"Public T cell receptors confer high-avidity CD4 responses to HIV controllers"

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1- SUPPLEMENTAL DISCUSSION

Public clonotype occurrence should statistically be an extremely rare event, given the huge number of TCRs that can be generated by V(D)J recombination (>10^{15}) and the extensive genetic diversity observed in human TCR repertoires, with an estimated >10^{7} distinct clonotypes per individual (1). However, public clonotypes have been described in several chronic viral infections of humans, especially those caused by members of the herpesviridae family (1-4). CD8 public clonotypes specific for conserved regions of Gag have also been identified in the context of Controlled HIV-1 infection, particularly in patients expressing the protective alleles HLA-B57 and B27 (5-7), though they can also be detected in patients carrying non-protective HLA-B alleles (8). Recent findings indicate that the frequency of HIV-specific public clonotypes correlates with the magnitude of the CD8 response, suggesting an important contribution to antiviral efficacy (8). Whether CD8 public clonotypes are generally more abundant in controlled rather than progressive HIV infection remains debated (9, 10), but it has become clear that the particular set of CD8 public clonotypes present in controllers is more efficient at suppressing viral replication and at recognizing viral escape mutants than that of progressor patients (7, 11). A high frequency of Gag-specific CD8 public clonotypes has also been associated with a favorable outcome in the SIVmac model, in primary infection as well as post-vaccination (12). The finding that the Gag-specific CD4 repertoire of controllers is more biased than the corresponding CD8 repertoire and is enriched in highly efficient public clonotypes supports the notion that public clonotypes contribute to HIV/SIV control. A reason for the advantage conferred by public clonotypes in the antiviral response may lie in their intrinsically high frequency. Analyses of the naive TCR repertoire have shown that public clonotypes, which are by definition shared by several individuals, are also present at significantly higher frequencies than private clonotypes in the naive repertoire of each individual (13). The presence of a larger pool of naive T cells ready to respond to a given pathogen is thought to trigger a more rapid initiation of the immune response, which can provide a key advantage to limit viral dissemination at an early stage. This advantage may be particularly critical in the cases of viruses such as HIV and SIV, which can induce a massive CD4+ T cell depletion and ensuing immunosuppression during the first week of infection (14). In effect, abundant public clonotypes endowed with efficient functions may act as a rapid antiviral response force, similar to populations of innate cells expressing conserved TCRs, such as iNKT or MAIT cells (15, 16).

The high prevalence of Gag293 public clonotypes may result from a high probability of being generated during V(D)J recombination. The most prevalent TRAV24 public clonotype, AFKAAGNKLTF, could be simply generated from germline sequences by limited nucleotide trimming, without requiring N/P mutations. In addition, 72% the 36 Gag293 specific public clonotypes were encoded by more than one nucleotide CDR3 sequence, compatible with the notion of convergent recombination (17). Interestingly, a study of the preimmune CD4+ T cell repertoire in healthy individuals identified several clones reactive with HIV antigens, including one that responded to Gag293 with high antigen sensitivity (18), supporting the idea that high-avidity Gag293-specific precursors may be comparatively abundant in the naive repertoire. Another reason for the high prevalence of Gag293-specific public clonotypes may lie in their extensive HLA cross-restriction. The Gag293 peptide shows promiscuous binding to at least 14 HLA-DR and DQ

allomorphs, enabling multiple possibilities for cross-restriction (19-21). Functional analyses indicated that the F24 TCR bound at least 5 distinct Gag293-MHC II complexes, with an efficient recognition of DR1, DR11, DR15, DRB5, and a limited but consistent recognition of DR7. The correlation between the degree of cross-restriction and the antigen sensitivity of the 8 TCRs tested suggests that broad HLA cross-restriction is a characteristic of high-affinity TCRs, which may better tolerate punctual MHC polymorphisms. This notion is supported by a study of human CD4 responses to JC virus, where HLA II cross-restricted clones showed higher antigen sensitivity and greater *in vivo* expansion than clones with a more narrow restriction (22). Widespread cross-restriction may help explain why HLA II allele frequencies are not strongly biased in carriers of chronic viral infections. HIV controllers show a highly significant enrichment for protective HLA I alleles, while biases in HLA II allele distribution have been reported but appear less prominent (21, 23, 24). Considering the evidence for broad HLA II cross-restriction of HIV-specific public TCRs, the limited HLA II biases in the controller population does not rule out a significant contribution of CD4+ T cells to HIV control.

