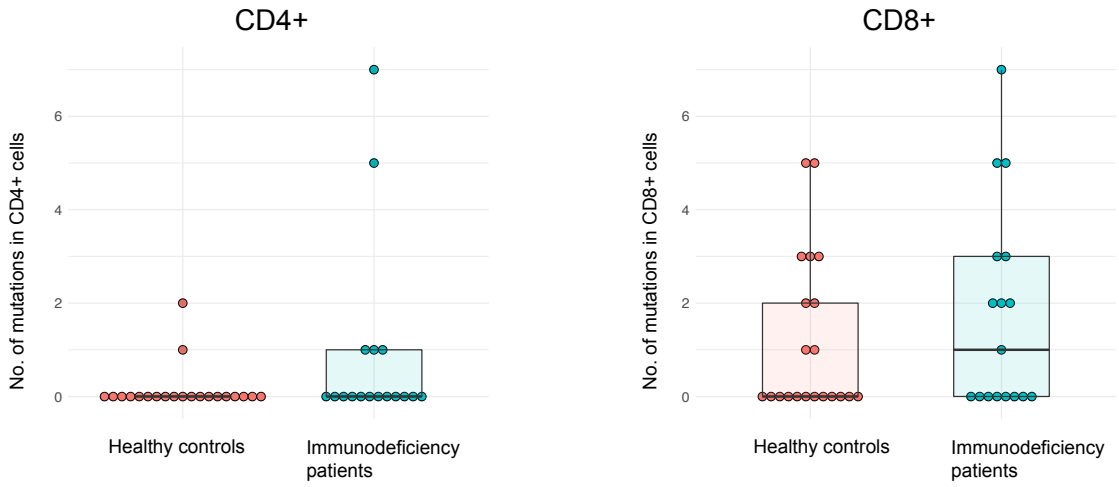
Patient	Gene	AA change	Variant allele frequency			
			CD3+CD4+	CD3+CD8+	CD14+	$CD3^{neg}CD14^{neg}$
Pt.2	*STAT5B*	N418K	0.069	0*	0	0
Pt.13	*STAT5B*	T628S	0.048	0	0	0
Pt.26	*KRAS*	T58I	0	0.075	0	Not sorted

Flow-cytometry-mediated sorting was used to extract CD3+ T cells and other cell types for sequencing. The *STAT5B* mutations occurred only in CD3+CD4+ cells, and the KRAS only in CD3+CD8+ cells. *For patient 2, CD3+CD8+ T cells were sorted also according to the largest CD3+CD8+Vbeta expansion, but both Vbeta+ and $Vbeta^{neg}$ fractions were negative. Abbreviations: AA, amino acid.

Supplementary Figure S1. T-cell clones and convergence of clones.

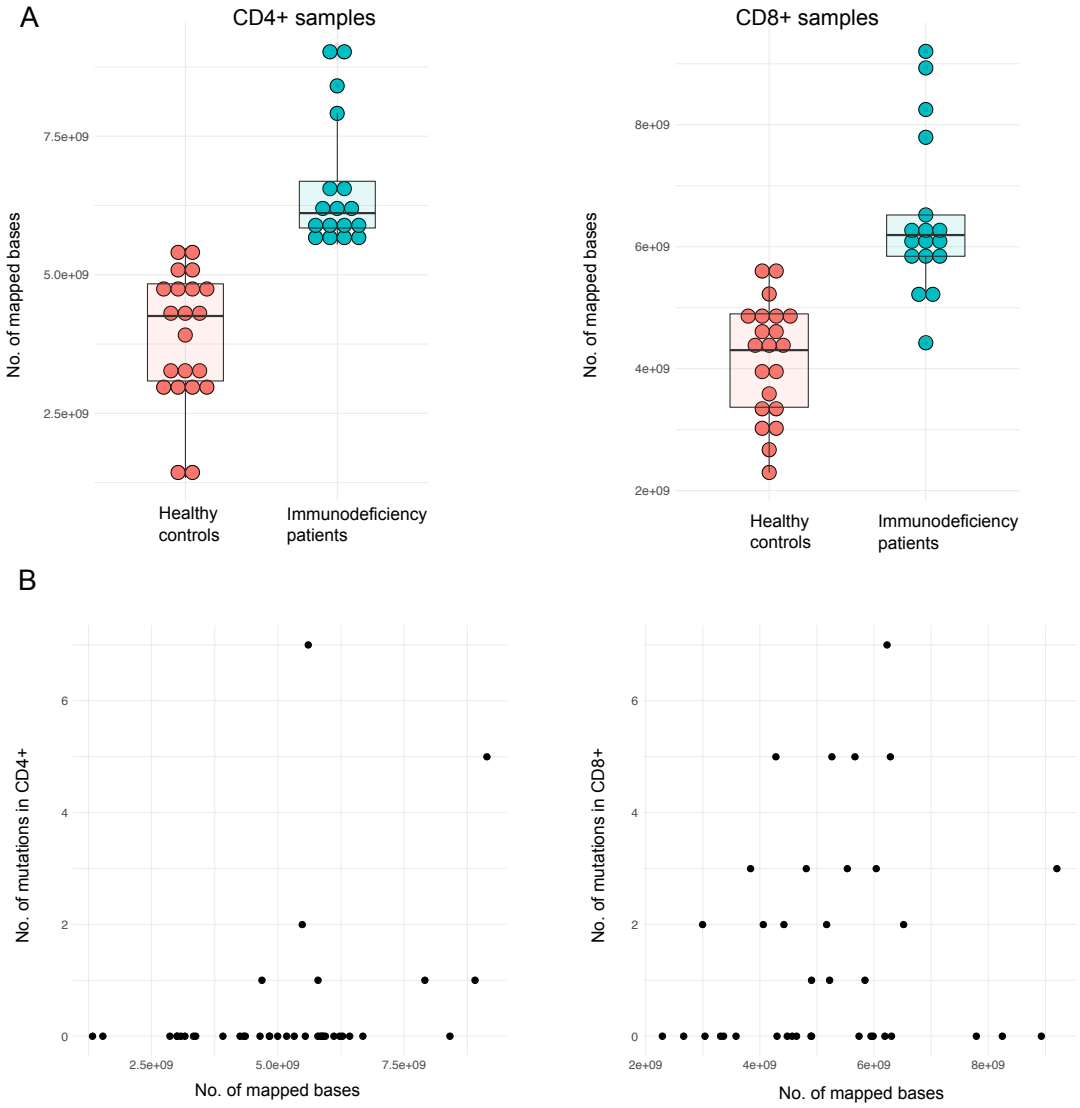


Supplementary Figure S2. The number of discovered mutations in patients and controls.



