immunology.sciencemag.org/cgi/content/full/3/24/eaar4526/DC1

Science Immunology

Supplementary Materials for

Identification and characterization of HIV-specific resident memory CD8$^+$ T cells in human lymphoid tissue

Marcus Buggert,* Son Nguyen, Gonzalo Salgado-Montes de Oca, Bertram Bengsch, Samuel Darko, Amy Ransier, Emily R. Roberts, Daniel del Alcazar, Irene Bukh Brody, Laura A. Vella, Lalit Beura, Sathi Wijeyesinghe, Ramin S. Herati, Perla M. Del Rio Estrada, Yuria Ablanedo-Terrazas, Leticia Kuri-Cervantes, Alberto Sada Japp, Sasikanth Manne, Shant Vartanian, Austin Huffman, Johan K. Sandberg, Emma Gostick, Gregory Nadolski, Guido Silvestri, David H. Canaday, David A. Price, Constantinos Petrovas, Laura F. Su, Golnaz Vahedi, Yoav Dori, Ian Frank, Maxim G. Itkin, E. John Wherry, Steven G. Deeks, Ali Naji, Gustavo Reyes-Terán, David Masopust, Daniel C. Douek, Michael R. Betts*

*Corresponding author. Email: betts@pennmedicine.upenn.edu (M.R.B.); marcus.buggert@ki.se (M.B.)

Published 1 June 2018, *Sci. Immunol.* **3**, eaar4526 (2018)
DOI: 10.1126/sciimmunol.aar4526

This PDF file includes:

Supplementary Materials and Methods

Human samples

Lymph node (LN) biopsies, peripheral blood, and TDL were collected from individuals classified as HIV^{-} (n = 47), HIV^{+} chronic and naïve to ART (n = 35), HIV^{+} chronic on ART (n = 19), HIV^{+} elite controllers (n = 9), and HIV^{+} acute/early seroconverters (Fiebig IV–VI; n = 8). Recruitment occurred at four sites: INER-CIENI in Mexico City (HIV^{+} ART^{+}/ART^{-} blood and matched cervical LNs); Case Western Reserve University (HIV^{-} mesenteric LNs); University of Pennsylvania (HIV^{-} blood, spleen, iliac LNs, tonsils, and TDL; HIV^{+} blood, iliac LNs, and TDL); and University of California, San Francisco (HIV^{+} elite controllers inguinal LNs). Subject grouping, tissue types, and clinical parameters are summarized in Table S1. All participants enrolled in this study provided written informed consent as per protocols approved by the INER-CIENI Ethics Committee and the Federal Commission for the Protection against Sanitary Risk (COFEPRIS), and the Institutional Review Boards of the University of Pennsylvania and Case Western Reserve University. HIV^{-} LN and TDL samples were obtained from following procedures/conditions: tonsils (non-enlarged tonsils from sleep apnea patients), mesenteric LNs (normal structures from patients undergoing abdominal surgery), iliac LNs (normal structures from kidney transplant donors), spleen (splenectomy due to trauma or surgical intervention), and TDL (patients with chylopericardium and chylothorax due to trauma or idiopathic disease).

Non-human primate samples

Rhesus macaque samples were obtained from two sites: University of Pennsylvania (SIV^{-} blood, TDL, and LTs) and Yerkes National Primate Research Center (SIV^{+} blood and LTs). All procedures were conducted in accordance with the Animal Welfare Act and other federal statutes and regulations relating to animals.

For studies of matched blood, LTs, and lymph in SIV^{-} primates, rhesus macaques of Indian origin (n = 4) were housed in facilities at the University of Pennsylvania Children's Hospital. TDL was first cannulated under anesthesia (see below for more details), and tissues were then removed at necropsy. SIV-infected rhesus macaques were housed and studied at the Yerkes National Primate Research Center as described previously (*59*).

Mouse samples

C57BL/6J (B6) and B6.SJL-Ptprc^{a}Pepc^b/BoyJ (CD45.1) female mice were purchased from The Jackson Laboratory and National Cancer Institute and housed in specific pathogen-free conditions at the University of Minnesota. Animals were maintained in accordance with regional ethical guidelines, and protocols were approved by the Institutional Review Board (*19*).

Cells and tissues

Peripheral blood mononuclear cells (PBMCs) were purified from whole blood or leukapheresis products using Ficoll-Hypaque density gradient centrifugation. Lymph node mononuclear cells (LNMCs) and splenocytes were isolated using mechanical disruption. PBMCs and LNMCs were cryopreserved and stored at –140°C for human and primate studies and stained fresh in all studies on mice.

TDL was accessed as described previously (*60*). In short, a 25-gauge spinal needle was advanced into an inguinal LN under ultra-sound guidance and an oil-based contrast agent (Ethiodol, Savage Laboratories) was injected under fluoroscopic guidance at a rate of approximately 1 mL per minute. After opacification of the cisterna chyli, access was gained via an anterior transabdominal approach using a 21–22-gauge Chiba needle (Cook Medical Inc.). A V18 control guide wire (Boston Scientific) was then advanced into the thoracic duct and manipulated cephalad. Over the wire, a 60-cm 2.3F Rapid Transit microcatheter (Cordis Corp.) was advanced further into the thoracic duct to aspirate TDL. Aspirated TDL was stored in heparin tubes and centrifuged over a Ficoll-Hypaque density gradient on the same day to remove contrast agents. TDL samples were cryopreserved as described above or used directly in flow cytometry experiments.

Conventional flow cytometry (FACS)

Human cryopreserved PBMCs, LNMCs, and TDL samples were thawed and rested in RPMI-1640 media supplemented with 10% FBS, 1% L-glutamine, and 1% penicillin/streptomycin for at least 1 hour. Cells were then washed with PBS and pre-stained for chemokine receptors and adhesion molecules at 37ºC for 10 minutes. After staining with LIVE/DEAD Aqua (Invitrogen) for 10 minutes, an optimized antibody cocktail was added for a further 20 minutes to detect additional surface markers. Cells were then washed with FACS buffer (PBS containing 0.1% sodium azide and 1% BSA), fixed, and permeabilized using a Cytofix/Cytoperm Buffer Kit (BD Biosciences) or a FoxP3 Transcription Factor Buffer Kit (eBioscience). An optimized antibody cocktail was then added for 1 hour to detect intracellular markers. In the relevant experiments, tetramers were added for 10 minutes at room temperature immediately before pre-stain. Stained cells were fixed in PBS containing 1% paraformaldehyde (Sigma-Aldrich) and stored at 4ºC. All samples were acquired within 3 days using an LSRII (BD Biosciences). Data were analyzed with FlowJo software (version 9.8.8 or higher, TreeStar). The gating strategies are depicted in the relevant figures.

For sorting experiments, thawed and rested PBMCs and/or LNMCs or fresh splenocytes were stained in 15-mL conical tubes following the procedure described above with higher concentrations of antibodies (i.e. not diluted 1:50 in FACS buffer). Cells were then washed with PBS and suspended in RPMI-1640 media without phenol red. All sorting experiments were carried out using a FACSAriaII (BD Biosciences).

Rhesus macaque cells were stained as previously described (*59*). Mamu A*01 tetramers were also added for 10 minutes at immediately before pre-stain.

Mouse splenocytes were stained as previously described (*19*).

Mass cytometry (CyTOF)

Cryopreserved cells were thawed in 0.025 U/mL benzonase (Sigma-Aldirch), washed, incubated in 1 μM cisplatin (Fluidigm) for 5 minutes, and stained with an optimized surface antibody cocktail for 30 minutes at room temperature. For intracellular staining, cells were fixed and permeabilized using a FoxP3 Transcription Factor Buffer Kit (eBioscience), and incubated with an optimized intracellular antibody cocktail for 1 hour at room temperature. Cells were then washed three times with PBS, resuspended in 2% paraformaldehyde (Electron Microscopy Sciences) in the presence of 125 nM iridium intercalator (Fluidigm), and incubated overnight at 4ºC. After three further washes, including a final wash in distilled water, cells were resuspended in PBS containing bead standards (Fluidigm) before acquisition using a CyTOF 2 (Fluidigm).

CyTOF FCS files were normalized using bead standards and the Matlab-based Nolan laboratory normalizer (*61*). Single unstimulated Iridium$^+$ CD3$^+$ CD19$^-$ TCR$\alpha\beta^+$ CD8$^+$ T cells were discriminated from doublets and beads using FlowJo (TreeStar).

Dimensionality reduction and cell clustering were performed in R using the “cytofkit” package of the tSNE and Phenograph algorithms. The analysis used a maximum of 1635 cells from 17 individuals, giving a total of 27,576 cells.

Flow antibodies

The following antibodies were used for human FACS experiments: α-CCR7 APC-Cy7 (clone G043H7, BioLegend), α-CD49a PE-Cy7 (clone TS2/7, BioLegend), α-CXCR6 BV421 (clone K041E5, BioLegend), α-CX3CR1 PE (clone 2A9-1, BioLegend), α-CCR5 BV650 (clone 3A9, BD Biosciences), α-CXCR3 BV711 (clone G025H7, BioLegend), α-CD14 BV510 (clone M5E2, BioLegend), α-CD19 BV510 (clone HIB19, BioLegend), α-CD3 AF700 or APC-R700 (clone UCHT1, BD Biosciences), α-CD3 (clone UCHT1, BioLegend), α-CD4 PeCy5.5 (clone S3.5, Invitrogen), α-CD8a BV570, BV605, BV711, or BV785 (clone RPA-T8, BioLegend), α-CD27 AF700, BV650 or BV785 (clone O323, BioLegend), α-CD45RO BV650 or PE-CF594 (clone UCHL1, BD Biosciences), α-CD45RA BV650, PE or PE-CF594 (clone HI100, BD Biosciences), α-CD69 BV421 or PE-Cy5 (clone FN50, BioLegend), α-CD69 PE-Cy5 (clone TP1.55.3, Beckman Coulter), α-CD103 BV605 or PE-Cy7 (clone Ber-ACT8, BioLegend), α-CD52 FITC (clone HI186, BioLegend), α-CXCR5 AF488 or AF647 (clone RF8B2, BD Biosciences), α-PD-1 BV421 or PE (clone EH12.2H7, BioLegend), α-HLA-DR BV605 or BV650 (clone G46-6, BD Biosciences), α-CD38 APC or BV711 (clone HIT2, BioLegend), α-CD25 PE (clone M-A251, BD Biosciences), α-4-1BB BV421 (clone 4B4-1, BioLegend), α-OX40 APC (clone ACT35, BD Biosciences), α-ICOS PE-EF610 (clone ISA-3, eBioscience), α-PD-L1 BV785 (clone 10F.9G2, BioLegend), α-CD95 BB515 (clone DX2, BD Biosciences), α-IFNγ Alexa700 (clone B27, Invitrogen), α-TNF PE-Cy7 (clone MAb11, BD Biosciences), α-perforin BV421 or PE-Cy7 (clone B-D48, BioLegend), α-perforin PE-Cy7 (clone dG9, eBioscience), α-granzyme B Alexa700 (clone GB11, BD Biosciences), α-T-bet PE (clone 4B10, eBioscience), α-T-bet PE-Dazzle 594 (clone 4B10, BioLegend), α-Eomes AF647 (clone WD1928, eBioscience), and α-Ki67 FITC (clone B56, BD Biosciences). LIVE/DEAD Aqua (Invitrogen) was used to discriminate dead cells.

The following antibodies were used for mouse FACS experiments: α-CD69 (clone H1.2F3, eBioscience) α-CD62L (clone MEL-14, Biolegend) α-CD8a (clone 53-6.7, eBioscience), α-CD3 (clone 145-2C11, Biolegend), α-Thy1.1 (clone HIS51, eBioscience), α-CD44 (clone IM7, eBioscience), α-CD45.1 (clone A20, eBioscience).

The following antibodies were used for non-human primate FACS experiments: α-CD14 BV650 (clone M5E2, BioLegend), α-CD16 BV650 (clone 3G8, BioLegend), α-CD20 BV650 (clone 2H7, BioLegend), α-CD3 APC-Cy7 (clone SP34-2, BD Biosciences), α-CD4 PE-Cy5.5 (clone S3.5, Invitrogen), α-CD8a BV570 (clone RPA-T8, BioLegend), α-CD28 ECD (clone CD28.2, Beckman Coulter), α-CD69 BV605 or PE (clone FN50, BioLegend), α-CD95 PE-Cy5 (clone DX2, BD Biosciences), and α-Ki-67 BV786 (clone B56, BD Biosciences). LIVE/DEAD Aqua (Invitrogen) was used to discriminate dead cells.

For mass cytometry (CyTOF), purified antibodies were conjugated to isotope-loaded polymers using an X8 Maxpar Kit (Fluidigm) and diluted to 0.2 mg/mL in antibody stabilization buffer (Candor bioscience). The following antibodies were used for human CyTOF experiments: α-CD57 ^{113}In (clone HCD57, BioLegend), α-CD3 ^{141}Pr (clone UCTH1, BD Biosciences), α-CD5 ^{142}Nd (clone UCTH2, BioLegend), α-CD8 ^{143}Nd (clone SK1, BioLegend), α-CD4 ^{144}Nd (clone SK3, BioLegend), α-CD19 ^{145}Nd (clone HIB19, BioLegend), α-IgD ^{146}Nd (clone IA6-2, BioLegend), α-IFNg ^{147}Sm (clone 4S.B3, eBioscience), α-CCR6 ^{148}Nd (clone G034E3, BioLegend), α-CD14 ^{149}Sm (clone M5E2, BioLegend), α-CD69 ^{150}Nd (clone FN50, BioLegend), α-Granzyme A ^{151}Eu (clone CB9, BioLegend), α-TNF ^{152}Sm (clone MAb11, BioLegend), α-CD45RO ^{153}Eu (clone UCHL1, BioLegend), α-CD27 ^{154}Sm (clone LG.7F9, eBioscience), α-TCRαβ ^{155}Gd (clone T10B9.1A-31, BD Biosciences), α-CCR5 ^{156}Gd (clone J418F1, BioLegend), α-Ki-67 ^{157}Gd (clone B56, BD Biosciences), α-Ki-67 ^{157}Gd (clone B56, BD Biosciences), α-BLYS ^{158}Gd (clone 1D6, BioLegend),), α-BCL6 ^{159}Tb (clone K112-91, BD Biosciences), α-IL-4 ^{160}Gd (clone 8D4-8, BD Biosciences), α-CD25 ^{161}Dy (clone M-A251, BD Biosciences), α-Eomes ^{162}Dy (clone wd1928, eBioscience), α-ICOS ^{163}Dy (clone c398-4A, BioLegend), α-IL-5 ^{164}Dy (clone TRFK5, BioLegend), α-FOXP3 ^{165}Ho (clone PCH101, eBioscience), α-CD95 ^{166}Er (clone DX2, BioLegend), α-CD45RA ^{167}Er (clone H100, eBioscience), α-CCR7 ^{168}Er (clone G043H7, BioLegend), α-CXCR5 ^{169}Tm (clone RF8B2, BD Biosciences), α-T-bet ^{170}Er (clone 4B10, BioLegend), α-PD-1 ^{171}Yb (clone EH12.2H7, BioLegend), α-IL-21 ^{172}Yb (clone 3A3-N2, BioLegend), α-IL-2 ^{173}Yb (clone MQ1-17H12, eBioscience), α-CD24 ^{174}Yb (clone ML5, BioLegend), α-CXCR3 ^{175}Lu (clone G025H7, BioLegend), and α-CD38 ^{176}Yb (clone HIT2, BioLegend).

Tetramers

MHC class I tetramers conjugated to PE or BV421 were used to detect CD8^{+} T cells specific for HIV-SLYNTVATL (SL9)/HLA-A*0201, HIV-ILKEPVHGV (IV9)/HLA-A*0201, HIV-FLGKIWPSHK (FK10)/HLA-A*0201, HIV-TLNAWVKVV (TV9)/HLA-A*0201, HIV-NLVPMVATV (NV9)/HLA-A*0201, HIV-RYPLTFGW (RW8)/HLA-A*2402, HIV-KYKLKHIVW (KW9)/HLA-A*2402, HIV-GPGHKARVL (GL9)/HLA-B*0702, HIV-HPRVSSEVHI (HI10)/HLA-B*0702, HIV-SPAIFQSSF (SM9)/HLA-B*0702, HIV-KRWIILGLNK (KK10)/HLA-B*2705, HIV-KAFSPEVIPMF (KF11)/HLA-B*5701, HIV-TSTLQEQIGW (TW10)/HLA-B*5701, HIV-ISPRTLNAW (ISW9)/B*5701, and HIV-QASQEVKNW (QW9)/HLA-B*5701. All fluorochrome-conjugated peptide-HLA-monomers were received from the NIH Tetramer Core Facility at Emory University or as gifts from Dr. David Price. All monomers were produced and tetramerized as previously described (*58*).