2- SUPPLEMENTAL MATERIALS AND METHODS

Antibodies

The following antibodies were used for membrane or intracellular staining: CD8-AlexaFluor488 (AF488, clone RPA-T8), CD3-eFluor® 780-Allophycocyanin (eF780-APC, clone UCHT1), TCR-Allophycocyanin (APC, clone IP26) and IL-2-APC (clone MQ1-17H12) (all from eBioscience); CD4 BD Horizon™ R-phycoerythrin-CF594 (PE-CF594, clone RPA-T4), CD4-R-phycoerythrin-cyanine 7 (PE-Cy7, clone SK3), CD69-R-phycoerythrin (PE, clone FN50), CD107a-AlexaFluor700 (AF700, clone H4A3), Perforin-AF488 (clone δG9), IFNγ-PE-Cy7 (clone B27), MIP1β-PE (clone D21-1351) (all from BD Biosciences); CD14-Viogreen (clone TÜK4), and CD19-VioGreen (clone LT19) (from Miltenyi Biotec); TRBV2-PE (clone IMMU 546, Beckman Coulter); CD14-Brilliant Violet 510™ (BV510, clone M5E2), and CD19-BV510 (clone HIB19), CD8-Brilliant Violet 785™ (BV785, clone RPA-T8), HLA-DR-PE-Cy7 (clone LN3), CD45RA-Brilliant Violet 421™ (BV421, clone HI100), CCR7-PE-Cy7 (clone G043H7), and TNFα-BV421 (clone MAb11) (all from Biolegend). The fixable viability dye eFluor® 506 (eF506, eBioscience) was added to restrict the analysis to live cells.

Cell culture

Transformed cell lines: The mutant Jurkat cell line J76, which lacks endogenous TCR expression, was provided by Dr Mirjam Heemskerk (Leids Universitair Medisch Centrum, The Netherlands) (25). J76 cells were maintained in RPMI 1640 medium supplemented with100 ug/ml penicillin/streptomycin, 1% Hepes buffer, and 2 mM L-glutamine (complete RPMI) in the presence of 10% fetal bovine serum (FBS). Murine fibroblasts (L cells) stably transfected to express a single human HLA-DR allele (DR1, DR3, DR4, DR7, DR11, DR15, or DRB5) were used as antigen presenting cells (26). L cells were maintained in complete RMPI supplemented with 10% FBS and 1% Non-Essential Amino Acids (Life Technologies).

Primary cells: Peripheral blood mononuclear cells (PBMC) were isolated from heparinized blood via density gradient centrifugation on Ficoll-Paque PLUS (GE Healthcare Life Sciences) and were either cryopreserved or used freshly for the preparation of monocyte derived dendritic cells (MDDC). The latter were obtained by positive selection of CD14+ monocytes using magnetic Microbeads (Miltenyi Biotec). Monocytes were plated at $2x10^6$ cells per mL in synthetic AIM-V medium (Life Technologies) supplemented with 10 ng/mL GM-CSF and 20 ng/mL IL-4 (both from Miltenyi Biotec) and incubated for 5-7 days at 37°C in a 5% CO2 incubator. Differentiated immature MDDC were collected and cryopreserved until further use.