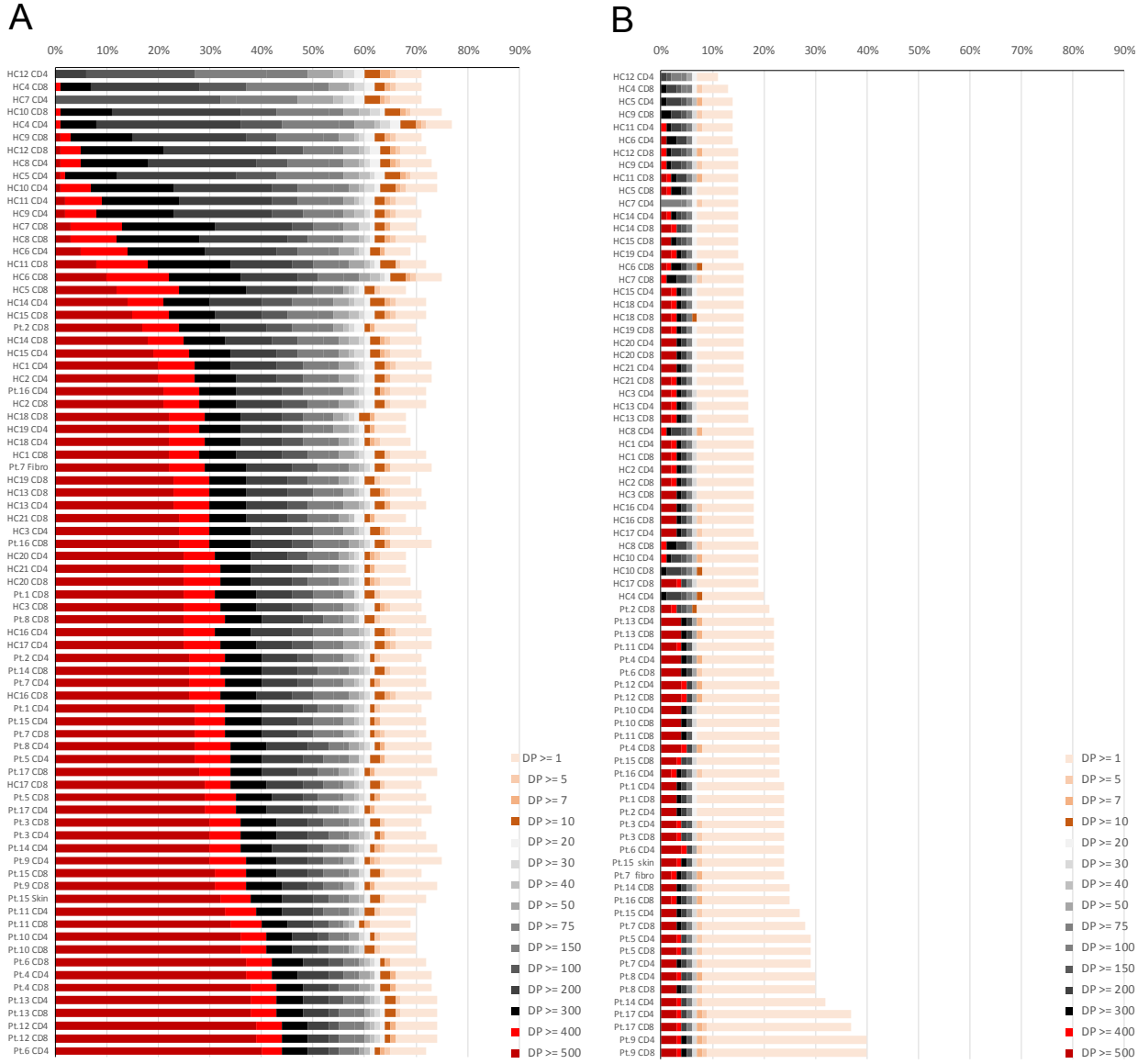
The number of somatic mutations in CD4+ or CD8+ cells did not differ between immnunodeficiency patients and controls (Mann-Whitney test). The plots show the number of mutations in each studied individual, with vertical lines representing the median, box hinges interquartile ranges, and whiskers reasonable extremes of the data.

Supplementary Figure S3. The numbers of mapped bases in CD4+ and CD8+ cells.



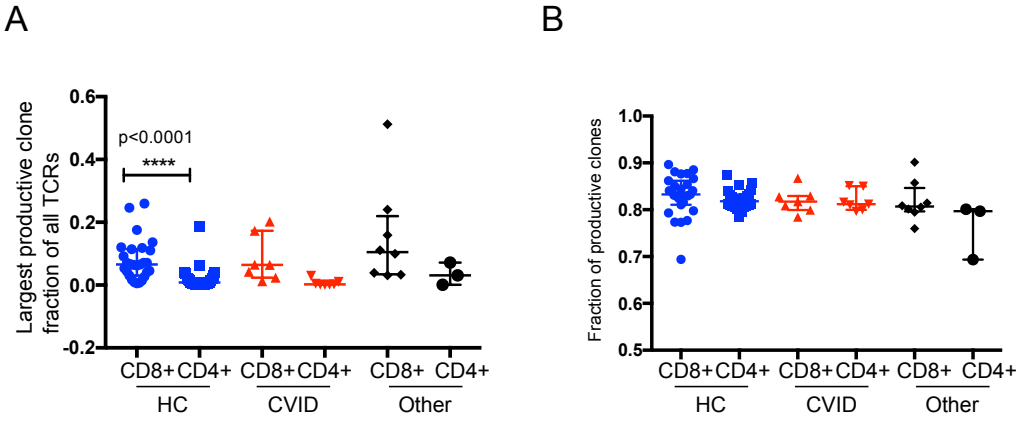
The numbers of mapped bases in immunogene sequencing for healthy controls and immunodeficiency patients. Results for CD4+ and CD8+ samples are shown separately. A. Immunodeficiency patients had higher numbers of mapped bases in CD8+ samples (p-value = 4.753e-08, Mann-Whitney test) and in CD4+ samples (p-value = 6.949e-11, Mann-Whitney test). Boxplot hinges represent interquartile medians and the vertical line the median. B. The number of mapped bases did not correlate with the number of detected mutations in CD8+ cells (Spearman correlation), although a statistically significant correlation existed in CD4+ cells (Spearman correlation p= 0.02955).

Supplementary Figure S4. Vertical and horizontal coverage of the custom gene sequencing panel.