SIV-TTPESANL (Tat-TL8)/Mamu A*01 APC conjugated tetramers and SIV-CTPYDINQM (Gag-CM9)/Mamu A*01 monomers were supplied by the NIH Tetramer Core Facility at Emory University. Gag-CM9 Mamu A*01-BV421 tetramers were prepared in our laboratory as previously described (*58*).

Multiparameter confocal imaging

Confocal imaging was performed with fixed OCT embedded lymph node sections ~10um in thickness. Briefly, after allowing the tissue sections to dry for 1h/RT, antigen retrieval was performed at 90°C for 20 minutes using Borg RTU (Biocare Medical). Tissue sections were then blocked for 1 hour at room temperature and stained with the following primary and conjugated antibodies: anti-CD69 (mouse IgG1, clone 8B6), anti-CD8 (mouse IgG2b, clone 4B11), CD103 (rabbit IgG, clone EPR4166(2)), anti-PD-1 Alexa Fluor 488 (goat polyclonal, R&D) and anti-CD20 efluor615 (clone L26). The nuclear marker JOJO-1 (Life Technologies) was also used. The primary antibodies were incubated first (overnight at 4°C), followed by staining with the appropriate secondary antibodies; goat anti-mouse IgG1 Alexa Fluor 647, goat anti-mouse IgG2b Alexa Fluor 546 and donkey anti-rabbit IgG BV421. Conjugated antibody staining was performed for 2 hours at room temperature, after which sections were stained with Jo-Pro-1 for nucleus identification. Images were acquired (512- x 512-pixel density) using a 40x objective (NA 1.3) on a NIKON C2si confocal microscope running NIS-elements AR. Fluorophore spectral spillover was corrected by acquiring single stained tissue controls and creation of an emission spectrum database which was subsequently utilized by the program to separate the emission of different fluorophores (spectral unmixing, NIKON).

HistoFlow and imaging analysis

Post-acquisition analysis was performed using the Imaris software (Bitplane, version 8.3.1). Histocytometry was performed as previously described (*39*). In brief, imaging objects were segmented based on their nuclear staining signal and average voxel intensities for all channels were extrapolated in Imaris after iso-surface generation. Data were then exported to Microsoft Excel, concatenated into a single comma separated value (cmv) files and imported into FlowJo version 10 for further analysis.

Activation experiments

PBMCs were thawed, rested overnight and stimulated with anti-CD3 (BioRad) and anti-CD28/CD49d (BD Biosciences). After 3-days of stimulation, cells were stained for multiple activation markers and subsequently used as a positive control in experiments comparing the activation status of LT CD69$^-$ and CD69$^+$ cells.

Kinetics of CD69 expression

Memory CD69$^–$ and CD69$^+$ CD8$^+$ T cells were isolated from LTs using a FACSAriaII (BD Biosciences). Cells were then cultured for 9 days in 96-well plates in the presence or absence of 10 ng/mL rhIL-7 (R&D Systems).

CXCL19/21 stimulations

Memory CD69$^–$ and CD69$^+$ CD8$^+$ T cells were isolated from LTs using a FACSAriaII (BD Biosciences). Cells were then cultured for up to 9 days in 96-well plates in the presence or absence of 100 ng/mL rhCCL19 and 100 ng/mL rhCCL21 (R&D Systems).

Adoptive transfers, infections and microarray in mice

P14 immune chimeras were generated by transferring 5X10^4 P14 (LCMV gp33-41specific) CD8$^+$ T cells into naive C57BL/6J mice. Next day, mice were infected with 2X10^5 plaque-forming units (PFU) LCMV Armstrong via intraperitoneal (i.p.) injection.

Murine spleen CD8$^+$ Thy1.1$^+$ P14 SLO T$_{RMs}$ (CD62L$^-$CD69$^+$) and T$_{CMs}$ (CD62L^{hi}CD69$^-$) were sorted similarly as described above. Sorted cell populations were homogenized using QIAshredder columns (Qiagen) and RNA was extracted with the RNeasy kit (Qiagen). RNA quality was assessed using a 2100 Bioanalyzer (Agilent). Total RNA samples were processed using the GeneChip® 3' IVT Pico Kit (Affymetrix). Samples were hybridized and loaded onto Affymetrix Genechip Mouse Genome 430 2.0 arrays.

Microarray analysis. All Affymetrix raw data passed the data quality control steps. The probe data set were next pre-processed and normalized with RMA (Robust Multiarray Average) from the R package, "affy". Prior to performing differential expression analysis, genes with average expression across all samples less than the background expression level (expression < 3.5) were filtered out. Differential gene expression (z-score) analysis was performed using the limma package in R.

RNA sequencing (RNA-seq)

Memory CD69$^–$ and CD69$^+$ CD8$^+$ T cells from MesLNs (250 cells per subset) were sorted using a FACSAriaII (BD Biosciences) directly into lysis buffer provided with the SMART-Seq v4 Ultra Low Input RNA Kit (Takara) and snap frozen. RNA-seq libraries were prepared using the SMART-Seq v4 Ultra Low Input RNA Kit (Takara) according to manufacturer's protocols. Briefly, 3' SMART-Seq CDS (oligo-dt) Primers were hybridized to the poly(A) tail of all the mRNA and reverse transcribed with the SMARTScribe RT enzyme. cDNA was pre-amplified using SeqAmp DNA polymerase and frozen. Amplified material was purified using Agencourt AMPure XP beads (Beckman) and cDNA quantity was assessed on a Qubit 3.0 (Thermo) and fragment size was evaluated on a 2100 BioAnalyzer (Agilent). The PCR products were next indexed using the Nextera XT DNA Library Prep Kit (Illumina) according to manufacturer's protocol. Briefly, products were tagmented using the Amplicon tagment mix, containing Tn5 transposase, and indexed using Nextera index 1 (i7) and index 2 (i5) primers. The libraries were again cleaned-up with Agencourt AMPure XP beads, pooled, quantified and sequenced across 75 base pairs (bp) using a paired-end strategy with a 150-cycle high output flow cell on a NextSeq 550 (Illumina). Three biological replicates were sequenced per experiment. Fastq files from three sequencing runs were concatenated and aligned using STAR 2.5.2a and hg38 to generate a final unique paired mapped read depth ranging from 8 million to 13.6 million reads per sample. The aligned files were normalized using Deseq2.

Differentially expressed genes

Differentially expressed genes on normalized RNA-seq counts between bulk LN CD69$^-$ and CD69$^+$ CD8$^+$ T cells were assessed using a t-test ($P < 0.05$) with the R limma package (v3.28.21). Genes of interest were then submitted to ingenuity pathway analysis (IPA, Qiagen Bioinformatics) to identify overrepresented pathways and upstream predictors. Differentially expressed genes with a larger than 2-fold difference between LN CD69$^-$ and CD69$^+$ CD8$^+$ T cells were visualized using the Pheatmap package in R (v. 1.0.8).

Gene set enrichment analysis (GSEA)

Normalized bulk and single cell RNA-seq counts from sorted LN CD69$^-$ and CD69$^+$ CD8$^+$ T cells were subjected to GSEA using Broad Institute software (http://www.broadinstitute.org/gsea/index.jsp). Gene signatures from bulk LN CD69$^-$ and CD69$^+$ CD8$^+$ T cells were compared with gene signatures indicative of lung T_{RM} programs (*37*).

ATAC sequencing (ATAC-seq)

ATAC-seq was performed as described previously with minor modifications (*62*). Memory CD69$^-$ and CD69$^+$ CD8$^+$ T cells from hepLNs (30,000–50,000 cells per subset) were sorted using a FACSAriaII (BD Biosciences) directly into R10 media. Cells were pelleted, washed with PBS, and treated with lysis buffer (10 mM Tris-HCl pH 7.4, 10 mM NaCl, 3 mM $MgCl_2$, 0.1% IGEPAL CA-630). Nuclear pellets were resuspended in a transposition reaction with Tn5 transposase (Illumina) for 30 minutes to tag and fragment accessible chromatin, and the reaction was incubated in a water bath at 37°C. Tagmented DNA was purified using a MinElute Reaction Cleanup Kit (Qiagen) and amplified using PCR. Libraries were then purified using a QIAQuick PCR Purification Kit (Qiagen) and paired-end sequenced (38bp + 37bp) on a NextSeq 550 (Illumina). Two biological replicates per sorted memory CD8+ T cell population was sequenced from n=1 hepatic LN.

ATAC-seq analysis for each cell type was performed in duplicates. Macs2 with *'-p 1e-7 --nolambda --nomodel'* was applied on each ATAC-seq replicate separately to identify accessible chromatin. Peaks were subsequently merged using BEDTools and ATAC-seq read counts were calculated in the merged peaks for every replicate. The resulting count table was used to identify differentially enriched regions in ATAC-seq signal between CD69+ and CD69- cells with DESeq2 after applying fold change

> 2; P < 0.05. De novo motif analysis was performed using Homer to assess the enrichment of cell-specific transcription factors. In each case, genomic regions shared between two cell types were used as background control. T_{RM}-specific open chromatin regions were also linked to genes based on proximity (<10kbp) in order to enable GO term enrichment analysis using the GSEA website. Visualization of ATAC-seq tracks (peaks) was conducted using Integrative genomics viewer (igv) version 2.3.93

Single-cell RNA sequencing

Single-cell clonotypic analysis was derived from a previously published method (*63*). In brief, single HIV-tetramer$^+$ cells were index sorted using a FACSAria II (BD Biosciences) directly into 96-well microtiter plates containing lysis buffer. In total, 552 cells were sorted, and full genome was sequenced from 221 cells. Cellular nucleic acids were recovered by processing the lysates with an RNEasy Plus Micro Kit (Qiagen) and then binding to RNAClean (SPRI) beads (Beckman Coulter). ERCC RNA control (Ambion) was diluted 1 in 10^7 from stock, and 10% by volume was added to the RNAClean beads prior to purification. mRNA was then reverse transcribed from an anchored oligo-dT primer that includes a universal priming site at the 5' end. RT reactions also included a template-switch oligonucleotide to allow the incorporation of the universal priming site at cDNA 3' ends. Whole transcriptome cDNA was then amplified by PCR for 22–24 cycles using universal priming sites primers and Kapa HiFi Hot Start ReadyMix. After post-PCR clean-up, amplified whole transcriptome cDNA was incorporated into barcoded Illumina Nextera libraries and sequenced to a depth of about 2 million 150bp paired-end reads/cell on a HiSeq 4000 (Illumina).

Single-cell RNA-seq analysis

Data were initially filtered for quality. Paired-end sequencing reads were then trimmed to remove adaptor sequences and low-quality basecalls using the utility Trimmomatic. Reads were subsequently aligned using Bowtie against a genomic repeat element database derived from RepeatMasker software to quantify and remove transcript reads considered to be irrelevant for the analysis in hand (rRNA, rRNA, LINEs, SINEs, etc). The remaining reads were aligned against the most recent human genome build, hg38, using the splice-site aware aligner, STAR. As a bioinformatic measure of library quality, the total frequency of reads that could be mapped to the transcriptome was determined, and outliers were excluded from further analysis. Transcripts were then quantified and normalized using the bioinformatics package, Cufflinks. In our experience, a small number of libraries display low complexity and lack expression of highly expressed housekeeping genes. In most systems, a set of housekeeping genes should be expressed in every cell. We therefore use qPCR to identify viable samples expressing two distinct housekeeping genes. Samples with low or no expression of these genes are removed from Nextera library construction. To further ensure exclusion of data from single cells for which library construction was unsuccessful, we determined diversity (Shannon entropy and count of detected genes) using the R package, Vegan, and discarded outliers.

For differential gene expression analysis of CD69$^-$ and CD69$^+$ HIV-specific CD8$^+$ T cells, raw counts were normalized using the R package, SCnorm. The normalized data was then transformed using z-transformation and analyzed for differential expression using the R package, ROTS.

Analysis of TCR sequences

For clonotype analysis of CD69$^-$ and CD69$^+$ HIV-specific CD8$^+$ T cells, the software package, MiXCR, was used to assemble and annotate TCR sequences from the pool of reads which had not aligned to the reference genome in the previous step. After assembly, low quality and low frequency TCR chains were removed. Clonotypes were then built for each cell using the refined chain information. An average of 55 (range 23–143) TCRBV sequences were analyzed per patient.

General statistical analysis

Mann-Whitney or unpaired t-tests were used to compare differences between unmatched groups, and Wilcoxon matched-pairs single rank or paired t-tests were used to compare differences between matched samples. Spearman or Pearson tests were used for correlation analyses. Non-parametric or parametric tests were conducted based on normal distribution of the data points (Shapiro-Wilk normality test). All analyses were performed using R studio or Prism v7.0 (GraphPad). Cell ACCENSE (Automatic Classification of Cellular Expression by Nonlinear Stochastic Embedding) analyses were conducted to visualize phenotypic relationships within multivariate data sets (http://www.cellaccense.com).

SUPPLEMENTARY FIGURES

Figure S1

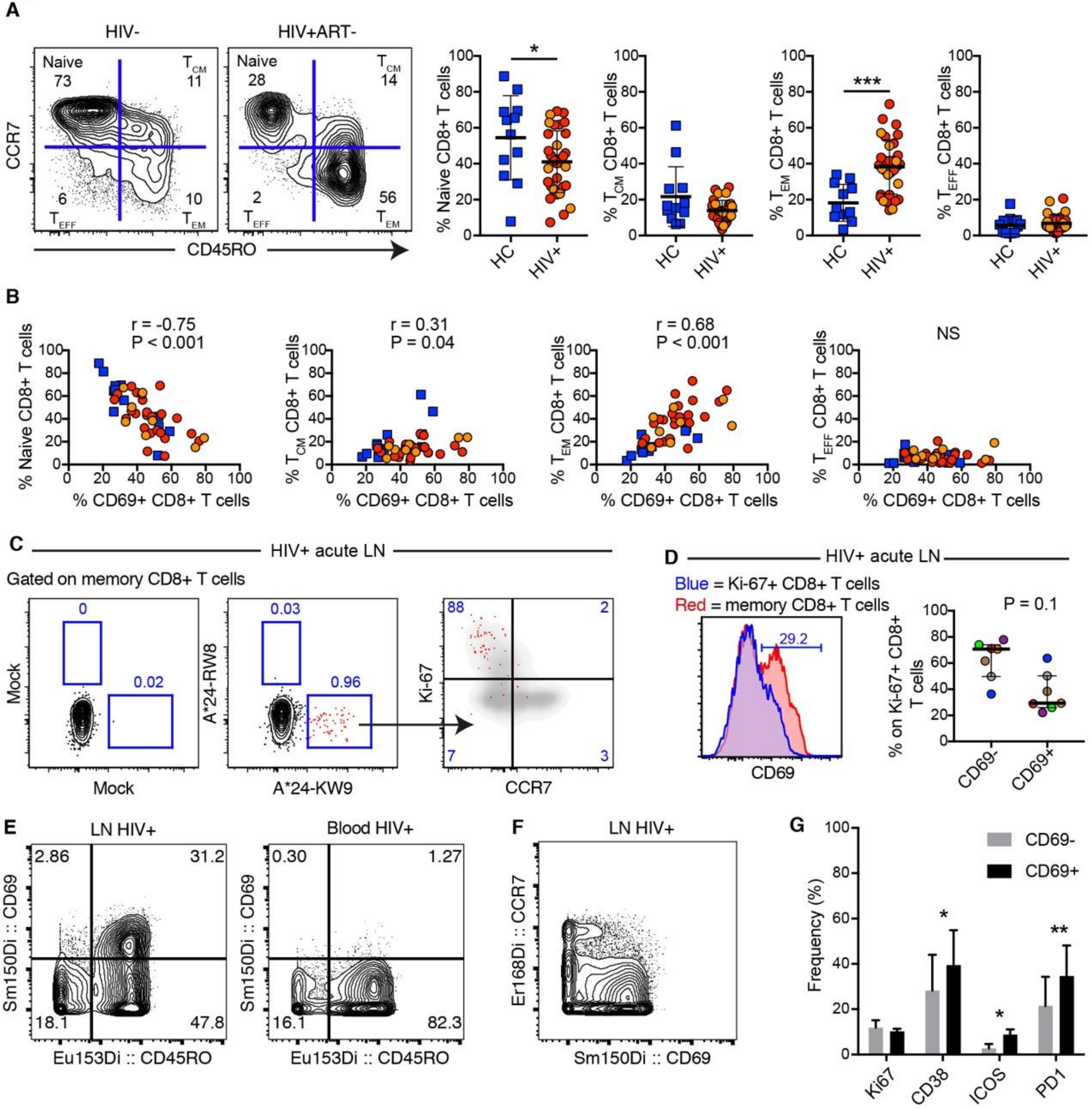

Fig. S1. Maturation of and cycling of LN CD8$^+$ T cells.