Primary CD4+ T cell lines: The 20-mer Gag293 peptide (FRD YVD RFY KTL RAE QAS QE), spanning amino acids 293 to 312 in HIV-1 HXB2 Gag, was used in highly purified form (>99% pure; Proteogenix SAS) to stimulate Gag-specific CD4+ T cell lines. PBMCs from HIV-1 infected patients were plated at

$2x10^6$ cells per well in 24-well plates in the presence of decreasing amount of Gag293 peptide (10^{-5}M to 10^{-11}M) in complete RPMI supplemented with 10% human AB serum, 0.5 μM AZT, 5 nM Saquinavir and 5 ng/ml recombinant IL-7 (Cytheris). Recombinant IL-2 (Chiron, Novartis) was added to a final concentration of 100 U/ml starting from day 2, and every 2 days afterwards. When CD4+ T cell lines reached doubling time (observed number of cells = 2 x number of input cells), they were tested for Gag293 specificity by IFN-γ ELISPOT assay, as described previously (27).

MHC class II tetramer labeling

The 20-mer Gag293 peptide (FRDYVDRFYKTLRAEQASQE), spanning amino acids 293-312 in HIV-1 HXB2 Gag, was used to stimulate Gag-specific CD4+ T cell lines, as previously described (27). Cell lines were tested for Gag293 specificity by IFN-γ ELISPOT assay and, if positive, labeled with an HLA-DR-matched Gag293-loaded tetramer and sorted.

Patients were genotyped for the HLA-DRB1 gene at a 4 digit resolution using the INNO-LiPA HLA-DRB1 Plus kit (Fujirebio). Patients were included in the study if their genotype matched at least one of the following alleles: DR1, DR11, DR15, or DRB5. APC-labeled MHC II tetramers for the DR1, DRB15, DRB5, DRB1*0301 (DR3), and DRB1*0701 (DR7) alleles were obtained through the NIH Tetramer Core Facility at Emory University, USA. HLA-DRB1*0401 (DR4) biotinylated monomers were provided by Dr Fabrice Lemaître (Institut Pasteur, Paris). DR11 biotinylated monomers were obtained through the tetramer Core laboratory of the Benaroya Research Institute (Seattle, USA). Monomers were loaded with 0.2 mg/ml peptide by incubation at 37°C for 72 h in the presence of 2.5 mg/ml n-octyl-β-D-glucopyranoside and protease inhibitors. Peptide-loaded monomers were tetramerized using APC-conjugated streptavidin (eBioscience). For each tetramer loaded with the Gag293 peptide, a corresponding control tetramer was loaded with an irrelevant peptide (either the CLIP peptide PVSKMRMATPLLMQA for the DR1, DR15, DR11 tetramers; or an Annexin II peptide DVPKWISIMTERSVPH for the DRB5 tetramer).

The MHC II tetramer labeling protocol was adapted from (28). Primary CD4+ T cells lines were incubated with 1μg MHC II tetramer/10^6 cells at a concentration ≥1 μg/mL in complete RPMI supplemented with 15% human AB serum for 90 min at 4°C. Antibodies for surface markers were added for the last 30 min of labeling, using the following combination: CD3-eF780-APC, CD4-PE-CF594, CD8-BV785, CD45RA-BV421, CCR7-PE-Cy7, CD14-VioGreen, and CD19-VioGreen. Gag293-specific tetramer-labeled (Tet+) cells were visualized in the CD3+, CD4+, CD14-, CD19-, CD8- lymphocyte gate, and were sorted using a FACSAria II cell sorter (BD Biosciences) installed in a microbiological safety cabinet. Each Gag293-tetramer labeled sample was matched with a control-tetramer labeled sample processed in identical conditions. Sorted Tet+ cells were resuspended in RLT buffer (Qiagen) and kept frozen at -80°C until RNA extraction. Sorted samples that yielded a minimum of 20,000 Tet+ events were selected for clonotypic analysis. Patient PBMC were labeled ex vivo with MHC II tetramer and sorted as described above, with a

minimum of 10^7 cells labeled per sample. Sorted PBMC samples that yielded a minimum of 2,000 Tet+ events were used for clonotypic analysis.