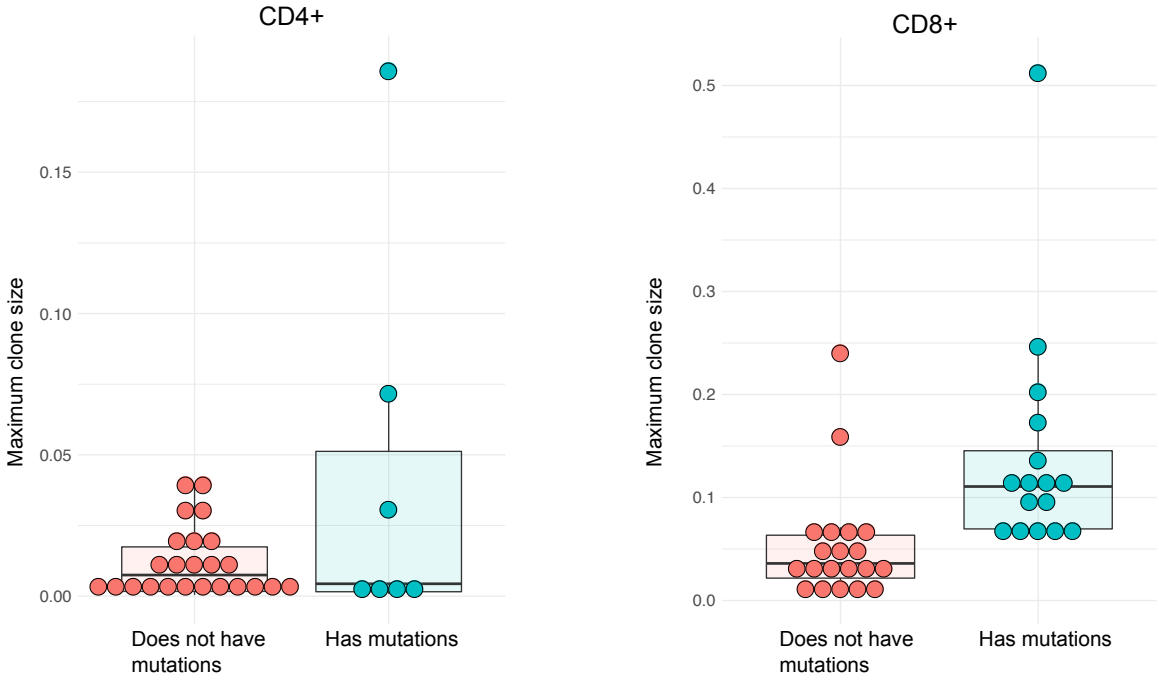
The percentage of bases covered by the given number (or more) of sequencing reads, presented as cumulative percentage. Colors show the depth. A. Coverages over the custom, targeted gene panel positions. B Coverages over all RefSeq genes. Abbreviations: DP, depth (the number of reads)

Supplementary Figure S5. The largest clones and fraction of productive sequences in the sample.



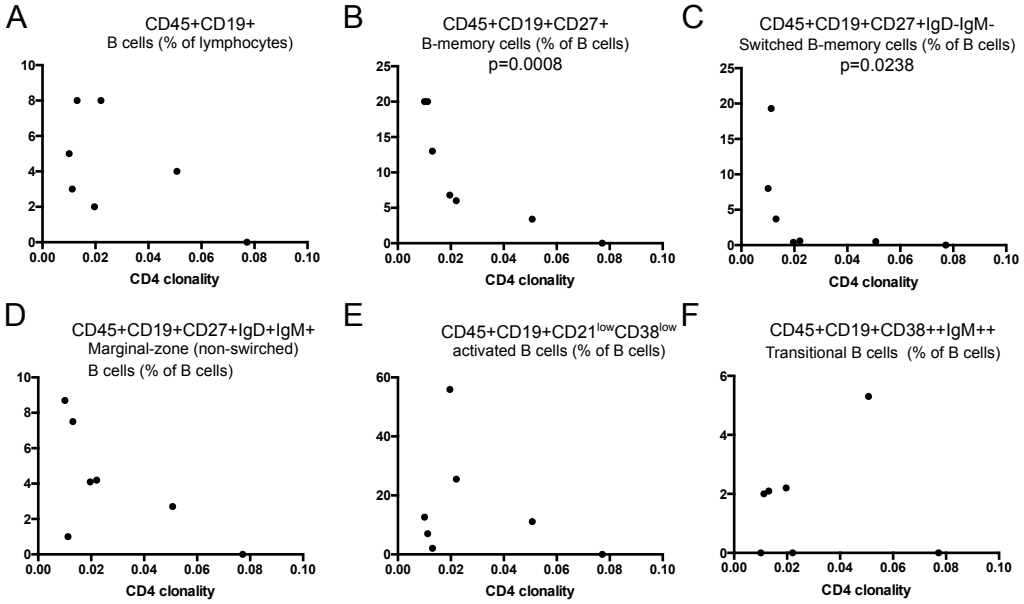
A. The largest clone (as frequency of all TCRB rearrangements in the sample) for each patient is shown. B. The fraction of productive TCRB rearrangements in the sample (frequency). Statistical tests comprised of Kruskall-Wallis test as an omnibus test and Dunn's multiple comparison tests as post-hoc tests. Statistically significant results are marked in the figure. The panels show group median, and error bars represent interquartile ranges.

Supplementary Figure S6. Individuals with mutations have larges T-cell clones.



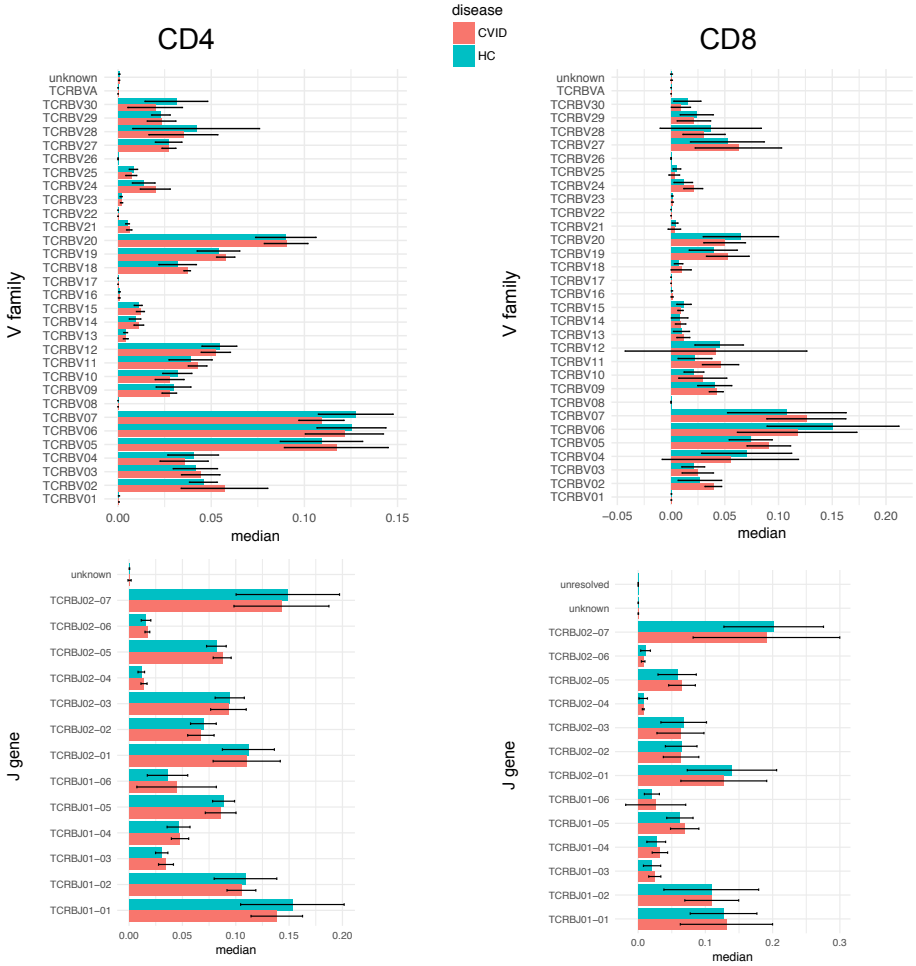
All individuals (both healthy controls and patients) were grouped using the existence of somatic mutations as a grouping factor. The sizes (frequency of all TCR rearrangements in the sample) of the largest T-cell clone in the sample were compared. In CD4+ cells, the clone sizes did not differ, but in CD8+ cells, individuals with mutations had larger T-cell clones (Mann-Whitney test p= 4.991e-05). Vertical lines in the plot represent the median, boxplot hinges interquartile ranges and whiskers reasonable extremes of the data.