(A) Frequency of LN naïve (CCR7$^+$ CD45RO$^–$/CD45RA$^+$), T$_{CM}$ (CCR7$^+$ CD45RO$^+$/CD45RA$^–$), T$_{EM}$ (CCR7$^–$ CD45RO$^+$/CD45RA$^–$), and T$_{EFF}$ (CCR7$^–$ CD45RO$^–$/CD45RA$^+$) of total CD8$^+$ T cells in HIV$^–$ and HIV$^+$ subjects. Blue: HIV$^–$ subjects; red: HIV$^+$ ART$^–$ subjects; orange: HIV$^+$ ART$^+$ subjects. **(B)** Correlation between LN naïve, T$_{CM}$, T$_{EM}$, and T$_{EFF}$ frequencies and CD69 expression on total CD8$^+$ T cells. Blue: HIV$^–$ subjects; red: HIV$^+$ ART$^–$ subjects; orange: HIV$^+$ ART$^+$ subjects. **(C)** Representative flow cytometry plots showing background (mock) and an HIV-tetramer$^+$ CD8$^+$ T cell response in an acutely HIV-infected LN. **(D)** Frequency of Ki-67$^+$ CD69$^–$ and CD69$^+$ CD8$^+$ T cells. **(E)** CYTOF plots showing the expression intensity of CD69 and CD45RO on total CD8$^+$ T cells between LN and blood. **(F)**

CYTOF plot (gated on total $CD8^+$ T cells) showing the expression intensity of CD69 and CCR7. **(G)** The frequency of several activation markers on/in CD69- and CD69+ CD45RO+ CD8+ T cells in HIV-infected subjects (n = 14) using CYTOF. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.

Related to Fig. 1

Figure S2

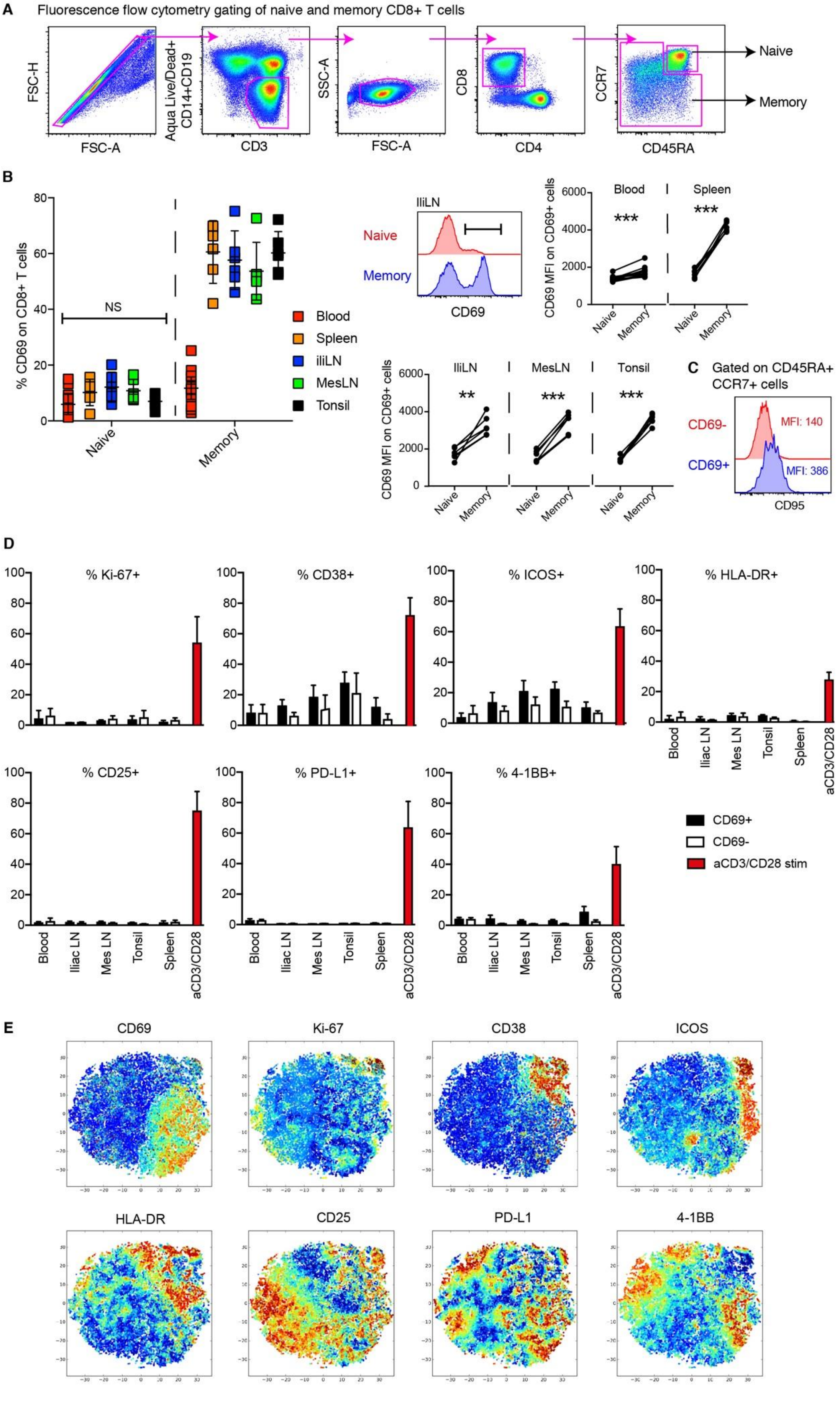
A
Fluorescence flow cytometry gating of naive and memory CD8+ T cells
FSC-H
FSC-A
Aqua Live/Dead+ CD14+CD19
CD3
SSC-A
FSC-A
CD8
CD4
CCR7
CD45RA
Naive
Memory
B
% CD69 on CD8+ T cells
80
60
40
20
0
NS
Naive
Memory
Blood
Spleen
iliLN
MesLN
Tonsil
IliLN
Naive
Memory
CD69
CD69 MFI on CD69+ cells
6000
4000
2000
0
Blood
Spleen
***
***
Naive
Memory
IliLN
MesLN
Tonsil
**
***
***
C
Gated on CD45RA+ CCR7+ cells
CD69-
CD69+
MFI: 140
MFI: 386
CD95
D
% Ki-67+
% CD38+
% ICOS+
% HLA-DR+
% CD25+
% PD-L1+
% 4-1BB+
100
80
60
40
20
0
Blood
Iliac LN
Mes LN
Tonsil
Spleen
aCD3/CD28
CD69+
CD69-
aCD3/CD28 stim
E
CD69
Ki-67
CD38
ICOS
HLA-DR
CD25
PD-L1
4-1BB
30
20
10
0
-10
-20
-30

Fig. S2. CD69 expression on naïve CD8$^+$ T cells and immune activation profile of CD69$^-$ and CD69$^+$ CD8$^+$ T cells in LTs.

(A) Gating strategy to detect naïve and memory CD8$^+$ T cells in blood and LTs for all human analysis. **(B)** CD69 frequency (left) and MFI (right) on naïve and memory CD8+ T cells from different sites. **(C)** CD95 MFI on naïve-like (CD45RA+CCR7+) CD69- (red) and CD69- (blue) cells. **(D)** Frequency of different immune activation markers on CD69$^-$ (white) and CD69$^+$ (black) CD8$^+$ T cells in blood and LTs; all data points are derived from HIV$^-$ subjects in Fig. 2A. Anti-CD3-CD28 stimulated blood memory CD8$^+$ T cells (red) were used as a positive control (n = 4). Median and IQR are shown for all bar plots. **(E)** Expression intensity of CD69 and multiple activation markers on CD8+ T cells. tSNE plots were derived using 30000 randomly selected CD8+ T cells (n = 5 subjects), merged from blood, iliac LN, mesenteric LN, spleen and tonsils. **$P < 0.01$; ***$P < 0.001$.

Related to Fig. 2

Figure S3

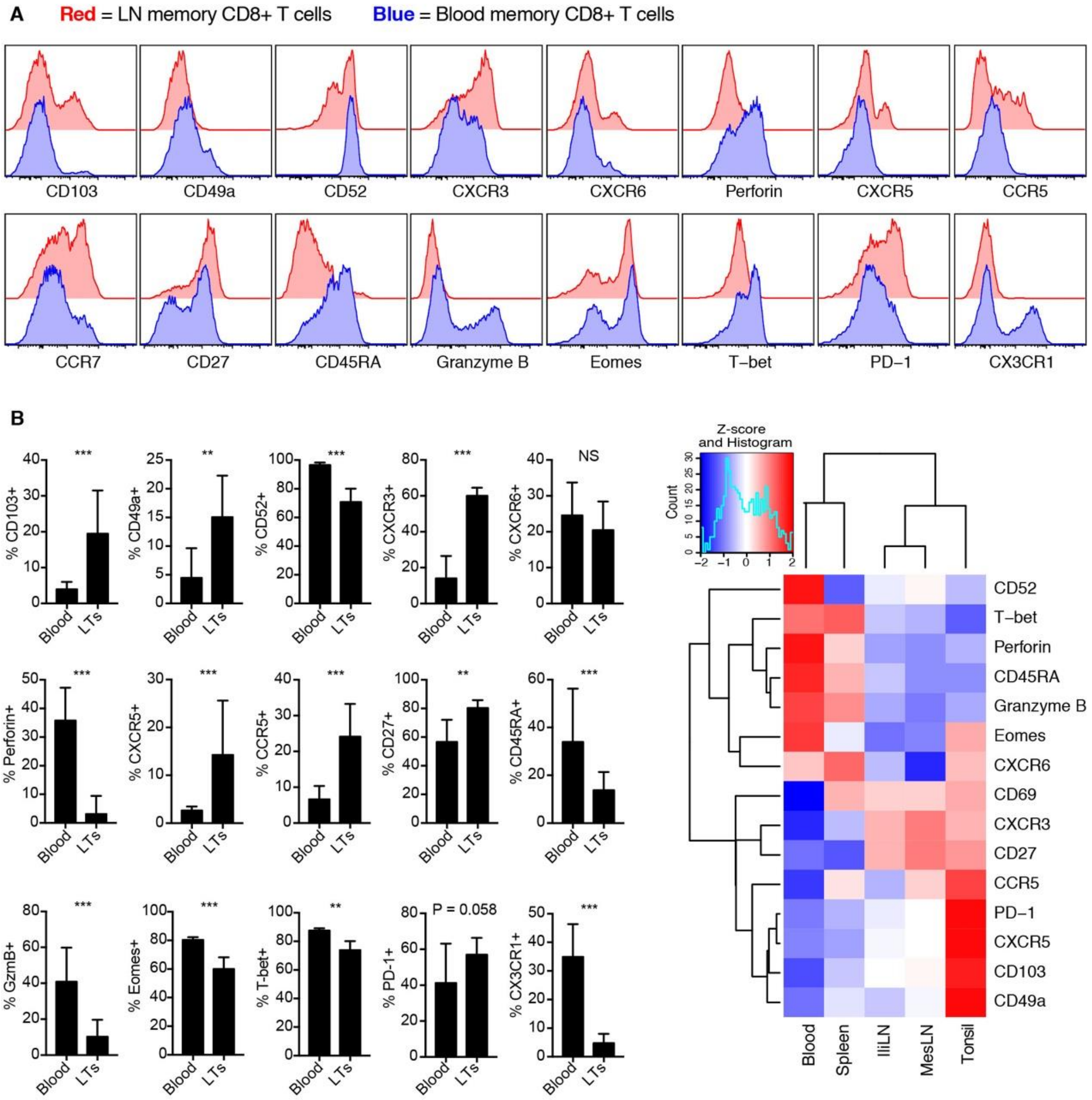

Fig. S3. Phenotypic characteristics of memory CD8$^+$ T cells in blood and LTs. **(A)** Representative histograms of all assessed markers between memory CD8+ T cells from LN (red) and blood (blue). **(B)** Frequency of multiple markers linked to residency, trafficking, effector function, and transcriptional regulation in blood and LTs on memory CD8+ T cells. Data points for LTs are derived from spleen, IliLN, MesLN, and tonsils merged together from Fig. 2A. Median and IQR are shown for all bar plots. The heat-map (right) shows hierarchical clustering of blood and different LTs based on the assessed markers. **P* < 0.05; ***P* < 0.01; ****P* < 0.001.

Related to Fig. 2

Figure S4

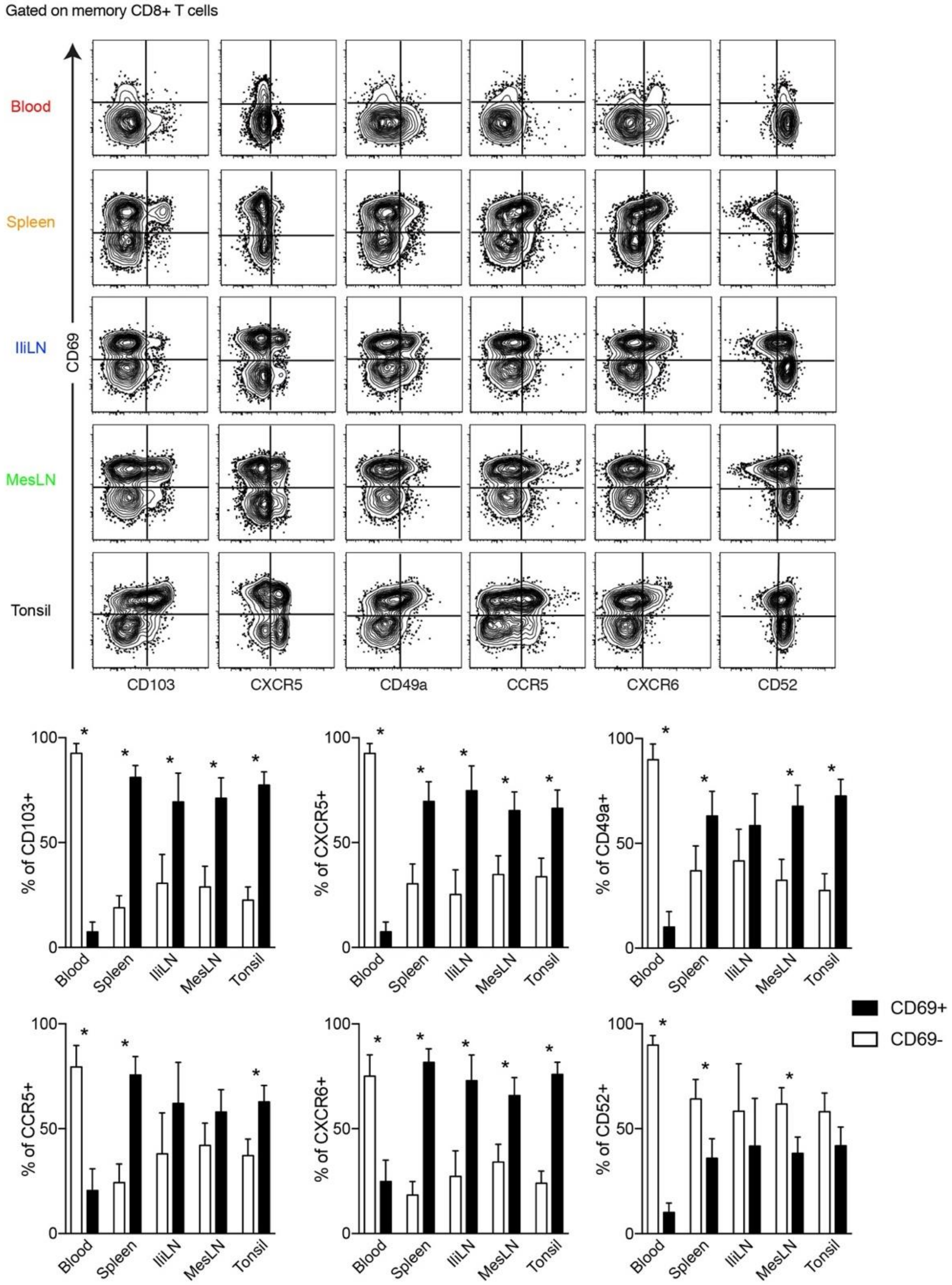

Fig. S4. Residency characteristics of CD69$^-$ and CD69$^+$ CD8$^+$ T cells.

Representative flow cytometry plots showing co-expression patterns between CD69 and multiple markers linked to NLT T$_{RMs}$ on memory CD8+ T cells. The bar plots show all residency markers on gated CD69$^-$ (white) and CD69$^+$ (black) memory CD8+ T cells. **P* < 0.05.