J76 cells expressing recombinant TCRs were labeled as above, except that incubation with the MHC II tetramer was performed in complete RPMI supplemented with 15% FBS for 1h at 37°C, followed by incubation for 30 min at 4°C with the following antibody combination: CD3-eF780-APC, CD4-PE-Cy7, αβTCR-APC and eF506-viability dye. The percentage of Tet+ cells was measured in the live CD3+, CD4+ gate after acquisition on an LSR Fortessa cytometer (BD Biosciences).

TCR CDR3 length polymorphism analysis and sequencing

TCR diversity was evaluated in sorted Tet+ cell RNA by the Immunoscope technique, as previously described (2, 29). The expression of 35 TCRα variable gene (TRAV) families and of 24 TCRβ variable gene (TRBV) families was measured by quantitative RT-PCR, followed by an analysis of the length distribution of the amplified CDR3 products on a capillary sequencer. Briefly, total RNA was extracted from Tet+ cells using the RNeasy mini or micro kits (Qiagen), depending on available cell number. Next, cDNA was obtained by reverse transcription with 500μg/mL oligo (dT)17 and 200 U of Superscript II reverse transcriptase (Life technologies). A cDNA aliquot was amplified with each of 35 TRAV and 24 TRBV family-specific primers, in combination with a constant region TRAC or a TRBC primer, respectively (2, 29). Amplification was performed in the presence of a family-specific TaqMan probe on an ABI 7300 real time PCR device (Applied Biosystems). An aliquot of each PCR reaction was used as template in a run-off reaction with a nested fluorescent TRAC- or TRBC-specific primer, to generate TRAV- or TRBV-specific single stranded DNA products. These fluorescent DNA samples were separated on an ABI-PRISM 3730 DNA analyzer (Applied Biosystems) and quantified for size and intensity with the Immunoscope software. Fluorescence intensity (in arbitrary units) was plotted in function of the CDR3 length in amino acids.

PCR products corresponding to the two amplified families, TRAV24 and TRBV2, were cloned and sequenced. The primers used to amplify the full-length chains were: TRAV24 forward primer: 5'-CCG AGG CCT TGT TTG TAA TG-3'; TRAC reverse primer: 5'GTG AAT AGG CAG ACA GAC TTG T-3'; TRBV2 forward primer: 5'-GGT CCG GAA TGG ATA CCT GGC TCG TAT GCT GGG C-3'; TRBC reverse primer: 5'-CCG GTC GAC CTA GCC TCT GGA ATC CTT TCT CTT GAC C-3'. PCR products were cloned into the pCR-Blunt-II-TOPO vector (Life technologies), transformed in E. coli, and analyzed by DNA sequencing (Eurofins Genomics).

Bioinformatic analysis of the TCR clonotypic repertoire

TRA and TRB sequences were analyzed with the software suite from the International ImMunoGeneTics (IMGT) Information System (30). The V(D)J gene nomenclature used is that of the IMGT database

(www.imgt.org). Clonotypic diversity of the TRAV24 and TRBV2 repertoires was evaluated (i) by counting the number of unique amino acid clonotypes (clonotypes AA) per 100 CDR3 nucleotide sequences (ii) by computing Simpson's diversity index, using the EstimateS software version 9.1.0 (31). Simpson's diversity index takes into account both the number of clonotypes and the frequency of each clonotype in the dataset, and is maximal when all clonotypes have an equal representation. The number of N and P mutations introduced during the V(D)J recombination process was determined by comparing the observed CDR3 sequences to their germline counterparts, using the Junction analysis module of the IMGT/HighV-QUEST software (30). The distribution of TRAV, TRAJ, TRBV, TRBJ, and TRBD genes in the sequence set was computed with the statistics module of IMGT/HighV-QUEST. The CDR3 lengths corresponded to the number of a.a. comprised between, but not including, the two conserved residues C104 and F/W118, as defined by the IMGT-ONTOLOGY unique numbering system. In contrast, the "CDR3 junctions" included the conserved C104 and F/W118 residues. Kurtosis, which measures the "peakedness" of a distribution, was used to evaluate biases in CDR3 lengths. Kurtosis was measured in the Prism v6.0 software (GraphPad). A Gaussian distribution has a kurtosis of zero, while a flatter distribution has negative kurtosis, and a more "peaked" distribution has positive kurtosis.