Supplementary Figure S7. CD4+ clonality correlations with B-cell subtype frequencies.



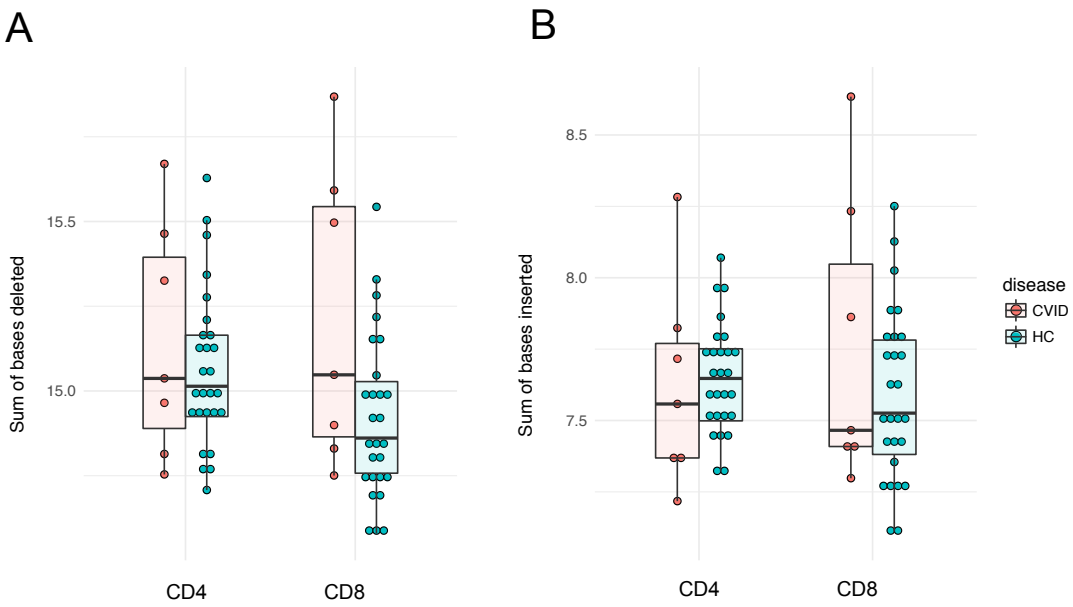
CD4+ clonality in CVID patients was plotted and correlated with the frequency of different B-cell subsets. Statistically significant correlations existed between B-memory and switched B-memory cells (Spearman correlation p=0.0008 and p=0.0238), but the associations were not linear.

Supplementary Figure S8. V-family and J-gene usage in CVID patients and controls.



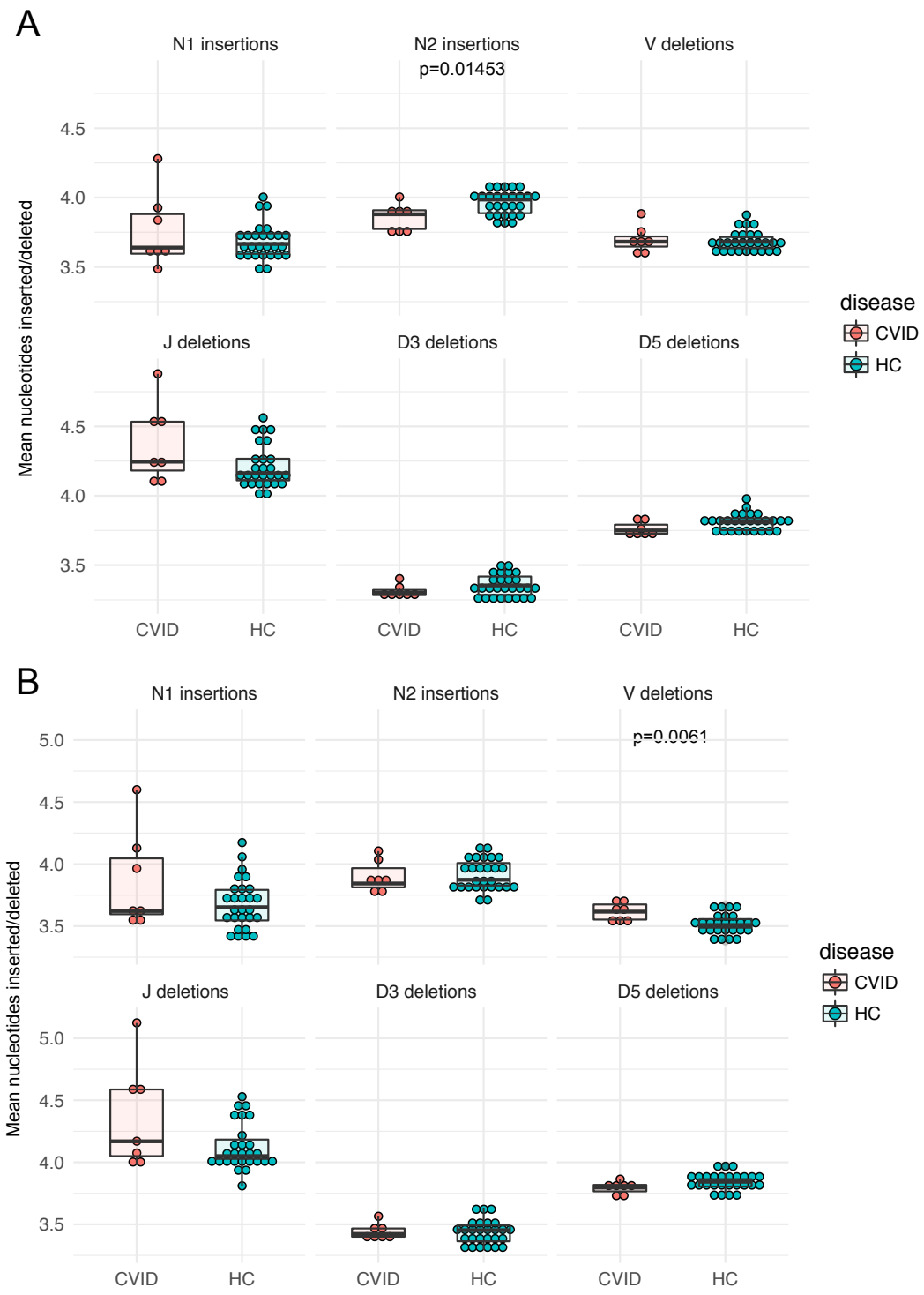
For each individual, the abundance of all TCRs that were classified to different V-families and J-genes were calculated. The graphs show the medians for CVID patients and healthy controls, and error bars represent interquartile ranges. No statistically significant differences were observed between patients and controls in neither V-family nor J-gene usage (Mann-Whitney test for each V-family and J-gene; p-values corrected for multiple comparisons with the Benjamini-Hochberg method).