Related to Fig. 2

Figure S5

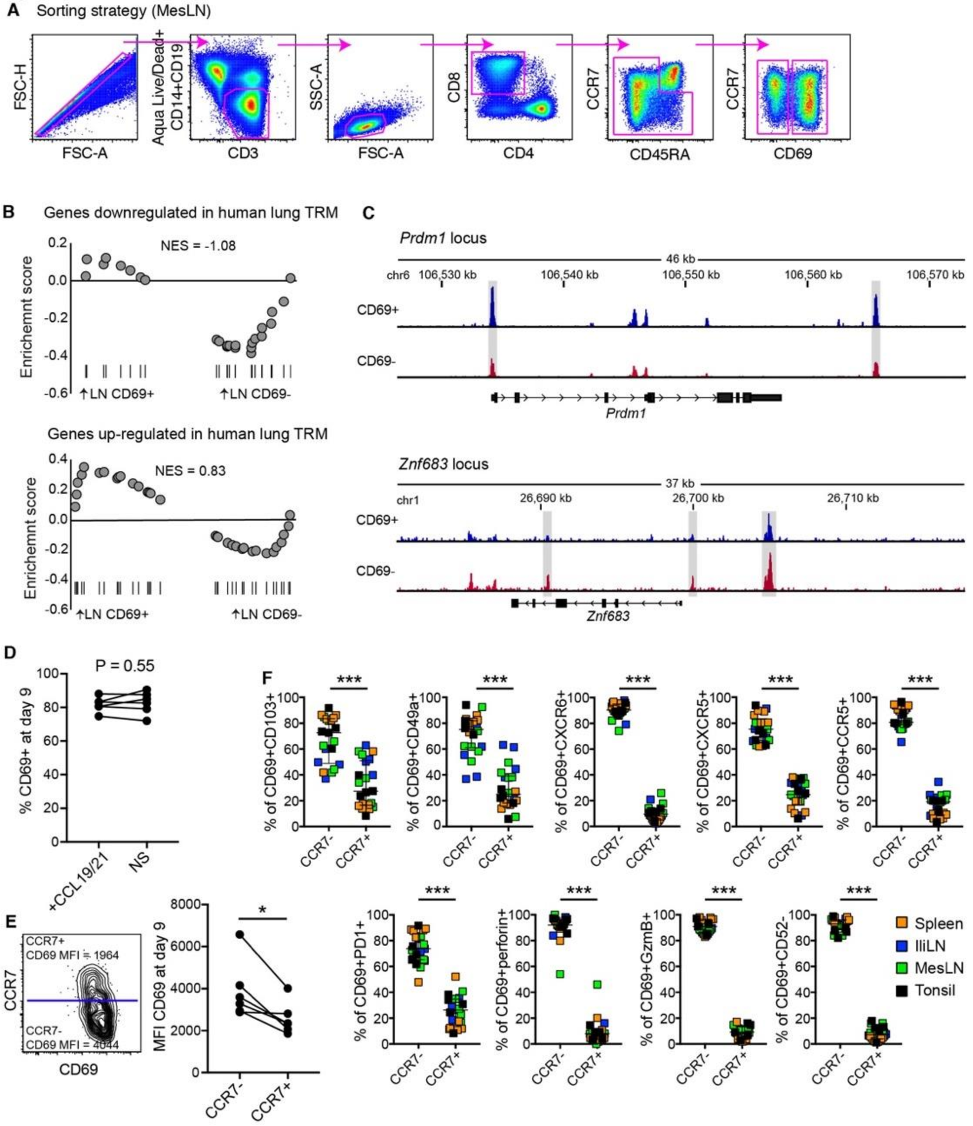

Fig. S5. RNA-seq, ATAC-seq, and CCR7 analysis of LN T_{RMs}.

(A) Gating strategy for RNA-seq and ATAC-seq sorts to acquire pure LN memory CD69$^-$ and CD69$^+$ CD8$^+$ T cell populations. **(B)** Normalized enrichment score (NES) of upregulated and downregulated gene sets from lung T_{RMs} (CD69$^+$ CD103$^+$) (*37*) in MesLN memory CD69$^-$ versus CD69$^+$ CD8$^+$ T cells. **(C)** ATAC-seq tracks for the *Prdm1 (Blimp-1)* and *Znf683 (Hobit)* locus. **(D)** Frequency of CD69 expression on sorted CD69$^+$ CD8$^+$ T cells after 9 days in culture with rhIL-7 in the presence or absence of CCL19/21. **(E)** Median fluorescence intensity **(**MFI) of CD69 expression on CCR7$^-$ and CCR7$^+$ CD69$^+$ CD8$^+$ T cells after 9 days in culture with rhIL-7. **(F)** Expression of residency and effector molecules on CCR7$^-$ and CCR7$^+$ CD69$^+$ CD8$^+$ T cells. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.

Related to Fig. 3

Figure S6

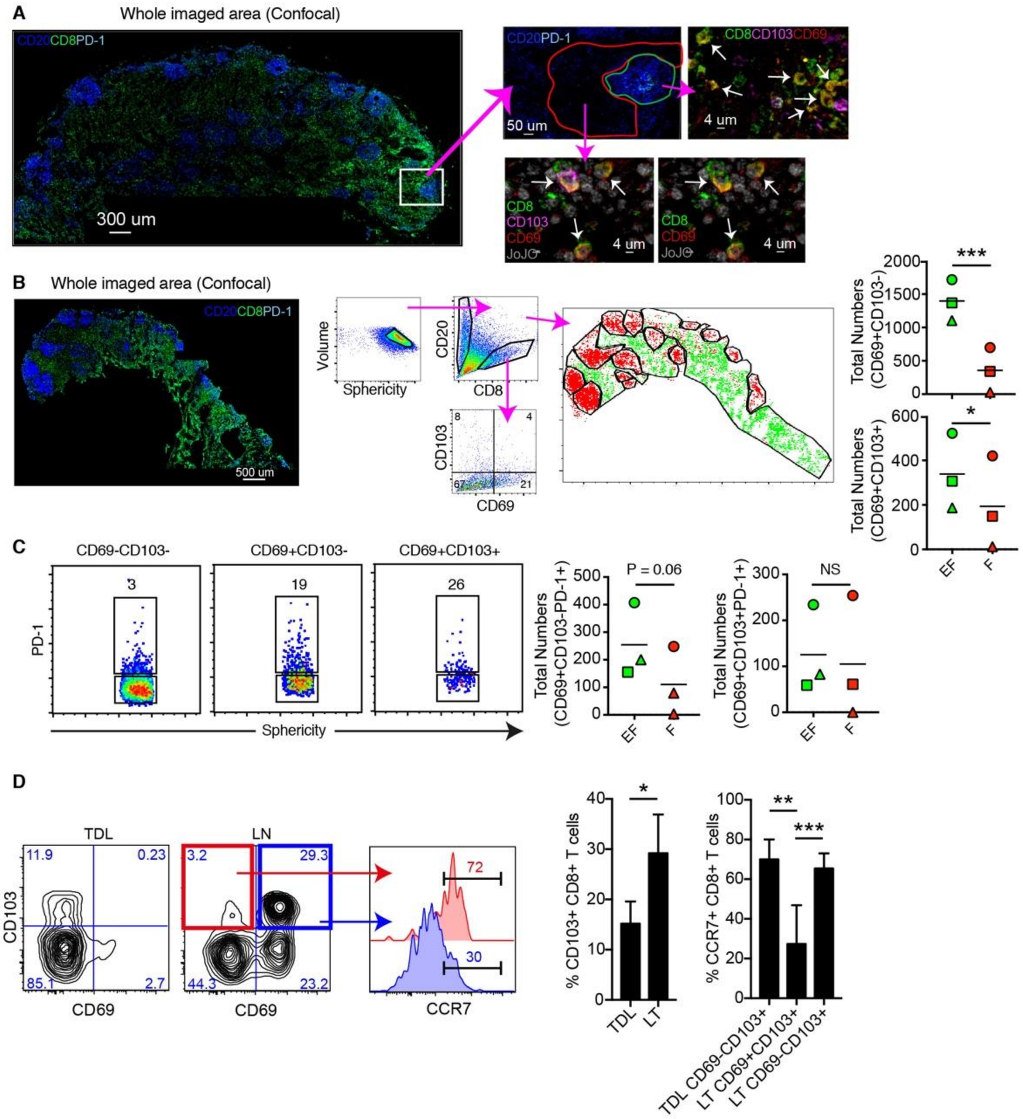

Fig. S6. Imaging analysis and CD103 expression in TDL.

(A) Whole imaged area of a mesLN from human (left) and zoomed in area (right) of a T cell zone (red) and B cell zone (green). Further zooming shows the co-expression pattern of CD8, CD103 and CD69. Cells expressing both CD69 and CD8 (yellow cells) are highlighted with the white arrows. **(B)** Whole imaged area of another mesLN (left) and subsequent histocytometry gating strategy to identify B cell follicles based on CD20 expression (red) and extra-follicular areas (green) in the whole imaged area using histocytometry (middle). Right graphs, shows the absolute numbers of CD69^{+}CD103^{-} and CD69^{+}CD103^{+} within the extra-follicular (EF) or B cell follicular (F) area for all imaged LNs. **(C)** PD-1 expression based on histocytometry for CD69^{-}CD103^{-}, CD69^{+}CD103^{-} and CD69^{+}CD103^{+} CD8^{+} cells (left). Right graphs, shows the absolute numbers of CD69^{+}CD103^{-}PD-1^{+} and CD69^{+}CD103^{+} PD-1^{+} within the extra-follicular (EF) or B cell follicular (F) area for all imaged LNs. **(D)** Conventional flow cytometry plots of CD103 *versus* CD69 on human thoracic duct lymph (TDL) and lymph node (LN) memory CD8$^+$ T cells from two unmatched subjects (left). The histogram demonstrates CCR7 expression levels on CD103$^+$CD69$^-$ (red) and CD103$^+$CD69$^+$ (blue) cells from LN CD8+ T cells. Frequency of CD103$^+$ CD8$^+$ T cells (left graph) and CCR7$^+$ of CD103$^+$CD69$^{+/-}$ CD8$^+$ T cells (right graph) in TDL (n = 7 subjects) and LTs from all subjects (n = 25) in Fig. 2A. *P < 0.05; **P < 0.01; ***P < 0.001.

Related to Fig. 4

Figure S7

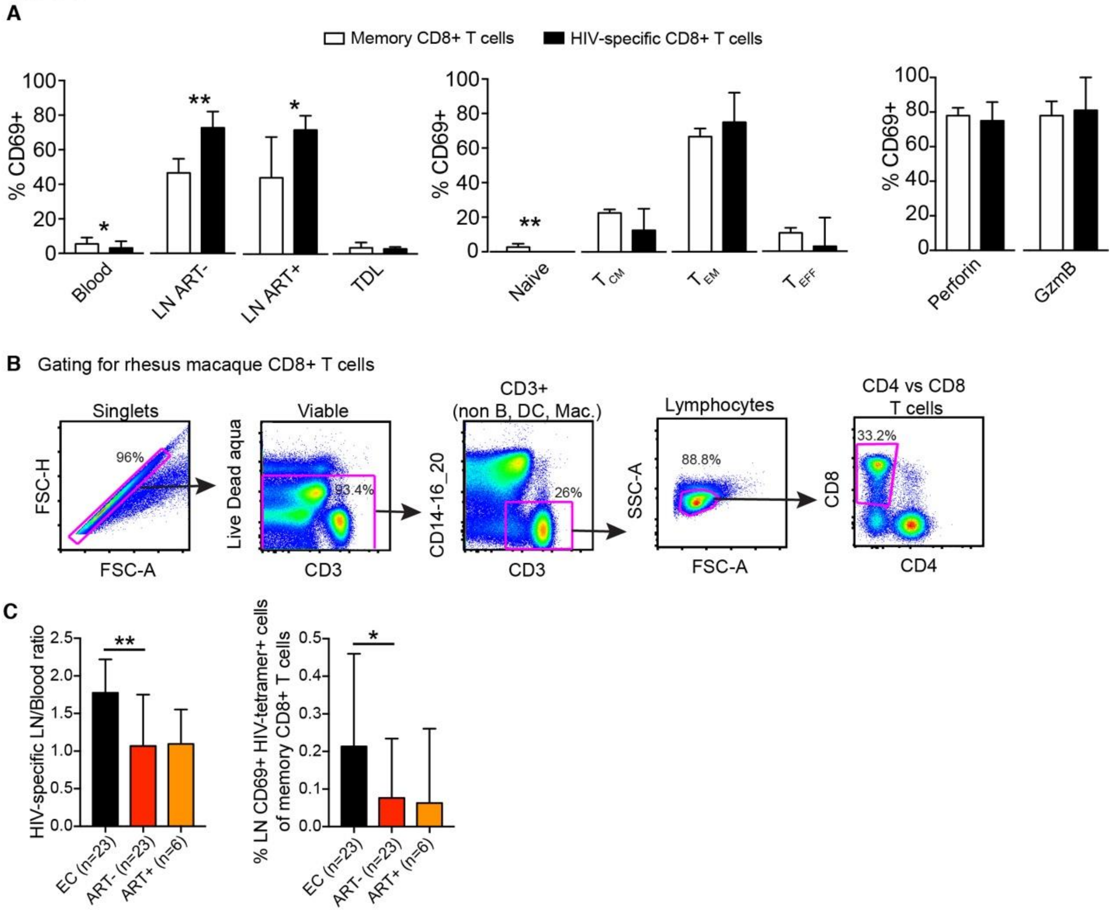

Fig. S7. Bulk and HIV-specific analysis and rhesus gating strategy.

(A) Frequency of CD69+ cells between bulk memory and HIV-specific CD8^{+} T cells (n = 17). **(B)** Gating strategy to detect total LT and blood CD8^{+} T cells for all rhesus macaque analysis. **(C)** Relative distribution of HIV-specific CD8^{+} T cells in blood and LNs from elite controllers (black), ART^{-} (red) and ART^{+} (orange) HIV^{+} subjects (left) and magnitude of LN HIV-tetramer^{+} CD69^{+} CD8^{+} T cell responses in elite controllers (black), ART^{-} (red) and ART^{+} (orange) HIV^{+} subjects. *$P < 0.05$; **$P < 0.01$.

Related to Fig. 5-7

Figure S8

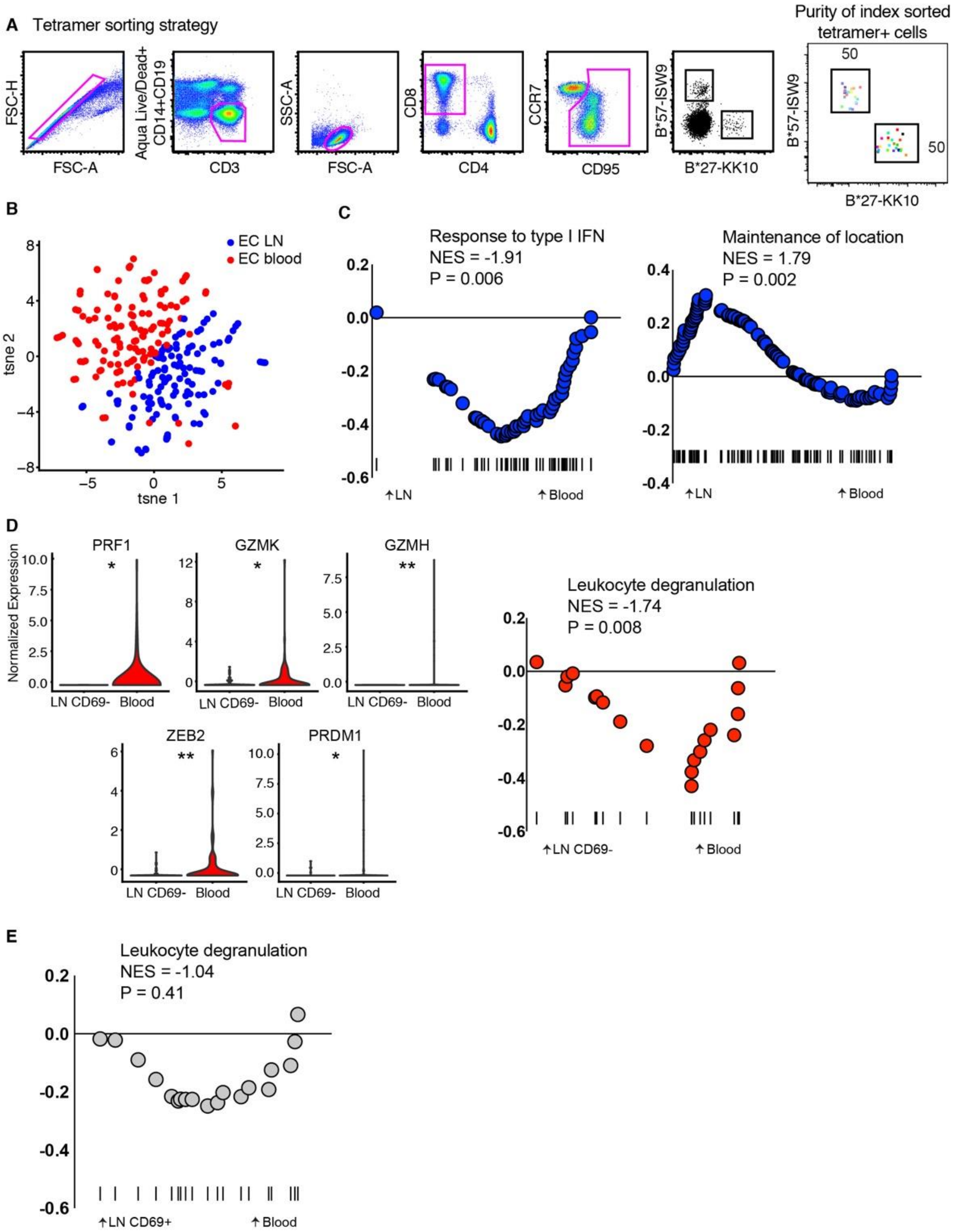

Fig. S8. Index sorting strategy and scRNA-seq analysis.