Motifs enriched in the TRAV24 and TRBV2 CDR3 sequence sets were first identified with the MEME motif discovery software version 4.10.0 (32) available at http://meme-suite.org. The MEME software chooses the width and number of occurrence of each motif automatically in order to minimize the "E-value" of the motif, i.e. the probability of finding an equally well conserved pattern in random sequences. Motifs were searched in discriminative mode, to identify public motifs enriched in the HIC compared to the HAART dataset. Motifs were represented as sequence logos, where the relative sizes of the letters indicate their frequencies in the sequence set, and the total height of the letters represents the information content of the position, in bits. Based on the initial motif analysis, simpler public motifs included within the MEME motifs were identified and counted using the "Protein Pattern Find" module of the Sequence Manipulation Suite (33).

Analysis of soluble recombinant TCRs by surface plasmon resonance (SPR)

The affinity of the soluble TCRs for immobilized Gag293-loaded HLA-DR monomers (DR11, DRB5, and DR1) was measured by SPR. Soluble TCRs were engineered by inserting disulfide linkage between the TRAC and TRBC constant domains and truncating the transmembrane and cytoplasmic regions, as previously described (34). The soluble TCRα and TCRβ chains were expressed separately in bacteria as inclusion bodies, refolded together, and purified before surface plasmon resonance (SPR) analysis. All SPR experiments were conducted at 25°C on a BIAcore 3000 instrument in the presence of TBS buffer (10mM Tris-HCl, pH 8, 150mM NaCl and 0.005% surfactant P20). The TBS buffer was supplemented with 1% BSA to prevent non-specific binding. The pHLA-II complexes were immobilized onto a Streptadivin-coated sensor chip with 1,000-1,200 Response Unit (RU) per flow cell. A flow cell containing a pHLA-I

complex was used as negative control. Experiments were conducted as previously described (34), with a concentration range of 0.78-100 µM of pHLA-II complexes. The BIAevaluationVersion 3.1 software was used for data analysis with the 1:1 Langmuir binding model.

TCR lentivector construction

For functional studies, full-length TCRα and TCRβ chains amplified from Gag293-specific Tet+ cells were cloned into lentiviral expression vectors. Full-length TRAV24+ chains were amplified with a forward primer containing the TRAV24 leader sequence with an NheI restriction site and a Kosak sequence added in 5' (5'-CGG CTA GCC GCC ACC ATG GAG AAG AAT CCT TTG GCA GCC-3') and a reverse primer containing the 3' of TRAC and a NotI site (5'-TTA GCG GCC GCG CTG GAC CAC AGC CGC AGC G-3'). Full-length TRBV2+ chains were amplified with a forward primer containing the TRBV2 leader sequence and a BspEI site in 5' (5'- GGT CCG GAA TGG ATA CCT GGC TCG TAT GCT GGG C-3') and a reverse primer containing the 3' of TRAC and a SalI site (5'- CCG GTC GAC CTA GCC TCT GGA ATC CTT TCT CTT GAC C-3'). The TCRα and TCRβ chains were first cloned separately in the pCR-Blunt-II-TOPO vector, and then combined into the pCDH-EF1-MCS-T2A vector (SBI System Bioscience), with a self-cleaving T2A sequence inserted in between, ensuring an equimolar expression of the two chains from the same transcript. All constructs were verified by DNA sequencing.