Supplementary Figure S9. CVID patients do not have more n-insertions or deletions than controls.



The mean number of deletions (A) and non-templated insertions (B) was calculated for each individual and compared between controls and CVID patients. No statistically significant differences (Mann-Whitney test) existed between CVID patients and healthy controls. In the figure, medians, interquartile ranges, and reasonable extremes of the data are shown. Abbreviations: HC, healthy control; CVID, common variable immunodeficiency.

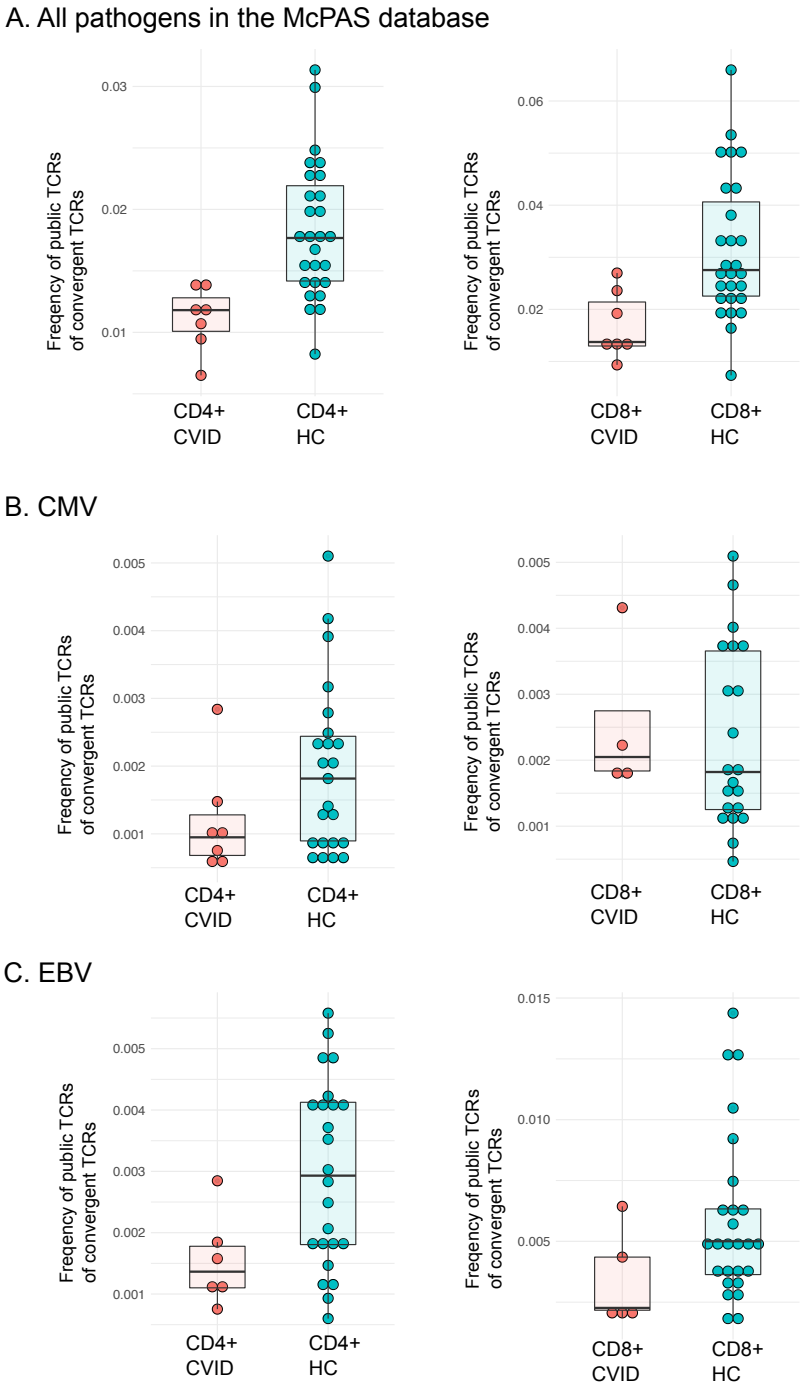
Supplementary Figure S10. All base editions in CVID and HC TCRs.



The mean number of base deletions and insertions are shown for CD4+ (A) and CD8+ cells (B). Medians, interquartile ranges, and reasonable extremes of the data are also shown. In most cases, no statistically significant differences occurred between CVID and healthy controls, but CVID CD4+ cells may have less N2 insertions and CVID CD8+ cells more V deletions than in healthy controls (Mann-Whitney test). Tests were not corrected for multiple comparisons, and thus caution in

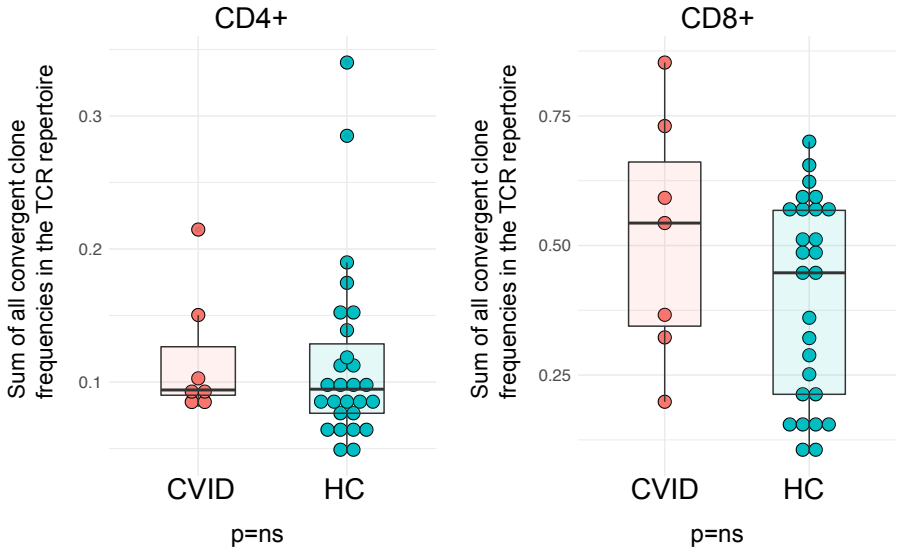
interpretation is needed. Abbreviations: HC, healthy control; CVID, common variable immunodeficiency.

Supplementary Figure S11. Healthy controls show higher frequencies of public, pathogen-specific TCRs in their convergent TCRs than CVID patients.