(A) Gating strategy for index sorting of LN and blood HIV-specific CD8$^+$ T cells and purity of index-sorted HIV-specific CD8$^+$ T cells. Memory cells were gated as non-CCR7^{hi} non-CD95$^-$ to include stem-cell memory T cells (T$_{SCMs}$). **(B)** tSNE plot of single HIV-specific CD8$^+$ T cells from LN (blue) and blood (red) from elite controllers (n=2). The plot is based on the top 200 significant genes differentially expressed between groups in the scRNA-seq data set. **(C)** Significant GSEAs of gene sets involved in immunological reactions and trafficking from LN versus blood HIV-specific CD8$^+$ T cells. **(D)** Violin plots and GSEAs for genes and gene sets involved in cytolytic T cell responses from LN CD69$^-$ and blood HIV-specific CD8$^+$ T cells. **(E)** Leukocyte degranulation GSEA between LN CD69$^+$ and blood HIV-specific CD8$^+$ T cells.

Related to Fig. 8

Figure S9

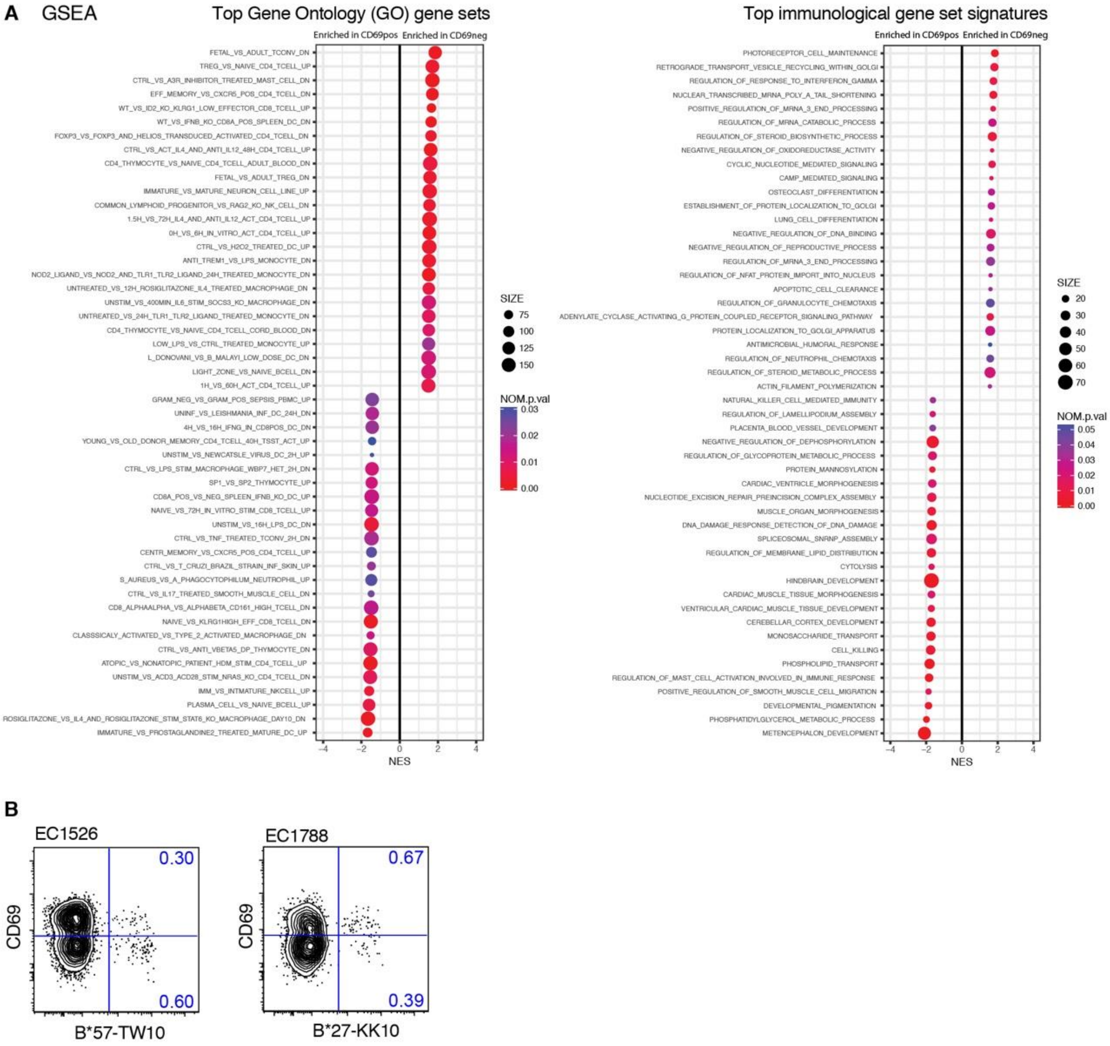

Fig. S9. scRNA-seq analysis of LN HIV-specific CD8$^+$ T cells.

(A) Gene set enrichment analysis (GSEA) between the two CD8$^+$ T cell subsets of all significantly enriched gene signatures from the Gene Ontology (GO) and Immunological Signature database. **(B)** CD69 expression on Gag-ISW9-specific CD8$^+$ T cells from subjects EC1526 and EC1788 (left).

Related to Fig. 8

Table S1. Cohort characteristics.

	HIV-	**HIV+ acute (Fiebig IV-VI)**	**HIV+ chronic ART-**	**HIV+ chronic ART+**	**HIV elite controllers**
Number of individuals	51	8	36	19	9
Sites of collection	University of Pennsylvania, Case Western Reserve University	INER-CIENI	University of Pennsylvania, INER-CIENI	University of Pennsylvania, INER-CIENI	UCSF, INER-CIENI
Types of tissues	Blood (n=11), spleen (n=8), tonsil (n=7), iliac LNs (n=7), mesenteric LNs (n=9), hepatic LNs (n=2), matched blood and TDL (n=7)	Matched blood and cervical LNs (n=8)	Matched blood and cervical LNs (n=34), matched blood and iliac LNs (n=1), matched blood and TDL (n=1)	Matched blood and cervical LNs (n=11), matched blood and TDL (n=8)	Matched blood and inguinal LNs (n=8), matched blood and cervical LNs (n=1)
Age*	N/A	23 (21-27)	29 (23-33)	29 (28-39)	49 (39-63)
CD4 count (cells/mL)*	N/A	306 (238-370)	348 (248-497)	382 (367-811)	835 (643-1111)
Viral load (copies/mL)*	0	1,996,027 (1,297,461-4,421,034)	75,043 (22,429-203,904)	<40 (<40-230,948)	<40 (<40-<40)
Log viral load*	N/A	6 (6.11-6.63)	4.90 (4.46-5.32)	<1.6 (<1.6-5.36)	<1.6 (<1.6-<1.6)

* All values = median and IQR

Table S2. List of significant genes up-regulated/down-regulated from RNA-seq.

EntrezGeneID	Gene name	FoldChange: (CD69+/CD69-)	P-value
817	CAMK2D	3.908224116	0.014685002
1647	GADD45A	3.560060748	0.02032066
1901	S1PR1	-4.881264449	0.006484687
1955	MEGF9	5.394509019	0.00441564
2043	EPHA4	-5.730196718	0.003486607
2591	GALNT3	-3.38533766	0.024087524
2595	GANC	-5.109049649	0.005448088
2635	GBP3	-6.144331082	0.002644247
2838	GPR15	2.829498872	0.042750171
2857	GPR34	-8.052667069	0.000879656
2937	GSS	3.299371014	0.026236322
3310	HSPA6	-2.802603634	0.044009595
3384	ICAM2	-3.467960182	0.02221301
3566	IL4R	-3.080580261	0.032786152
3590	IL11RA	-4.479423789	0.008952138
3638	INSIG1	9.643180989	0.000414506
3640	INSL3	-18.62786107	2.47792E-05
3678	ITGA5	-3.123653733	0.03135947
4293	MAP3K9	5.701837017	0.003555349
4515	MTCP1	-4.005162055	0.013458441
4528	MTIF2	-2.735594654	0.047335252
4616	GADD45B	-4.708224746	0.007432374
4621	MYH3	-4.029960755	0.013164347
4668	NAGA	3.982086603	0.013739089
4734	NEDD4	3.480574034	0.021942045
4913	NTHL1	-2.876456267	0.040648519
5367	PMCH	9.218949204	0.0005007
5395	PMS2	-3.276444454	0.026846467
5830	PEX5	3.690611349	0.017951726
5914	RARA	-4.639165158	0.007856213
5921	RASA1	-3.478197316	0.021992805
5932	RBBP8	-5.149195382	0.005286616
6019	RLN2	-3.003081042	0.03554561
6314	ATXN7	-4.113235185	0.01223085
6375	XCL1	3.749921904	0.016983402
6402	SELL	-9.535111395	0.000434621
6541	SLC7A1	2.867385589	0.041045131
6843	VAMP1	2.756772284	0.046254287
6877	TAF5	4.006716964	0.013439774

7433	VIPR1	-5.096113773	0.005501373
7476	WNT7A	-22.77170937	1.03749E-05
7678	ZNF124	-6.067215939	0.002780695
7692	ZNF133	-3.935841741	0.014322594
8879	SGPL1	-3.302054084	0.026165974
9046	DOK2	-3.431161944	0.02302607
9110	MTMR4	-2.727653048	0.047747983
9136	RRP9	3.798906349	0.016229682
9200	HACD1	6.661607006	0.001911444
9425	CDYL	-2.914347379	0.039038423
9531	BAG3	-2.972686453	0.036700037
9827	RGP1	3.839030605	0.015641473
9975	NR1D2	-2.809220234	0.043695885
10077	TSPAN32	-5.436404846	0.004284683
10172	ZNF256	2.814572059	0.043444003
10235	RASGRP2	-4.44346449	0.009223383
10296	MAEA	5.421206591	0.004331643
10420	TESK2	-2.703846466	0.049009886
10509	SEMA4B	-2.749827452	0.046605652
10516	FBLN5	-3.438614662	0.022858637
10527	IPO7	-3.647981906	0.018687824
10750	GRAP	-17.8684944	2.96656E-05
10802	SEC24A	2.934783594	0.038200383
11035	RIPK3	5.273344119	0.004822348
11094	CACFD1	4.146185737	0.011883241
11133	KPTN	-7.233174996	0.00136792
22821	RASA3	-3.754180925	0.01691626
22879	MON1B	2.990163224	0.036031076
23059	CLUAP1	-4.584439618	0.008212658
23312	DMXL2	-2.900650144	0.03961189
23334	SZT2	-3.403909489	0.023650609
23353	SUN1	-5.02072808	0.005824618
23368	PPP1R13B	-3.297395288	0.026288263
23400	ATP13A2	-2.883712443	0.040334395
23594	ORC6	-5.816043399	0.003288063
23643	LY96	-3.724709321	0.017387345
23708	GSPT2	-4.385570709	0.009680907
25888	ZNF473	5.330812599	0.004624078
25914	RTTN	2.894038511	0.039892145
25939	SAMHD1	-3.353722048	0.024853095
25940	FAM98A	-4.198314418	0.011356898
25945	NECTIN3	6.540180507	0.002058721

25966	C2CD2	-2.759256244	0.046129346
26048	ZNF500	-3.811938921	0.01603582
26128	KIF1BP	3.942818005	0.014232723
27018	BEX3	-5.253322034	0.004893811
27153	ZNF777	3.01660433	0.035045419
28658	TRAV25	5.417604693	0.004342863
28802	IGLV3-12	-3.678605637	0.018155538
28990	ASTE1	-3.534271691	0.020830873
29803	REPIN1	-3.508976096	0.021345924
29925	GMPPB	3.181963067	0.02954076
29933	GPR132	-2.843748289	0.042099588
29966	STRN3	-6.864850872	0.001692417
29994	BAZ2B	-4.336062621	0.01009368
30009	TBX21	2.849439052	0.041842926
50632	CALY	3.929375072	0.014406497
51274	KLF3	-2.742195066	0.046995303
51333	ZNF771	3.474397116	0.02207425
51360	MBTPS2	-3.271990435	0.026966902
51439	FAM8A1	-3.520283656	0.02111387
51651	PTRH2	3.629367272	0.01902031
53405	CLIC5	-17.47841338	3.26345E-05
54434	SSH1	3.118709863	0.031519531
54762	GRAMD1C	-8.00892208	0.000899707
54790	TET2	-5.032938802	0.005770747
54892	NCAPG2	-4.520470679	0.00865403
55170	PRMT6	2.752115998	0.046489532
55175	KLHL11	3.159454225	0.030227999
55293	UEVLD	3.222665209	0.028343391
55317	AP5S1	-4.632804491	0.007896681
55364	IMPACT	2.87430331	0.040742259
55571	CNOT11	-2.857495104	0.041482634
55609	ZNF280C	4.789894965	0.006965829
55703	POLR3B	3.081242339	0.032763664
55790	CSGALNACT1	-4.556288734	0.008403508
55825	PECR	-3.288419389	0.026525748
56478	EIF4ENIF1	3.634555437	0.018926949
56895	AGPAT4	-5.806663816	0.003309081
56899	ANKS1B	3.110524138	0.031786625
56911	MAP3K7CL	4.280098954	0.010585701
57085	AGTRAP	-5.033691843	0.005767444
57171	DOLPP1	15.1206543	6.09596E-05
57178	ZMIZ1	3.560797748	0.020306296

57205	ATP10D	3.413323627	0.023432662
57463	AMIGO1	-3.405775938	0.023607212
57496	MKL2	-2.737723214	0.047225318
57558	USP35	-2.755003435	0.046343493
59338	PLEKHA1	-4.295448366	0.010447973
64131	XYLT1	-4.29867959	0.010419252
64332	NFKBIZ	-2.734316664	0.047401396
64412	GZF1	4.324707859	0.010191276
64753	CCDC136	-3.70194973	0.017761703
64794	DDX31	3.207855909	0.028772431
65083	NOL6	-4.119352849	0.012165412
79081	LBHD1	-3.766827248	0.016718723
79567	FAM65A	-3.020038642	0.034919684
79600	TCTN1	-2.896082363	0.039805268
79711	IPO4	2.879111053	0.040533269
79803	HPS6	2.989115715	0.036070776
79862	ZNF669	4.248539928	0.010875702
80007	C10orf88	2.932124163	0.038308266
80267	EDEM3	-3.287185279	0.026558594
80833	APOL3	-2.866850698	0.041068657
81537	SGPP1	4.297787407	0.010427173
81931	ZNF93	3.569739498	0.020132956
83743	GRWD1	2.824557368	0.042978456
83888	FGFBP2	-6.287899165	0.002411117
84033	OBSCN	-2.987394385	0.036136121
84318	CCDC77	-5.410438446	0.004365289
84343	HPS3	-3.552033147	0.020477897
84766	CRACR2A	4.353692673	0.009944337
84883	AIFM2	-5.420249822	0.00433462
84969	TOX2	3.48648486	0.0218164
90673	PPP1R3E	-2.81752238	0.043305854
91151	TIGD7	3.012052957	0.035212854
91316	GUSBP11	-3.997342438	0.01355278
91351	DDX60L	-3.862521875	0.015308746
91687	CENPL	3.771207581	0.016650935
91694	LONRF1	3.104954376	0.031969855
93624	TADA2B	-3.324737811	0.025579902
113655	MFSD3	-3.102174541	0.032061759
114625	ERMAP	-5.047077805	0.005709111
116447	TOP1MT	3.828594895	0.01579201
116988	AGAP3	-3.255765825	0.027410942
117145	THEM4	-2.702224979	0.049097201

124044	SPATA2L	3.104789473	0.031975298
127544	RNF19B	4.585589255	0.008204974
128346	C1orf162	-4.018304231	0.013301629
132720	C4orf32	-2.890907921	0.040025635
143888	KDELC2	3.754465861	0.016911779
145864	HAPLN3	-3.983865603	0.013717208
147699	PPM1N	-7.037835905	0.001529568
153241	CEP120	3.704289107	0.017722791
153733	CCDC112	-3.092348268	0.032389076
158399	ZNF483	-2.756944249	0.046245625
158584	FAAH2	-3.901089179	0.014780379
161823	ADAL	-3.385809628	0.024076305
200933	FBXO45	-2.795143316	0.044366388
219844	HYLS1	-3.150308162	0.030512512
221322	TBC1D32	-4.154645011	0.011795895
222658	KCTD20	-3.218192393	0.028472188
223082	ZNRF2	2.885160089	0.040272058
252969	NEIL2	7.141260497	0.001441259
257101	ZNF683	-4.030256135	0.01316089
283377	SPRYD4	31.61993425	2.48814E-06
285540	SEPSECS-AS1	8.39060885	0.000741756
286437	#N/A	-2.733954151	0.047420177
339559	ZFP69	-2.692504819	0.049624325
339745	SPOPL	-2.763694181	0.045907074
342926	ZNF677	3.254295093	0.02745161
348654	GEN1	-3.144011028	0.030710199
374879	ZNF699	-3.058829154	0.033534932
374928	ZNF773	2.73611856	0.047308167
400073	C12orf76	-3.193391611	0.029198747
401612	SLC25A53	-5.228297503	0.004984924
646719	NIPBL-AS1	-5.137879022	0.005331544
729218	#N/A	2.898097571	0.039719821
100505746	ITGB2-AS1	-4.257817581	0.010789481
101927156	#N/A	-3.616007022	0.019263219
101929206	#N/A	-9.410939969	0.000459224
102606465	#N/A	-3.846535704	0.015534255
102724316	SVIL-AS1	2.965450085	0.036981187
104472713	PCAT29	4.623094132	0.007958942
105221694	BISPR	-2.893490813	0.039915462
105369174	#N/A	4.851368907	0.006637611

Table S3. List of significant ATAC-seq tracks.