TCR lentivector and HIV-1 pseudotype preparation

TCR lentivectors were transfected in 293T cells with Lipofectamine 3000 (Life technologies) in the presence of the pPACKH1 Packaging Plasmid Mix (SBI System Bioscience). 48h after transfection, supernatants were collected, filtered using a 0.45 µm filter, and concentrated by ultracentrifugation at 23,000 g for 90 min at 4°C on a 20% sucrose cushion. Viral particles were resuspended in PBS and frozen in aliquots at -80°C until use. Gag p24 concentration was measured with the Alliance HIV-1 p24 Antigen ELISA kit (Perkin Elmer).

Single cycle pseudotyped HIV-1 particles (ΨHIV-1) were produced by calcium phosphate transfection of 25 µg of pNL4-3-deltaEnv-EGFP (from the NIH AIDS Reagent Program) and 10 µg of pVSV-G plasmids in 293T cells. Virus-like particles (VLP) expressing Vpx were obtained similarly by co-transfection of the pSIV3+ vector (35) with pVSV-G. Viruses were harvested at 48h later and concentrated as described above.

TCR transduction

For TCR transfer, 0.5 x 10^6 J76 cells were resuspended in 0.5 mL complete RPMI medium supplemented with 10% FBS in a 24-well plate. TCR lentiviral particles (200 ng of p24) were added to each well and thoroughly resuspended by pipetting. After 3h, 0.5 mL fresh medium was added to each well. Transduced J76 cells were analyzed at day 3 by staining with CD4-PE-Cy7, TCR-APC, CD3-eF780-APC antibodies and the eF510-viability dye. Samples were acquired on an LSR Fortessa flow cytometer (BD Biosciences)

to determine TCR expression and relocalization of the CD3 complex to the cell surface as a measure of transduction efficiency.

To transfer TCRs in primary T cells, healthy donor PBMCs were pre-activated with 5 μg/mL PHA and 50 UI/mL IL-2 for 48h. PHA blasts were collected and plated at 10^5 cells/well in a 24-well plate. TCR lentiviral particles (400 ng of p24) were mixed with 5 µL Lentiblast solution A + 5 µL Lentiblast solution B (OZ Biosciences), and added to each well. Complete RPMI medium supplemented with 10% FBS and 50 UI/ mL IL-2 was added up to a volume of 0.5 mL and plates were centrifuged at 1,000 g for 1h at 32°C, before incubation o/n at 37°C. The following day, fresh medium and 50 UI/mL IL-2 were added up to a volume of 1 mL. 48 to 72h later, transduced PBMC were labeled with TRBV2-PE, CD4-PE-CF594, CD8-BV785, CD3-eF780-APC antibodies, and the eF506-viability dye. Samples analyzed by flow cytometry as above, and quantified for an increase in TRBV2 expression level in the live CD3+ CD4+ CD8- lymphocyte gate to measure transduction efficiency.

Analyses of TCR functions

J76 cell activation assay: L cells expressing a single HLA-DR allele were pulsed with serial dilutions (from 2 x 10^{-5} to 10^{-11} M) of Gag293 peptide. 5 x 10^4 TCR-transduced J76 cells and 5 x 10^4 peptide-pulsed L cells were co-cultured in a 96-well plate o/n at 37°C. On the next day, cells were labeled with CD69-PE, CD4-PE-Cy7, TCR-APC, CD3-eF780-APC antibodies and eF506-viability dye. Samples were acquired in a 96-well plate using a FACSCanto II flow cytometer and analyzed to estimate the induction of CD69 expression as a measure of J76 cell activation upon Gag293-HLA-DR recognition.