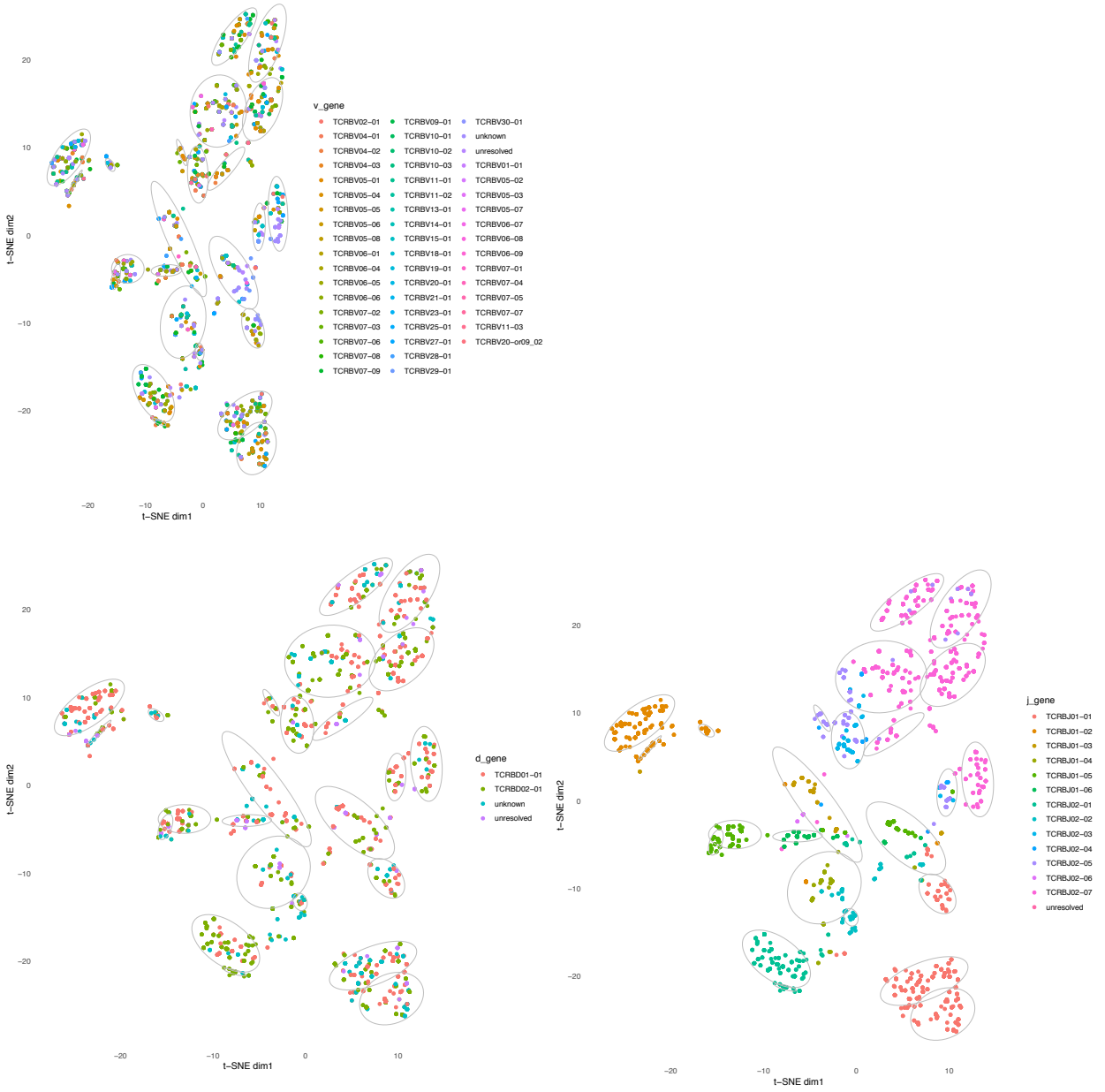
Frequency of public pathogen-specific TCRs of all convergent TCRs in both CVID patients' and healthy controls' CD4+ and CD8+ cells. Public pathogen-specific TCRs were extracted from the McPas database.[10] The pathogen-specific public TCRs comprised of TCRs targeting CMV, EBV, influenza, HIV, yellow fever virus, *Mycobacterium tuberculosis*, Herpes simplex 2 virus, and hepatitis C virus. Healthy controls harbored higher frequencies of public pathogen-specific TCRs in their repertoire of convergent TCRs (Mann-Whitney test p=0.0003454 for CD4+; p=0.003182 for CD8+) and EBV-specific CD4+ cells (p=0.03312). The plots show median as a vertical line, and boxplot hinges represent interquartile ranges and whiskers reasonable extremes of the data.

Supplementary Figure S12. Abundance of convergent clones.



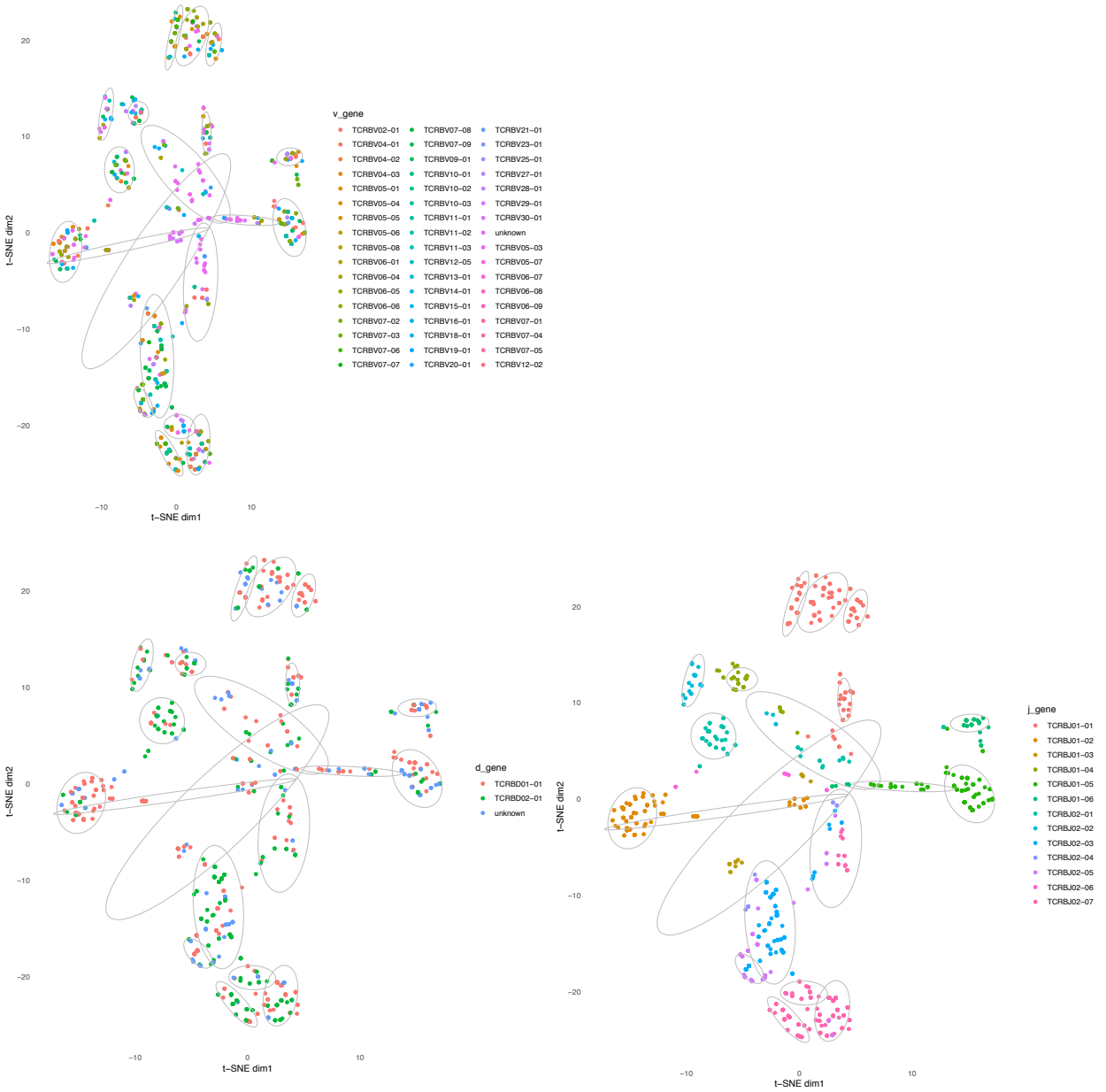
CVID patients did not show higher abundance (=sum of the frequencies of all rearrangements showing convergence) of convergent TCRs (Mann-Whitney test p= ns for CD4+ and CD8+). In the plots, vertical lines represent the median, box hinges interquartile ranges, and whiskers reasonable extremes of the data. Abbreviations: ns, not significant; HC, healthy control; CVID, common variable immunodeficiency.