	Gene	chr	start	end	log2FoldChange	pvalue
1	peakid_21109	chr2	9843224	9843819	2.25688	9.37E-21
2	peakid_4785	chr10	30024049	30025123	1.97059	1.11E-18
3	peakid_16122	chr17	2717797	2718710	2.05739	2.67E-18
4	peakid_7993	chr11	104034585	104035258	-1.46203	1.06E-15
5	peakid_28754	chr3	148727321	148728016	-1.24072	7.14E-14
6	peakid_18526	chr18	42686277	42686822	-1.79287	1.96E-12
7	peakid_31835	chr5	64317419	64317830	-1.98829	2.69E-12
8	peakid_39896	chr8	128990012	128990455	-1.40952	4.03E-11
9	peakid_10065	chr12	92270614	92271419	-0.89183	8.55E-11
10	peakid_30726	chr4	122175089	122176089	-1.15378	8.00E-11
11	peakid_16129	chr17	2952044	2952640	1.60056	1.35E-10
12	peakid_4783	chr10	29970587	29971319	1.76158	1.68E-10
13	peakid_1917	chr1	101178436	101179133	-1.12081	3.82E-10
14	peakid_34636	chr6	45553998	45554978	1.65793	5.49E-10
15	peakid_9855	chr12	68553214	68553926	-1.22141	7.23E-10
16	peakid_21485	chr2	36467492	36468247	-1.15202	6.46E-10
17	peakid_27840	chr3	67998272	67998988	1.47267	7.25E-10
18	peakid_23606	chr2	197107037	197107534	-1.25941	8.41E-10
19	peakid_34981	chr6	96947489	96948162	1.20211	8.24E-10
20	peakid_5149	chr10	64440985	64441601	-0.98448	1.01E-09
21	peakid_35043	chr6	106094052	106094844	-1.12729	1.09E-09
22	peakid_11574	chr13	80973552	80974400	-1.47944	1.44E-09
23	peakid_39636	chr8	105677412	105678221	-1.88020	1.87E-09
24	peakid_14705	chr16	2317743	2319015	1.04699	2.22E-09
25	peakid_6701	chr11	14599877	14600582	-1.06258	2.40E-09
26	peakid_28162	chr3	108524931	108525734	-0.94326	2.64E-09
27	peakid_40309	chr9	5558205	5558667	1.81780	2.68E-09
28	peakid_4782	chr10	29947892	29948432	1.35075	3.00E-09
29	peakid_21489	chr2	36582578	36583803	-0.88714	3.93E-09
30	peakid_14758	chr16	3184651	3185379	1.14190	4.08E-09
31	peakid_1740	chr1	91590480	91591006	-1.71857	4.25E-09
32	peakid_11187	chr13	41885031	41886212	-0.76656	5.38E-09
33	peakid_10888	chr13	22688671	22689250	-1.01598	5.64E-09
34	peakid_21064	chr2	7884983	7885436	-1.31965	6.61E-09
35	peakid_14634	chr16	729776	730616	1.13928	6.95E-09
36	peakid_10103	chr12	92987323	92988264	-0.80839	7.89E-09
37	peakid_41831	chr9	139257466	139258501	1.13982	8.12E-09
38	peakid_35626	chr6	138132503	138132973	-1.11406	8.47E-09
39	peakid_39635	chr8	105600974	105601790	-1.51729	9.29E-09
40	peakid_31566	chr5	40378487	40379012	-1.36044	1.01E-08

41	peakid_18517	chr18	42280625	42281012	-1.46001	1.13E-08
42	peakid_19740	chr19	17112514	17113106	1.51444	1.39E-08
43	peakid_3299	chr1	198136450	198137110	-1.00014	1.50E-08
44	peakid_4275	chr10	3846500	3847002	-1.18223	1.58E-08
45	peakid_26755	chr22	50945903	50947063	0.98160	1.56E-08
46	peakid_28200	chr3	111327286	111327633	-1.44460	1.53E-08
47	peakid_27062	chr3	18720792	18721214	-1.43252	1.67E-08
48	peakid_366	chr1	15850631	15851837	0.79840	1.83E-08
49	peakid_5153	chr10	64492598	64493196	-0.96747	1.94E-08
50	peakid_35397	chr6	130005118	130005567	-1.12424	2.05E-08
51	peakid_35618	chr6	138036718	138037391	-1.01536	2.07E-08
52	peakid_29269	chr3	187778901	187779478	-1.30268	2.63E-08
53	peakid_28203	chr3	111334972	111335818	-0.75819	2.98E-08
54	peakid_41591	chr9	131418742	131419493	1.26780	3.52E-08
55	peakid_29276	chr3	188057230	188058031	-1.18035	4.36E-08
56	peakid_27141	chr3	28367803	28368565	-0.87833	4.56E-08
57	peakid_34300	chr6	33377856	33379136	0.80888	4.90E-08
58	peakid_40907	chr9	84304288	84305106	-1.33202	5.25E-08
59	peakid_13861	chr15	60095735	60096384	1.67270	6.04E-08
60	peakid_1627	chr1	85464665	85465083	-0.98301	6.32E-08
61	peakid_28176	chr3	109525648	109526274	-0.91181	6.58E-08
62	peakid_2987	chr1	172668261	172668793	-1.05554	7.00E-08
63	peakid_20273	chr19	41256212	41257292	0.97391	6.99E-08
64	peakid_41838	chr9	139377210	139378643	0.85332	7.68E-08
65	peakid_14702	chr16	2264617	2265486	0.88774	8.11E-08
66	peakid_7996	chr11	104524041	104524573	-1.33087	8.46E-08
67	peakid_6707	chr11	14912598	14914129	-0.62929	9.45E-08
68	peakid_20852	chr19	54693161	54695323	0.66780	9.50E-08
69	peakid_32882	chr5	142166464	142166864	-1.30564	9.27E-08
70	peakid_17933	chr17	76356061	76356637	1.23503	9.79E-08
71	peakid_35590	chr6	137355042	137355461	-1.05326	1.03E-07
72	peakid_28175	chr3	109523600	109524026	-1.13097	1.08E-07
73	peakid_15150	chr16	29816594	29817464	1.02325	1.27E-07
74	peakid_2591	chr1	155292919	155294512	0.85675	1.40E-07
75	peakid_12496	chr14	64194272	64195205	-0.81034	1.39E-07
76	peakid_20351	chr19	42787490	42788813	0.80131	1.46E-07
77	peakid_1949	chr1	101804297	101804753	-1.49897	1.51E-07
78	peakid_26576	chr22	42475281	42476294	0.89327	1.52E-07
79	peakid_35600	chr6	137579277	137579632	-1.68464	1.58E-07
80	peakid_20161	chr19	38806350	38807029	1.00248	1.60E-07
81	peakid_23364	chr2	177796527	177797060	-1.17125	1.64E-07
82	peakid_19396	chr19	9902311	9903832	0.87051	1.75E-07

83	peakid_20443	chr19	45681264	45682425	0.76355	1.76E-07
84	peakid_2980	chr1	172608072	172608908	-0.85476	1.94E-07
85	peakid_31929	chr5	71530082	71530578	-1.10329	1.92E-07
86	peakid_11310	chr13	48611561	48612494	-0.65756	2.04E-07
87	peakid_41586	chr9	131218053	131219379	0.84487	2.02E-07
88	peakid_10097	chr12	92855657	92856327	-1.13904	2.20E-07
89	peakid_15941	chr16	88700167	88701540	0.93979	2.24E-07
90	peakid_14623	chr16	638962	640366	0.73197	2.37E-07
91	peakid_28251	chr3	112395682	112396107	-1.01421	2.43E-07
92	peakid_3624	chr1	207999201	207999659	-0.99828	2.47E-07
93	peakid_29678	chr4	10956320	10956827	-1.30364	2.50E-07
94	peakid_7762	chr11	81580423	81581497	-0.56637	2.56E-07
95	peakid_23201	chr2	169964157	169964752	-0.87366	2.59E-07
96	peakid_18984	chr19	796890	797670	0.93352	2.75E-07
97	peakid_39939	chr8	131080462	131081233	-0.94636	2.77E-07
98	peakid_18029	chr17	79818156	79819425	0.72803	2.81E-07
99	peakid_24128	chr2	231742168	231742990	-0.95327	3.10E-07
100	peakid_39426	chr8	91479748	91480366	-0.91349	3.14E-07
101	peakid_18544	chr18	43518408	43518996	-1.33955	3.49E-07
102	peakid_9865	chr12	68725796	68726623	-0.71742	3.62E-07
103	peakid_5146	chr10	64391800	64392584	-1.00616	3.73E-07
104	peakid_5714	chr10	98431137	98431636	-1.60890	3.82E-07
105	peakid_28261	chr3	112709525	112710519	-0.68037	3.98E-07
106	peakid_18021	chr17	79519056	79520609	1.04306	4.02E-07
107	peakid_12492	chr14	64009637	64010629	-0.67794	4.30E-07
108	peakid_4292	chr10	4003337	4003765	-1.07665	4.43E-07
109	peakid_14701	chr16	2255249	2256063	1.04381	4.45E-07
110	peakid_24678	chr20	19421794	19422209	-1.64368	4.49E-07
111	peakid_27001	chr3	16327573	16328103	-1.07342	4.50E-07
112	peakid_6352	chr11	506344	507704	0.88528	4.75E-07
113	peakid_11155	chr13	40962721	40963646	-0.75366	4.72E-07
114	peakid_31757	chr5	55354265	55355226	-1.49937	4.82E-07
115	peakid_40356	chr9	7976196	7976928	-0.72070	4.86E-07
116	peakid_14782	chr16	3930005	3931268	0.94936	5.36E-07
117	peakid_1895	chr1	100731321	100732180	-0.67020	5.70E-07
118	peakid_19727	chr19	16652897	16653773	1.04691	5.67E-07
119	peakid_20724	chr19	50379803	50381531	0.69134	5.66E-07
120	peakid_11305	chr13	47325831	47326520	-0.99964	5.92E-07
121	peakid_15218	chr16	30933644	30934938	0.70716	6.04E-07
122	peakid_7455	chr11	66233812	66234947	0.86753	6.24E-07
123	peakid_20497	chr19	46389028	46390332	0.97440	6.22E-07
124	peakid_20246	chr19	40696649	40697738	1.02702	6.41E-07

125	peakid_22903	chr2	144019533	144020357	-1.01839	6.77E-07
126	peakid_19716	chr19	16435142	16436113	0.81186	6.90E-07
127	peakid_26475	chr22	39715377	39716064	1.10542	7.10E-07
128	peakid_17874	chr17	75136379	75137393	0.84355	7.19E-07
129	peakid_32326	chr5	106822070	106822641	-0.99010	7.36E-07
130	peakid_17093	chr17	42295822	42296799	0.91418	7.48E-07
131	peakid_29807	chr4	26874844	26875488	-0.86736	7.50E-07
132	peakid_7355	chr11	64851335	64852160	1.18756	7.56E-07
133	peakid_11388	chr13	51250726	51251116	-1.47433	8.43E-07
134	peakid_14689	chr16	2041974	2042707	1.02655	8.67E-07
135	peakid_40908	chr9	84429812	84430390	-1.49027	8.64E-07
136	peakid_25885	chr21	45431852	45433043	0.87859	8.86E-07
137	peakid_1509	chr1	67798686	67799231	-1.17146	9.06E-07
138	peakid_18846	chr18	72040692	72041166	-0.87208	9.17E-07
139	peakid_29081	chr3	177370467	177371143	-1.28014	9.11E-07
140	peakid_19128	chr19	2950342	2951164	1.07186	9.25E-07
141	peakid_15958	chr16	88877739	88878952	0.93265	9.38E-07
142	peakid_6597	chr11	10319996	10320304	-1.08175	9.58E-07
143	peakid_9856	chr12	68557454	68557792	-1.57091	9.51E-07
144	peakid_19734	chr19	16738811	16739602	0.93689	9.66E-07
145	peakid_39191	chr8	66868026	66868355	-1.35339	9.80E-07
146	peakid_7472	chr11	66610396	66611333	0.93506	9.97E-07
147	peakid_7333	chr11	64512393	64512956	1.26304	1.04E-06
148	peakid_27037	chr3	17192985	17193784	-0.77345	1.05E-06
149	peakid_26743	chr22	50708494	50709238	1.15872	1.12E-06
150	peakid_35745	chr6	143718236	143719106	-0.81288	1.13E-06
151	peakid_12587	chr14	69201003	69201582	-1.32937	1.14E-06
152	peakid_19207	chr19	4342650	4343854	0.80044	1.21E-06
153	peakid_39899	chr8	129005079	129005852	-0.84936	1.22E-06
154	peakid_16340	chr17	8286320	8287283	0.95021	1.25E-06
155	peakid_19067	chr19	1855365	1855788	1.36598	1.25E-06
156	peakid_27580	chr3	49711081	49712030	0.74003	1.27E-06
157	peakid_32735	chr5	137794980	137795404	-1.07614	1.27E-06
158	peakid_42569	chrX	78514560	78515057	-1.01563	1.27E-06
159	peakid_824	chr1	32109987	32111096	0.89724	1.32E-06
160	peakid_16121	chr17	2699396	2699886	1.49752	1.30E-06
161	peakid_21554	chr2	38894025	38894723	-0.90295	1.32E-06
162	peakid_39678	chr8	116660324	116660912	-0.75110	1.31E-06
163	peakid_39863	chr8	126954109	126954923	-0.78576	1.35E-06
164	peakid_18363	chr18	20811244	20811795	-0.76136	1.37E-06
165	peakid_22939	chr2	145265921	145266212	-1.25932	1.39E-06
166	peakid_40862	chr9	79192569	79193144	-1.17584	1.39E-06

167	peakid_12515	chr14	65006951	65007604	-0.67921	1.42E-06
168	peakid_16253	chr17	7145716	7146634	1.02862	1.46E-06
169	peakid_26020	chr22	19434814	19435654	0.85898	1.48E-06
170	peakid_36490	chr7	13889631	13890196	-0.78850	1.49E-06
171	peakid_96	chr1	2517747	2518684	0.84151	1.50E-06
172	peakid_30787	chr4	124398936	124399470	-1.29353	1.55E-06
173	peakid_26170	chr22	24950812	24952101	0.71242	1.62E-06
174	peakid_3329	chr1	198648752	198649256	-0.92254	1.64E-06
175	peakid_16126	chr17	2756598	2757285	1.55787	1.67E-06
176	peakid_31591	chr5	40675719	40676364	-1.05739	1.67E-06
177	peakid_7248	chr11	62494378	62495823	0.76991	1.70E-06
178	peakid_2657	chr1	156736759	156737764	0.78342	1.71E-06
179	peakid_27318	chr3	39309158	39309818	1.17218	1.75E-06
180	peakid_18519	chr18	42309747	42310181	-1.11746	1.83E-06
181	peakid_3381	chr1	200857303	200857859	-0.92837	1.86E-06
182	peakid_36825	chr7	36824400	36824969	-0.92959	1.85E-06
183	peakid_1360	chr1	58857796	58858277	-1.38979	1.88E-06
184	peakid_39837	chr8	126010249	126011115	-0.59801	1.87E-06
185	peakid_38938	chr8	38795797	38796538	-0.77886	1.91E-06
186	peakid_4114	chr1	239750330	239750870	-1.21622	2.00E-06
187	peakid_7406	chr11	65419870	65420740	0.98129	2.11E-06
188	peakid_14531	chr15	98503442	98504149	-1.11956	2.12E-06
189	peakid_9040	chr12	22562223	22563279	-0.66971	2.13E-06
190	peakid_10201	chr12	96839534	96840433	-0.77880	2.25E-06
191	peakid_21486	chr2	36473488	36473942	-1.07908	2.30E-06
192	peakid_41574	chr9	130922148	130922817	1.00599	2.30E-06
193	peakid_20907	chr19	56825784	56827031	0.94493	2.37E-06
194	peakid_30646	chr4	114468529	114469168	-0.70781	2.47E-06
195	peakid_10066	chr12	92271737	92272058	-1.07697	2.49E-06
196	peakid_110	chr1	3541049	3542029	0.82137	2.65E-06
197	peakid_41647	chr9	132565114	132566021	1.01954	2.70E-06
198	peakid_39825	chr8	125649703	125650308	-0.81431	2.72E-06
199	peakid_7523	chr11	67572574	67573906	0.82484	2.76E-06
200	peakid_42590	chrX	82889918	82890647	-0.72090	2.75E-06
201	peakid_41695	chr9	134248565	134249314	0.87730	2.85E-06
202	peakid_1693	chr1	89738020	89738954	-0.86256	2.89E-06
203	peakid_1767	chr1	92781366	92782048	-0.92504	2.91E-06
204	peakid_1929	chr1	101414804	101415613	-0.86551	2.87E-06
205	peakid_19058	chr19	1651817	1653331	0.87280	2.91E-06
206	peakid_677	chr1	26946705	26948093	0.89201	3.03E-06
207	peakid_31044	chr4	154730336	154730979	-1.19982	3.04E-06
208	peakid_5045	chr10	52268087	52268604	-1.06918	3.11E-06