To measure J76 cell activation upon stimulation with HIV-1-derived, endogenously processed Gag proteins, MDDC were infected with single-cycle pseudotyped HIV particles (ΨHIV-1) and used as APC. ΨHIV-1 was obtained by cotransfection of the pNL4-3-deltaE-EGFP plasmid, obtained through the NIH AIDS Reagent Program from (Cat# 11100) from Drs. Haili Zhang, Yan Zhou, and Robert Siliciano (John Hopkins Hospital, Baltimore) (36), and a pVSV-G plasmid encoding the VSV envelope glycoprotein. For infection, MDDC were incubated for 3h with 50 ng p24 of ΨHIV-1 per 0.15 x 10^6 cells in presence of Vpx-containing virus-like-particles. Cells were then extensively washed to remove unbound viral particles and co-cultured o/n at 37°C with TCR-transduced J76 cells at a 1:1 ratio. After co-culture, cells were harvested, washed, treated with FcR Blocker (Miltenyi Biotec), stained with CD69-PE, HLA-DR-PE-Cy7, TCR-APC, CD3-eF780-APC antibodies and eF506-viability dye, and analyzed by flow cytometry as above.

Intracellular cytokine staining (ICS) in primary T cells: PBMC from healthy donors expressing at least one of 4 HLA-DR alleles (DR11, DR1, DR15, or DRB5) were transduced with TCR lentivectors and tested 7 to 9 days after transduction. Autologous MDDC (2.5 x 10^4) were pulsed with serial dilutions of from 10^{-5} to 10^{-11} M of Gag293 peptide and co-cultured at a 1:1 ratio with transduced PBMC. Cells were co-cultured for 1h at 37°C before addition of 1μg/ml Brefeldin A (eBioscience), and further incubated o/n. Negative

controls consisted in TCR-transduced PBMC incubated with unpulsed MDDC and in mock-transduced PBMC incubated with peptide-pulsed MDDC. Positive controls were obtained by pulsing MMDC with 1μg/ml Staphylococcal Enterotoxin A (Toxin Technology, Sarasota, FL), or by using TCR-transduced PBMC stimulated with 50 ng/mL phorbol 12-myristate 13-acetate (PMA) and 0.25 μg/ml ionomycin in the absence of MDDC.

For ICS, cells were washed, treated with FcR Blocker, and stained for surface antigens with CD4-PE-CF594, CD8-BV785, CD14-BV510, CD3-eF780-APC antibodies, and eF506-viability dye. Cells were fixed and permeabilized using the CytoFix/Cytoperm kit (BD Biosciences) before staining for intacellular cytokines with IL-2-APC, MIP1β-PE, IFNγ-PE-Cy7, TNFα-BV421, and CD107a antibodies. Fluorescence was acquired on an LSR Fortessa flow cytometer. Intracellular cytokine production was evaluated in the live CD14-CD3+CD4+CD8- or CD14-CD3+CD4-CD8+ lymphocyte gates. The percentage of cytokine-producing T cells was determined after subtracting the percentage of cytokine-positive events in unstimulated controls. All flow cytometry experiments were analyzed with the Flowjo v8.8 software (Tree Star). Polyfunctionality was assessed for a panel of 5 functions that included the production of IFN-γ, IL-2, MIP-1β, TNF-α and CD107a. All possible combinations of the 5 markers were analyzed by boolean gating in Flowjo. The resulting data table was converted to the matrix symmetric positive definite (SPD) format, and then analyzed using the SPICE software version 5.3 (37), with a cytokine positivity threshold of 0.1%.

HLA-blocking experiments in primary cells: MDDC were brought to a concentration of 5 x 10^6/mL in complete RPMI medium supplemented with 10% FBS. MDDC were pretreated with 10 μg/mL of an HLA-DR blocking antibody (Biolegend, clone: L243) or a pan-MHC I blocking antibody (Biolegend, clone: W6/32) for 1 h at 37°C prior to Gag293 peptide stimulation. Incubation with 10 μg/mL of an isotypic IgG2a control antibody (Biolegend, clone: MOPC-173) was used as a negative control for HLA blocking. MDDC were then pulsed with 10^{-5} M Gag293 peptide and cocultured at a 1:1 ratio with TCR-transduced PBMC, as described above. Cytokine production was evaluated by ICS in the CD8+ T cell gate.