Supplementary Figure S13. VDJ gene usage mapped to CD8+ TCR clustering analysis.



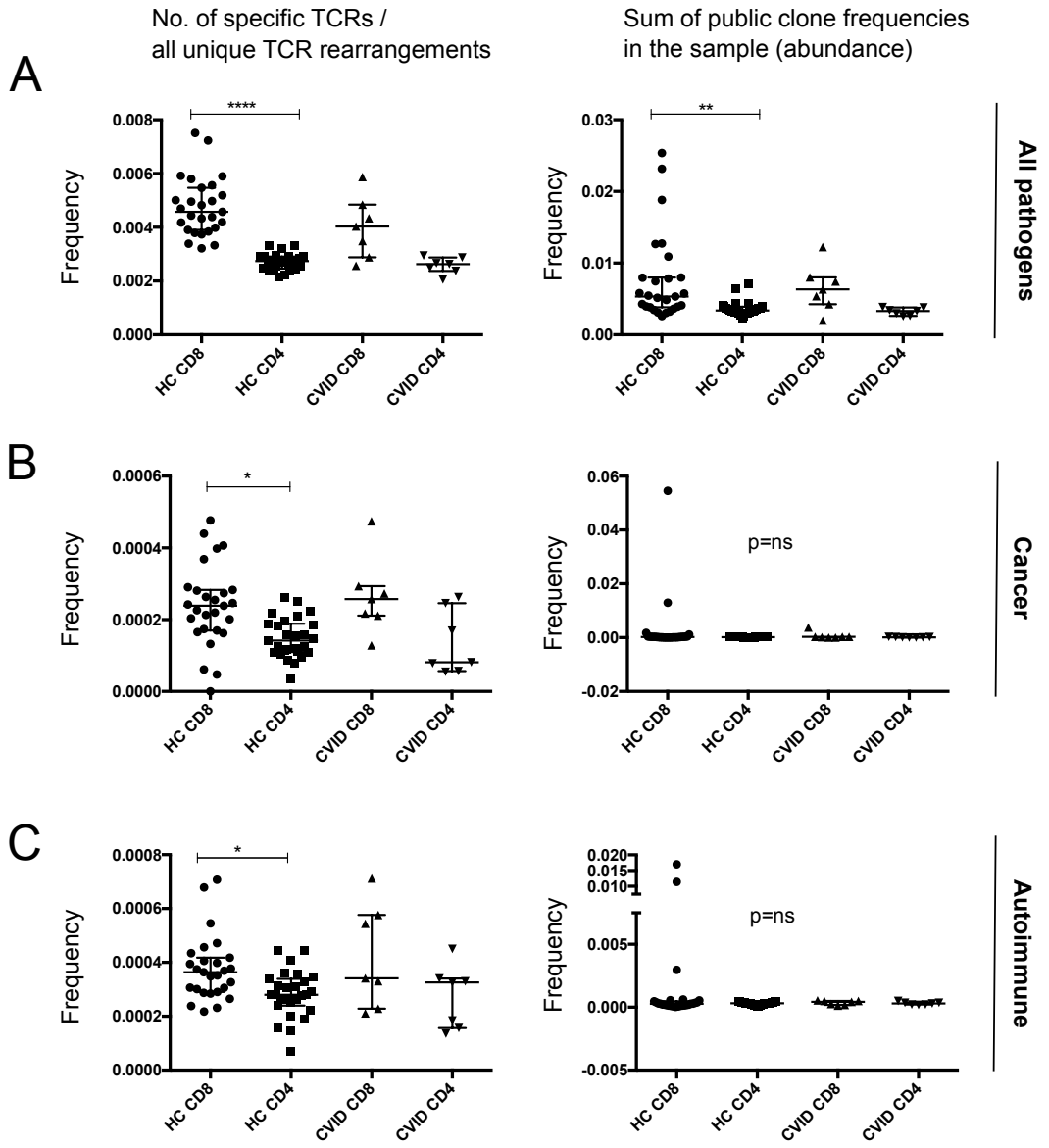
Physiochemical similarity analysis of selected CD8+ TCR CDR3 sequences by the GSKernel algorithm, presented as tSNE plots. TCRs are colored by their V-gene, D-gene, and J-genes. The V-gene does not clearly correlate with TCR similarity clusters, but the J-genes do. However, J-genes define a larger proportion of the TCR CDR3 than V- or D genes.

Supplementary Figure S14. VDJ gene usage mapped to CD4+ TCR clustering analysis.