209	peakid_30791	chr4	124538102	124538537	-1.11756	3.11E-06
210	peakid_11331	chr13	49106443	49107442	-0.60381	3.14E-06
211	peakid_2654	chr1	156710536	156711391	0.83583	3.26E-06
212	peakid_16196	chr17	4851250	4852787	0.91725	3.30E-06
213	peakid_14658	chr16	1358756	1359966	0.88503	3.42E-06
214	peakid_4296	chr10	4276802	4277383	-1.04665	3.54E-06
215	peakid_7440	chr11	66034886	66036312	0.77842	3.59E-06
216	peakid_20121	chr19	36705232	36706274	0.88749	3.58E-06
217	peakid_21062	chr2	7865433	7866120	-0.96594	3.65E-06
218	peakid_14714	chr16	2563439	2564510	0.87742	3.83E-06
219	peakid_23535	chr2	191980106	191980900	-0.92494	3.82E-06
220	peakid_29203	chr3	185826744	185827412	-0.72809	3.84E-06
221	peakid_14160	chr15	75074161	75074984	0.93536	3.87E-06
222	peakid_2641	chr1	156474692	156475437	0.91658	3.91E-06
223	peakid_9858	chr12	68574814	68575449	-1.22183	4.06E-06
224	peakid_24381	chr2	242576024	242577461	0.92667	4.06E-06
225	peakid_795	chr1	31190782	31191951	0.64083	4.11E-06
226	peakid_11059	chr13	31318333	31318933	-0.75150	4.12E-06
227	peakid_2875	chr1	167486768	167487261	-0.95955	4.19E-06
228	peakid_20142	chr19	37808234	37809129	0.87119	4.21E-06
229	peakid_35038	chr6	105906959	105907459	-1.13051	4.22E-06
230	peakid_12415	chr14	60618490	60618893	-0.98535	4.34E-06
231	peakid_29875	chr4	38655970	38656328	1.49837	4.44E-06
232	peakid_19349	chr19	7985008	7986098	0.89241	4.50E-06
233	peakid_20131	chr19	37263459	37264250	1.21078	4.49E-06
234	peakid_26412	chr22	38141842	38142552	0.90920	4.56E-06
235	peakid_14726	chr16	2826842	2827751	1.04018	4.62E-06
236	peakid_21514	chr2	37571667	37572555	-0.85303	4.66E-06
237	peakid_1948	chr1	101774853	101775900	-0.61269	4.72E-06
238	peakid_20975	chr19	58986959	58987879	0.76856	4.72E-06
239	peakid_19470	chr19	10981466	10982600	0.68656	4.81E-06
240	peakid_41835	chr9	139304795	139305332	1.11391	4.82E-06
241	peakid_19473	chr19	11071146	11072133	0.85005	4.96E-06
242	peakid_35379	chr6	128293020	128293731	-0.80111	4.95E-06
243	peakid_20849	chr19	54640650	54641658	0.63245	5.04E-06
244	peakid_775	chr1	28994974	28995829	0.99560	5.17E-06
245	peakid_10337	chr12	107421362	107421854	-1.37637	5.14E-06
246	peakid_15202	chr16	30669139	30670825	0.62990	5.09E-06
247	peakid_26042	chr22	20104472	20105412	0.85350	5.11E-06
248	peakid_29479	chr4	1241882	1243503	0.72866	5.16E-06
249	peakid_39102	chr8	59703319	59704000	-1.12708	5.24E-06
250	peakid_22925	chr2	145140432	145140970	-0.85789	5.34E-06

251	peakid_1320	chr1	54411054	54412403	0.63236	5.37E-06
252	peakid_32325	chr5	106812461	106813002	-1.00513	5.51E-06
253	peakid_9281	chr12	46608844	46609325	-0.87153	5.57E-06
254	peakid_18019	chr17	79481678	79482245	0.97086	5.68E-06
255	peakid_20344	chr19	42746539	42747604	0.67577	5.67E-06
256	peakid_20693	chr19	50003945	50004694	0.85039	5.80E-06
257	peakid_2984	chr1	172639623	172640325	-0.95779	5.94E-06
258	peakid_11158	chr13	41059760	41060373	-0.68208	6.05E-06
259	peakid_20115	chr19	36544845	36546029	0.73541	6.06E-06
260	peakid_30769	chr4	123653350	123654238	-0.49774	6.05E-06
261	peakid_3335	chr1	198757715	198758211	-1.16362	6.15E-06
262	peakid_6364	chr11	694833	696165	0.60543	6.17E-06
263	peakid_34307	chr6	33538620	33539429	0.82644	6.17E-06
264	peakid_28107	chr3	105787561	105788051	-1.20484	6.30E-06
265	peakid_20705	chr19	50094333	50094877	1.18120	6.42E-06
266	peakid_21530	chr2	37875639	37876167	-1.09643	6.49E-06
267	peakid_35025	chr6	102293540	102293985	-1.17970	6.50E-06
268	peakid_19068	chr19	1863466	1864545	0.68300	6.55E-06
269	peakid_20072	chr19	35759316	35759959	1.24331	6.58E-06
270	peakid_26467	chr22	39541382	39542244	0.93812	6.72E-06
271	peakid_27166	chr3	30686085	30686617	-0.99589	6.71E-06
272	peakid_7252	chr11	62538545	62539408	0.93778	6.75E-06
273	peakid_4789	chr10	30315901	30316705	-0.62003	6.81E-06
274	peakid_58	chr1	1709691	1710716	0.87266	6.92E-06
275	peakid_7430	chr11	65769547	65770435	0.85168	6.90E-06
276	peakid_7826	chr11	86511215	86511835	1.31656	7.04E-06
277	peakid_66	chr1	1981406	1982274	0.80600	7.21E-06
278	peakid_2981	chr1	172616152	172616709	-1.11488	7.32E-06
279	peakid_182	chr1	6844430	6846143	0.56767	7.52E-06
280	peakid_16182	chr17	4613311	4614227	0.70101	7.51E-06
281	peakid_34214	chr6	31633276	31634016	0.87629	7.55E-06
282	peakid_8324	chr11	122619756	122620036	-1.35303	7.80E-06
283	peakid_29866	chr4	38312054	38312597	-0.73614	7.81E-06
284	peakid_5595	chr10	90923244	90923988	-0.90521	7.87E-06
285	peakid_11291	chr13	46869729	46870709	-0.66274	8.03E-06
286	peakid_9864	chr12	68683953	68684426	-1.24671	8.09E-06
287	peakid_30302	chr4	83826539	83826776	-1.36961	8.35E-06
288	peakid_27741	chr3	58101840	58102324	1.35559	8.46E-06
289	peakid_26308	chr22	32366578	32367066	1.16425	8.57E-06
290	peakid_9853	chr12	68513511	68514132	-1.02269	8.66E-06
291	peakid_7425	chr11	65686233	65687504	0.74732	8.84E-06
292	peakid_4969	chr10	44806005	44806898	-0.87825	8.90E-06

293	peakid_14772	chr16	3507567	3508412	0.89881	8.94E-06
294	peakid_23600	chr2	197075881	197076622	-0.81727	9.00E-06
295	peakid_28165	chr3	108554003	108554374	-0.98400	8.97E-06
296	peakid_26021	chr22	19466576	19467590	0.75905	9.07E-06
297	peakid_489	chr1	21112834	21114173	0.72659	9.14E-06
298	peakid_18039	chr17	79934967	79936020	0.90716	9.20E-06
299	peakid_16458	chr17	17267004	17267468	1.44418	9.38E-06
300	peakid_17846	chr17	74497077	74497865	0.89655	9.60E-06
301	peakid_12176	chr14	39698238	39698884	-0.81833	9.70E-06
302	peakid_41573	chr9	130889736	130890995	0.76193	9.98E-06
303	peakid_10071	chr12	92424304	92424922	-0.80797	1.01E-05
304	peakid_28206	chr3	111393010	111393922	-0.53508	1.01E-05
305	peakid_1149	chr1	44678932	44679528	1.18971	1.04E-05
306	peakid_30790	chr4	124520988	124521562	-0.96744	1.05E-05
307	peakid_8830	chr12	10059459	10059926	-1.08361	1.05E-05
308	peakid_10063	chr12	92245945	92246294	-1.34595	1.06E-05
309	peakid_24866	chr20	32580839	32582139	0.67611	1.07E-05
310	peakid_6672	chr11	13689605	13690840	-0.52004	1.08E-05
311	peakid_6692	chr11	14402531	14403160	-1.08225	1.08E-05
312	peakid_25430	chr20	62289571	62290198	1.08619	1.09E-05
313	peakid_26016	chr22	19165777	19166723	0.81337	1.10E-05
314	peakid_121	chr1	3816426	3817783	0.66611	1.14E-05
315	peakid_1894	chr1	100714846	100715782	-0.57425	1.15E-05
316	peakid_7921	chr11	95890100	95890772	-1.05628	1.14E-05
317	peakid_15171	chr16	30194573	30195866	0.92462	1.13E-05
318	peakid_26600	chr22	43044924	43045861	0.92429	1.15E-05
319	peakid_20431	chr19	45542058	45542920	0.99820	1.17E-05
320	peakid_7242	chr11	62432247	62433071	0.92863	1.17E-05
321	peakid_11329	chr13	49079249	49080204	-0.93969	1.18E-05
322	peakid_15117	chr16	28833899	28834738	0.87499	1.19E-05
323	peakid_20291	chr19	41768914	41770462	0.63440	1.19E-05
324	peakid_33804	chr6	16320063	16320724	-0.91353	1.23E-05
325	peakid_7256	chr11	62598967	62599916	0.74277	1.24E-05
326	peakid_4412	chr10	8374064	8374828	-0.66869	1.25E-05
327	peakid_14681	chr16	1876161	1877415	0.80555	1.26E-05
328	peakid_20971	chr19	58919611	58920413	0.86883	1.25E-05
329	peakid_23073	chr2	160001673	160002201	-1.19156	1.26E-05
330	peakid_41785	chr9	136932671	136933976	0.80110	1.26E-05
331	peakid_18067	chr17	80408390	80408983	0.97048	1.27E-05
332	peakid_2983	chr1	172631718	172632367	-0.75815	1.29E-05
333	peakid_11585	chr13	84660052	84661224	-0.81537	1.30E-05
334	peakid_39984	chr8	134151061	134151596	-0.93544	1.32E-05

335	peakid_7516	chr11	67396834	67398408	0.74956	1.33E-05
336	peakid_9547	chr12	53773148	53774747	0.56404	1.34E-05
337	peakid_14691	chr16	2059435	2060115	0.97447	1.35E-05
338	peakid_14822	chr16	4783910	4785196	0.83223	1.34E-05
339	peakid_16216	chr17	5389282	5390356	0.82945	1.35E-05
340	peakid_40176	chr8	145159076	145160032	0.71898	1.34E-05
341	peakid_1560	chr1	77747428	77748398	1.26621	1.36E-05
342	peakid_41746	chr9	135996322	135997118	0.85451	1.38E-05
343	peakid_21595	chr2	42360037	42360784	-0.69493	1.39E-05
344	peakid_38037	chr7	138560464	138561065	-0.86467	1.40E-05
345	peakid_16982	chr17	39844683	39845970	0.66768	1.43E-05
346	peakid_10151	chr12	94638469	94639066	-0.97950	1.45E-05
347	peakid_28336	chr3	118753176	118754079	-0.93215	1.45E-05
348	peakid_7254	chr11	62559226	62559754	1.08904	1.47E-05
349	peakid_19622	chr19	14116505	14117939	0.69277	1.49E-05
350	peakid_14725	chr16	2802076	2803168	0.81461	1.49E-05
351	peakid_7237	chr11	62379669	62380847	0.75361	1.50E-05
352	peakid_7999	chr11	104576260	104577013	-0.61125	1.53E-05
353	peakid_26039	chr22	20067287	20068305	0.82921	1.54E-05
354	peakid_34936	chr6	90662145	90663000	-0.75721	1.55E-05
355	peakid_7360	chr11	64884911	64885552	0.82541	1.55E-05
356	peakid_41818	chr9	138799099	138800030	0.73485	1.57E-05
357	peakid_37326	chr7	87228722	87229051	-1.21624	1.60E-05
358	peakid_22807	chr2	133033282	133033653	-0.98616	1.62E-05
359	peakid_2982	chr1	172628062	172628473	-1.06074	1.64E-05
360	peakid_15237	chr16	31190941	31192310	0.85673	1.63E-05
361	peakid_15772	chr16	81557992	81558433	-1.08621	1.63E-05
362	peakid_18138	chr18	2963155	2963458	-1.16657	1.64E-05
363	peakid_20426	chr19	45457962	45458899	0.91446	1.63E-05
364	peakid_367	chr1	15852977	15853657	0.75867	1.72E-05
365	peakid_16006	chr16	89789069	89789446	1.20029	1.73E-05
366	peakid_17783	chr17	73401443	73402141	0.97162	1.74E-05
367	peakid_5581	chr10	90595245	90595815	-0.75370	1.75E-05
368	peakid_19184	chr19	3970858	3971540	0.96825	1.76E-05
369	peakid_40134	chr8	144650807	144651873	0.79076	1.76E-05
370	peakid_20319	chr19	42363565	42364574	0.78076	1.77E-05
371	peakid_11223	chr13	42979884	42980923	-0.85520	1.78E-05
372	peakid_34	chr1	1209013	1209779	0.92203	1.80E-05
373	peakid_5599	chr10	91011156	91012094	-0.52758	1.80E-05
374	peakid_18368	chr18	20886866	20887281	-1.17494	1.83E-05
375	peakid_15974	chr16	89283794	89284356	1.08089	1.83E-05
376	peakid_15163	chr16	30006577	30007782	0.81606	1.87E-05

377	peakid_6377	chr11	805047	805630	0.99589	1.88E-05
378	peakid_7235	chr11	62368760	62369749	0.77324	1.88E-05
379	peakid_15234	chr16	31153410	31154295	0.68536	1.89E-05
380	peakid_27193	chr3	32155841	32156909	-0.65549	1.90E-05
381	peakid_20403	chr19	44617297	44617823	1.04006	1.93E-05
382	peakid_29980	chr4	47533442	47534173	-0.76142	1.93E-05
383	peakid_4276	chr10	3847464	3847813	-1.02675	1.94E-05
384	peakid_11353	chr13	50017908	50018822	-0.50966	2.01E-05
385	peakid_26715	chr22	50311665	50312558	0.79374	2.02E-05
386	peakid_20029	chr19	34760862	34761542	1.29003	2.02E-05
387	peakid_5164	chr10	64615909	64616268	-1.29751	2.04E-05
388	peakid_7317	chr11	64072404	64073318	0.70339	2.03E-05
389	peakid_14832	chr16	5147557	5148841	0.68244	2.06E-05
390	peakid_20687	chr19	49972227	49972831	0.92571	2.08E-05
391	peakid_19342	chr19	7894361	7895341	0.65469	2.09E-05
392	peakid_7576	chr11	71497618	71498804	0.66633	2.10E-05
393	peakid_3302	chr1	198157126	198157849	-0.74475	2.11E-05
394	peakid_14621	chr16	577095	578024	0.71996	2.12E-05
395	peakid_7946	chr11	101785420	101786288	-0.50498	2.13E-05
396	peakid_26443	chr22	38966001	38966729	0.92620	2.14E-05
397	peakid_35	chr1	1243127	1244273	0.72700	2.16E-05
398	peakid_19279	chr19	6393076	6393984	0.87030	2.16E-05
399	peakid_28249	chr3	112362611	112363399	-1.07551	2.15E-05
400	peakid_34294	chr6	33285310	33286089	0.89864	2.16E-05
401	peakid_19191	chr19	4065223	4066245	0.73384	2.19E-05
402	peakid_32280	chr5	100003042	100003468	-1.18038	2.21E-05
403	peakid_27055	chr3	18486124	18487386	-0.56441	2.22E-05
404	peakid_29830	chr4	36280470	36280811	-1.33094	2.24E-05
405	peakid_40793	chr9	74397916	74398642	-0.64569	2.24E-05
406	peakid_20743	chr19	50887070	50887836	0.83549	2.25E-05
407	peakid_1776	chr1	92950132	92950594	-0.80355	2.28E-05
408	peakid_2287	chr1	144935433	144935793	-0.90093	2.29E-05
409	peakid_10079	chr12	92539116	92540371	-0.47289	2.29E-05
410	peakid_31881	chr5	67535302	67535913	-0.80181	2.29E-05
411	peakid_26749	chr22	50781263	50781990	0.89494	2.32E-05
412	peakid_3313	chr1	198533637	198534285	-1.10424	2.33E-05
413	peakid_18159	chr18	3297040	3297827	-0.74034	2.36E-05
414	peakid_20333	chr19	42497891	42498710	1.07396	2.36E-05
415	peakid_26540	chr22	41777157	41778448	0.67355	2.35E-05
416	peakid_16110	chr17	2295784	2297479	0.62387	2.39E-05
417	peakid_39669	chr8	116230838	116231651	-0.55095	2.38E-05
418	peakid_11716	chr13	100086474	100087181	-0.62924	2.40E-05

419	peakid_19275	chr19	6279723	6280477	0.80184	2.41E-05
420	peakid_17657	chr17	65821296	65822480	0.78527	2.50E-05
421	peakid_20874	chr19	55769883	55770982	0.78279	2.52E-05
422	peakid_23438	chr2	182321332	182322308	-0.69198	2.53E-05
423	peakid_21672	chr2	46666710	46667172	-1.05812	2.55E-05
424	peakid_29254	chr3	187520777	187521073	-1.27630	2.56E-05
425	peakid_29501	chr4	1872034	1873472	0.71780	2.58E-05
426	peakid_10950	chr13	26475813	26476222	-0.90855	2.63E-05
427	peakid_39978	chr8	134080748	134081185	-0.86974	2.64E-05
428	peakid_19146	chr19	3185274	3186375	0.84538	2.65E-05
429	peakid_25930	chr21	46644322	46644861	1.16444	2.66E-05
430	peakid_39848	chr8	126540961	126541565	-0.78851	2.67E-05
431	peakid_19410	chr19	10196668	10197205	0.90060	2.69E-05
432	peakid_35256	chr6	117803389	117804286	-0.59751	2.70E-05
433	peakid_39871	chr8	127568704	127569264	-0.82869	2.73E-05
434	peakid_2653	chr1	156697957	156699028	0.72011	2.77E-05
435	peakid_176	chr1	6673186	6674090	0.64829	2.80E-05
436	peakid_6047	chr10	115802962	115803995	-0.96622	2.79E-05
437	peakid_12087	chr14	31596947	31597376	-0.98013	2.80E-05
438	peakid_14676	chr16	1755758	1756618	0.87479	2.80E-05
439	peakid_15126	chr16	28961787	28962540	0.74217	2.89E-05
440	peakid_31565	chr5	40361609	40361893	-1.16258	2.89E-05
441	peakid_7314	chr11	64051985	64053551	0.70721	2.91E-05
442	peakid_25070	chr20	43513895	43514870	0.68186	2.90E-05
443	peakid_3262	chr1	194258630	194259190	-0.82010	2.93E-05
444	peakid_1783	chr1	93050052	93050368	-1.16305	2.93E-05
445	peakid_31713	chr5	54039875	54040625	-0.85406	2.95E-05
446	peakid_2656	chr1	156721073	156721962	0.83049	2.97E-05
447	peakid_1713	chr1	90098140	90099285	-0.56779	2.99E-05
448	peakid_18030	chr17	79828761	79829732	0.87674	2.98E-05
449	peakid_27578	chr3	49591547	49592388	0.89137	3.03E-05
450	peakid_9879	chr12	69004208	69005229	-0.64458	3.07E-05
451	peakid_12318	chr14	53385083	53385678	-0.89326	3.14E-05
452	peakid_40181	chr8	145514859	145515537	0.83865	3.14E-05
453	peakid_840	chr1	32403175	32404423	0.69412	3.16E-05
454	peakid_18975	chr19	610622	611584	1.07259	3.23E-05
455	peakid_20764	chr19	51611429	51612134	0.84857	3.26E-05
456	peakid_20093	chr19	36207787	36209165	0.64930	3.28E-05
457	peakid_81	chr1	2246027	2246967	0.92322	3.32E-05
458	peakid_15203	chr16	30709254	30710586	0.69501	3.34E-05
459	peakid_7362	chr11	64901816	64902840	0.83916	3.34E-05
460	peakid_13439	chr15	31657920	31658460	-0.80056	3.36E-05

461	peakid_36448	chr7	8165351	8166148	-0.62300	3.39E-05
462	peakid_39965	chr8	133772529	133773250	-0.85531	3.43E-05
463	peakid_28837	chr3	152016645	152017452	-0.81555	3.44E-05
464	peakid_12844	chr14	88461448	88461777	-1.02217	3.46E-05
465	peakid_13798	chr15	55513436	55514231	-1.00148	3.46E-05
466	peakid_2089	chr1	111991227	111992320	0.77567	3.48E-05
467	peakid_30724	chr4	122148532	122149081	-0.93279	3.47E-05
468	peakid_2505	chr1	153918185	153919431	0.79745	3.49E-05
469	peakid_32425	chr5	114505218	114506201	-0.63655	3.49E-05
470	peakid_35051	chr6	106533855	106534489	-0.75489	3.53E-05
471	peakid_16331	chr17	8113675	8114262	1.15987	3.56E-05
472	peakid_16613	chr17	26988664	26989529	0.87095	3.58E-05
473	peakid_17754	chr17	72868907	72869774	0.73966	3.58E-05
474	peakid_22716	chr2	122456897	122457637	-0.70627	3.57E-05
475	peakid_31945	chr5	72608370	72608772	-1.08866	3.58E-05
476	peakid_37366	chr7	92033195	92033906	-1.14699	3.57E-05
477	peakid_12223	chr14	50465961	50466339	-0.85628	3.63E-05
478	peakid_15939	chr16	88636348	88637234	0.89615	3.64E-05
479	peakid_19871	chr19	19431111	19431916	0.74883	3.64E-05
480	peakid_19434	chr19	10491042	10491757	0.75593	3.66E-05
481	peakid_29062	chr3	176917062	176917397	-0.98448	3.71E-05
482	peakid_12437	chr14	61746964	61748256	-0.67175	3.73E-05
483	peakid_23544	chr2	192071272	192071965	-0.71255	3.77E-05
484	peakid_17168	chr17	44270156	44271778	0.72678	3.82E-05
485	peakid_14675	chr16	1727930	1728683	0.76605	3.84E-05
486	peakid_19105	chr19	2475725	2476264	1.01335	3.84E-05
487	peakid_41541	chr9	130547356	130548542	0.66511	3.84E-05
488	peakid_27822	chr3	66633058	66633696	-0.80498	3.94E-05
489	peakid_16285	chr17	7517765	7518890	0.63023	3.99E-05
490	peakid_15622	chr16	70414877	70415792	0.70164	4.01E-05
491	peakid_8441	chr11	128194098	128195114	-0.71247	4.02E-05
492	peakid_14995	chr16	21512748	21514065	0.56580	4.09E-05
493	peakid_15159	chr16	29911280	29912016	1.09075	4.10E-05
494	peakid_9950	chr12	75874372	75874911	-0.65318	4.16E-05
495	peakid_26248	chr22	30162730	30163638	0.74997	4.20E-05
496	peakid_41612	chr9	131872818	131873890	0.72422	4.21E-05
497	peakid_20733	chr19	50528375	50529535	0.71484	4.24E-05
498	peakid_25399	chr20	61568809	61569967	0.74302	4.23E-05
499	peakid_7305	chr11	63993316	63993973	0.97043	4.31E-05
500	peakid_11576	chr13	81052139	81052637	-1.21496	4.31E-05

Table S4. List of top 200 significant genes up-regulated/down-regulated from scRNA-seq.

Gene name	Log FC: (LN/Blood)	P-value
TUBAP2	0.649504	0.000014
CFL1P2	-0.652373	0.000017
CD3D	0.60613	0.000046
HLA-DPB1	-0.610531	0.000053
HLA-E	-0.577799	0.000127
ANKLE2	0.546936	0.000223
CFL1	-0.549949	0.000259
FTH1	-0.544579	0.000297
AC022210.1	-0.54436	0.000299
TUBA1B	0.534247	0.000316
AC006483.1	0.530684	0.000347
IL32	0.529765	0.000356
LGALS1	0.506563	0.000638
TCEA1	-0.513658	0.00064
LMAN2	-0.512158	0.000664
C16orf54	-0.498763	0.000928
NOA1	0.488268	0.001015
PIP4K2A	-0.491602	0.001101
COX7A2L	-0.491267	0.00111
S100A11	0.484015	0.001128
CD8B	-0.486164	0.001249
MRPL52	-0.483101	0.001345
PHF3	-0.482516	0.001363
YIF1A	0.472704	0.001482
HDAC4	-0.473711	0.001678
SECISBP2	-0.469252	0.001859
CA5B	-0.46786	0.00192
AC005840.1	-0.461978	0.002202
CST7	-0.45949	0.002332
HNRNPA3P5	0.452534	0.002397
BHLHE40	-0.457094	0.002457
RPL30	-0.454698	0.002592
AF111169.1	-0.450351	0.002875
H3F3C	0.443112	0.002994
PRPF40A	-0.447788	0.003052
SOAT1	-0.443248	0.003383
C1orf174	-0.438552	0.003761
DENND2D	-0.436145	0.003967

UBC	0.429209	0.004124
RARRES3	-0.434219	0.004139
ATP6V1G1	-0.433918	0.004165
SPPL2A	-0.432567	0.00429
NSA2	-0.431998	0.004355
TRAF3IP3	-0.430648	0.004508
EIF3E	-0.429584	0.004615
ITSN2	-0.429546	0.00462
TRBV5-4	0.424132	0.004658
NEIL2	-0.425758	0.005029
PUM2	-0.425562	0.005048
RPS20P14	-0.424577	0.005162
HAUS1	-0.423996	0.005223
DUSP1	-0.421739	0.00549
OTUD7B	-0.421546	0.005512
SLC41A2	0.416575	0.005525
ELMSAN1	0.416422	0.005545
XPO4	0.416014	0.0056
RPL27A	-0.420202	0.005681
TRBV5-3	0.413615	0.005911
KMT2A	-0.418024	0.005966
ABCD4	-0.415755	0.006278
ENOX2	0.409979	0.006423
LINC00649	0.409374	0.006508
NFKBIB	0.408637	0.006615
MYO1G	0.406597	0.006927
CPSF1	-0.408685	0.007313
DDX5	0.403803	0.007369
AC245595.1	-0.406289	0.007709
USP48	-0.405684	0.007809
SRSF6	0.399556	0.00808
DPP6	-0.402798	0.008294
MRPL10	-0.40232	0.008377
RPL3P4	-0.402044	0.008434
SCMH1	0.396677	0.008605
SNRPGP10	0.396611	0.008618
RPSAP8	0.39638	0.008659
EVI2A	-0.398966	0.008985
LCP2	-0.397969	0.009203
AP001086.1	0.393541	0.00923
CDK5RAP2	-0.396647	0.009474
LSP1	-0.396429	0.009517

RSL1D1	0.391656	0.009614
TRBV5-5	0.387882	0.01042
BZW1P1	0.387207	0.010564
FCRL5	-0.390431	0.010776
RREB1	-0.390349	0.010792
AL591721.1	0.385604	0.010917
CAP1P2	-0.389121	0.011066
CUL4A	0.384363	0.011208
CHMP3	0.38181	0.011827
PYM1	-0.385409	0.011955
CHD1L	-0.38197	0.012965
AL355309.1	-0.381331	0.01314
MRPL50	-0.381327	0.013141
ERICH6-AS1	0.377227	0.013171
ZYX	-0.380448	0.013369
AC078777.1	0.375668	0.013602
EIF2D	-0.379566	0.013613
KIAA1671	0.374895	0.013829
CLPX	0.373675	0.014188
CDS2	-0.376705	0.014442
TRAV1-2	0.372753	0.014461
TRBV5-6	0.371646	0.014813
TTN	-0.37515	0.014918
CHIC2	-0.374285	0.015187
ATP5I	0.370176	0.015266
BLMH	-0.373481	0.015425
FCN1	-0.372613	0.0157
RAD21	-0.371824	0.015962
ADAR	0.367929	0.015995
EPHB6	0.367784	0.016044
HSPA8P11	0.367492	0.016179
TM9SF1	-0.370333	0.016515
PAXX	-0.370088	0.016602
RPL31P63	-0.368899	0.017052
ST6GALNAC6	-0.367843	0.017429
TRAF5	-0.366821	0.01779
C8orf33	0.361402	0.01841
DCAF11	-0.364722	0.018528
VPS33B	-0.364398	0.018658
PAK1IP1	0.359013	0.019342
MT-TM	-0.362384	0.019429
PDK1	-0.36138	0.019815

FYCO1	0.357252	0.020036
FRA10AC1	-0.360689	0.02008
CEP128	0.355627	0.02072
RPS19P1	-0.358492	0.020968
ZMAT1	-0.357904	0.021195
CLPTM1	-0.357449	0.021366
AC012236.1	0.353639	0.021527
NCF1	0.352521	0.021993
NACA	-0.355528	0.02219
AC117382.1	-0.355453	0.022218
YWHAZ	0.35126	0.022647
GARNL3	-0.354613	0.022697
RTF1	-0.353885	0.023036
MTERF2	-0.353446	0.023254
EDRF1	-0.353312	0.02331
AIFM2	0.349076	0.02368
POTEKP	-0.352027	0.023898
AC098935.1	0.348366	0.024032
NPIPB12	-0.35147	0.024153
DOCK9	-0.350144	0.024769
AC007238.1	-0.348296	0.025613
ZNF611	-0.345046	0.027166
THAP12P7	0.341552	0.027287
SNHG6	-0.344761	0.027306
MRPL53P1	-0.344619	0.02738
STAT5A	0.341106	0.027518
TMEM231	0.338766	0.028835
MTCO3P12	-0.341462	0.029106
AC226101.1	-0.341243	0.029297
CPT2	0.337891	0.02941
RPL7AP6	0.334891	0.031113
ZNF7	-0.337911	0.031181
DARS2	0.334616	0.031276
NCF1C	0.334227	0.031497
MAP3K4	0.333725	0.031806
AC022400.8	-0.336168	0.032203
TTC4P1	-0.336067	0.032268
BRWD3	0.332722	0.032411
RSBN1L	-0.335697	0.032479
RPL7P10	-0.335433	0.032625
ERBIN	0.33228	0.032669
DDAH2	-0.333658	0.033728

CNOT6LP1	0.330241	0.033965
MON1B	-0.333005	0.03415
PNPLA7	0.329018	0.034958
FAM122A	0.327539	0.036231
HMGA1P2	0.327343	0.036385
RPS24	-0.329456	0.037036
AC025198.1	0.325874	0.03747
ENSA	0.325594	0.037671
AC126755.1	0.325325	0.037875
PHKG1	0.324816	0.038253
RPS12	-0.324691	0.040483
PTMAP5	-0.323598	0.041311
TSC22D1	0.319371	0.042367
FGFRL1	-0.322117	0.042449
RGPD6	0.318964	0.042686
PTEN	0.316831	0.044417
C6orf62	0.315987	0.045152
DNM1P46	-0.318702	0.045213
AL031056.1	0.315844	0.045268
ETV3L	0.315467	0.0456
DEPDC5	-0.318043	0.045777
MTRNR2L8	0.3136	0.047182
MT-RNR2	0.312105	0.048664
TM2D1	-0.31279	0.050505
ANK3	-0.309967	0.053062
SNHG5	-0.308995	0.053929
LINC02536	-0.306197	0.056814
ENOSF1	-0.304954	0.058262
CCL5	-0.304714	0.058516
CFAP161	-0.30337	0.059945
HECTD4	-0.302914	0.060438
IFT52	-0.301805	0.06163
SLC36A3	-0.298066	0.065721
SNRPD2	-0.293977	0.070485
SCARNA7	-0.293105	0.071565
ABHD11	-0.292269	0.072551