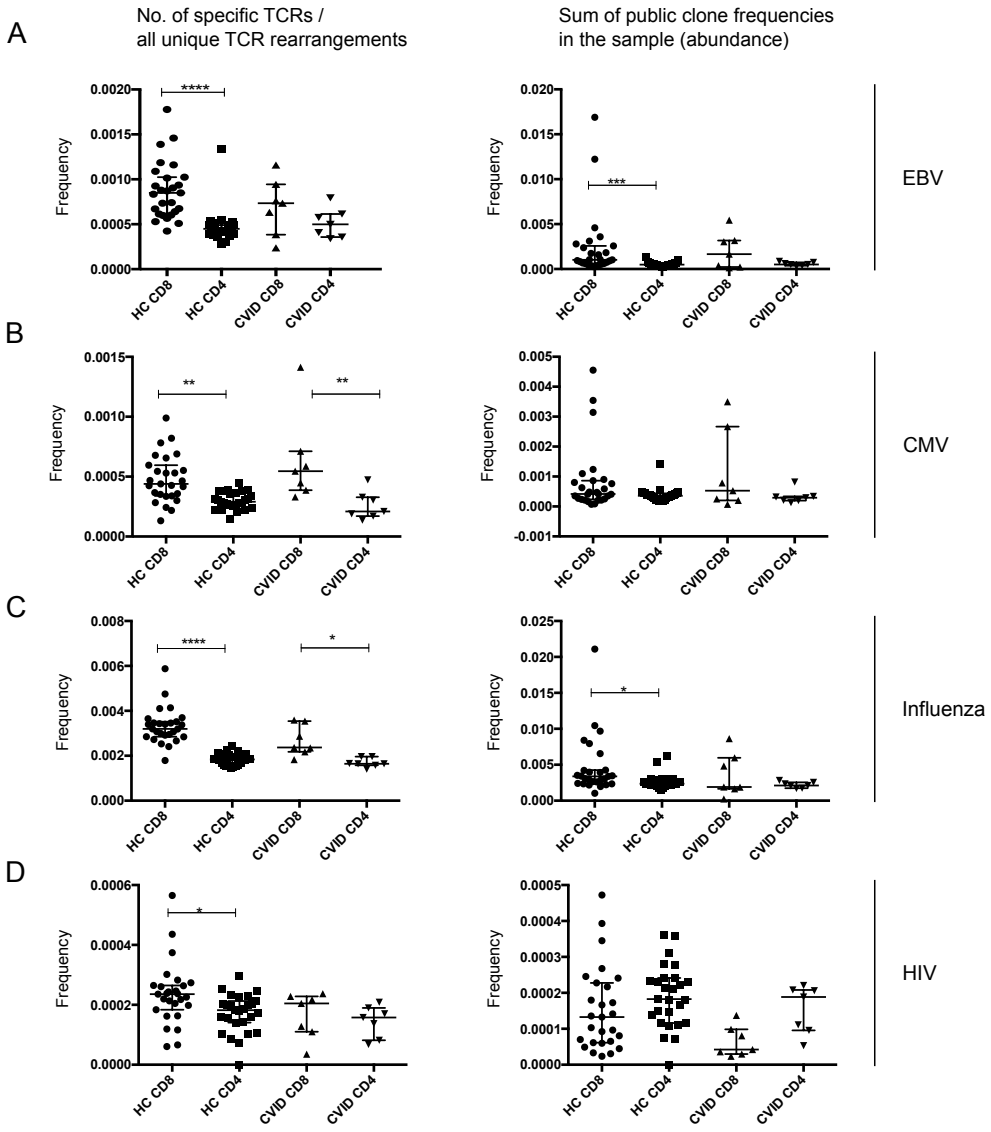
Physiochemical similarity analysis of selected CD4+ TCR CDR3 sequences by the GSKernel algorithm, presented as tSNE plots. TCRs are colored by their V-gene, D-gene, and J-genes. The V-gene does not clearly correlate with TCR similarity clusters, but the J-genes do. However, J-genes define a larger proportion of the TCR CDR3 than V- or D genes.

Supplementary Figure S15. Pathogen-specific TCRs are more common in CD8+ cells than in CD4+ cells.



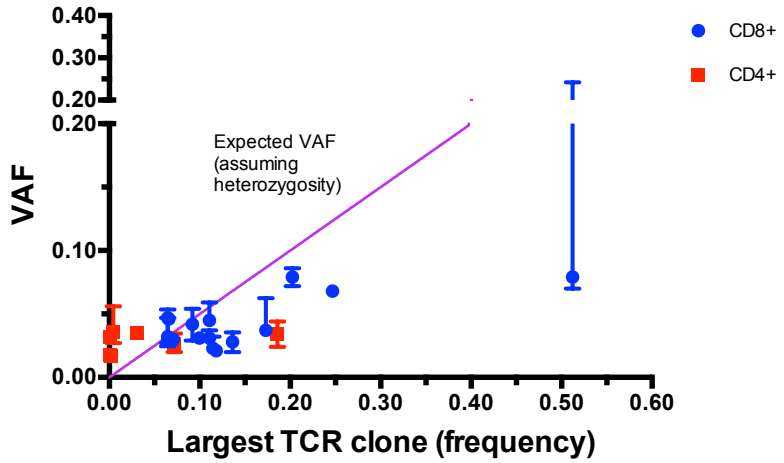
TCRB sequencing data was queried for matches for public, previously reported TCR sequences included in the McPas database. The numbers of all pathogen-, cancer-, or autoimmune-associated TCRs were pooled for each patient and normalized for repertoire size. For pathogen- and cancer-associated TCRs, only antigen-specific TCRs were queried (labels "1" and "2" in the McPAS database), but for autoimmune TCRs, all autoimmune-associated TCRs were included in the analyses. Statistical tests comprised of Kruskall-Wallis test with Dunn's multiple comparison tests. Panels A-C show the median and error bars represent interquartile ranges. Statistically significant results between comparisons (HC CD8+ vs HC CD4+, CVID CD8+ vs CD4+, CVID CD8+ vs HC CD8+, and CVID CD4+ vs HC CD4+) are shown. Abbreviations: ns, not significant; HC, healthy control; CVID, common variable immunodeficiency. *p<0.05;**p<0.01 ;***p<0.001; ****p<0.0001.

Supplementaryry Figure S16. Virus-specific TCRs are more frequent in CD8+ cells than in CD4+ cells.



TCRB sequencing data was queried for matches for public, previously reported TCR sequences included in the McPas database. Results for CMV, EBV, influenza, and HIV are shown. Only antigen-specific TCRs were queried (labels "1" and "2" in the McPAS database). Statistical tests comprised of Kruskall-Wallis test with Dunn's multiple comparison tests. Panels A-D show the median and error bars represent interquartile ranges. Statistically significant results between comparisons (HC CD8+ vs HC CD4+, CVID CD8+ vs CD4+, CVID CD8+ vs HC CD8+, and CVID CD4+ vs HC CD4+) are shown. Abbreviations: HC, healthy control; CVID, common variable immunodeficiency. *p<0.05;**p<0.01 ;***p<0.001; ****p<0.0001.

Supplementary Figure S17. T-cell clone size compared to variant-allele frequencies (VAFs)



For each patient, the median VAF of somatic mutations was plotted against the frequency of the largest T-cell clone in the same cell fraction of the same patient. Results for CD4+ and CD8+ cells are shown separately. The error bars represent interquartile range of the mutation VAFs in the patient. The purple line represents expected results, if (1) all mutations were heterozygous, (2) they occurred in the largest T-cell clone, and (3) they existed in all cells of that largest clone. The results from CD8+ cells were as expected and in line with our previous results.[37] However, some CD4+ cells harbor mutations with large VAFs compared to clone sizes.

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