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Patient ID	Age yrs	Duration of Infection yrs	CD4 /mm3	VL copies/mL	MHC Class II DRB1 alleles		Tetramer used for sort
HIC 1	56.4	25.0	850	<50	DRB1*1501/1507/1510 (DRB5)		DRB1*1501
HIC 2	50.8	24.2	1020	<50	DRB1*1122	DRB1*1501/ 1507/ 1510 (DRB5)	DRB5*0101
HIC 3	54.7	22.0	1050	<50	DRB1*0102	DRB1*1101	DRB1*1101
HIC 4	61.4	26.0	852	<50	DRB1*1501 (DRB5)		DRB1*1501
HIC 5	53.6	11.0	742	<50	DRB1*0101	DRB1*1607	DRB1*0101
HIC 6	34.6	13.1	1048	<50	DRB1*1101	DRB1*1204/ 1201/ 1202/ 1307	DRB1*1101
HIC 7	41.7	11.7	744	<50	DRB1*0701/ 0703/ 0704/ 0705/ 0706	DRB1*1501/ 1502 (DRB5)	DRB5*0101
HIC 8	48.5	21.0	799	<50	DRB1*0102	DRB1*1301	DRB1*0101
HIC 9	49.7	14.6	754	<50	DRB1*0101	DRB1*0701	-
HIC 11	45.0	26.0	!"#$	<50	DRB1*0101	DRB1*1501 (DRB5)	-
HIC 12	50.9	25.5	%#&	<50	DRB1*0301	DRB1*1359	-
HIC 13	34.0	9.8	&''	<50	DRB1*1360/ 1402	DRB1*1401 /1602 (DRB5)	-
HIC 14	56.6	18.3	!#""	<50	DRB1*1301/ 1302	DRB1*0703	-
HIC 15	43.6	14.7	!"%(	<50	DRB1*0101	DRB1*0703	-
Median HIC	50.3	19.6	875	<50			
HAART 1	41.4	7.1	516	<50	DRB1*0101/ 0107	DRB1*1502/ 1504/ 1506/ 1514 (DRB5)	DRB5*0101
HAART 2	44.5	10.2	432	<50	DRB1*1502 (DRB5)	DRB1*1608	DRB5*0101
HAART 3	52.5	25.3	682	<50	DRB1*0101/ 0107	DRB1*0703	DRB1*0101
HAART 4	53.0	14.5	570	<50	DRB1*0703	DRB1*1122	DRB1*1101
HAART 5	48.6	9.0	948	<50	DRB1*0102	DRB1*1410	DRB1*0101
HAART 6	54.5	6.8	266	<50	DRB1*0101/0107	DRB1*0322	DRB1*0101
HAART 7	55.9	18.1	846	<50	DRB1*0701	DRB1*1122	DRB1*1101
HAART 8	39.5	20.1	847	<50	DRB1*1501 (DRB5)		DRB5*0101
HAART 9	47.7	19.7	)(#	<50	N.A.	N.A.	-
HAART 10	54.0	11.2	#$$	<50	DRB1*0301	DRB1*1501 (DRB5)	-
HAART 11	52.1	12.9	'(*	<50	DRB1*0701	DRB1*1001	-
HAART 12	43.0	12.1	))&	<50	DRB1*1165	DRB1*1301	-
HAART 13	45.0	11.9	!)(#	<50	DRB1*0401	DRB1*1101	-
HAART 14	47.5	11.9	))*	<50	DRB1*0901	DRB1*1301	-
HAART 15	41.4	7.1	*&)	<50	DRB1*0101	DRB1*0301	-
Median HAART	47.7	11.9	570	<50			

Supplemental Table S1: MHC typing and clinical characteristics of patients included in the study

Primary CD4+ T cell lines were generated from 14 HIV controllers (HIC) and 15 treated patients (HAART) genotyped for HLA-DRB1.

For a subgroup of 8 HIC and 8 HAART patients, CD4+ T cell lines were sorted with HLA-matched tetramers loaded with the Gag293 peptide

The tetramer used for the sort is reported in the rightmost column. VL: viral load; N.A. not available.

Supplemental Table S2: List of TRAV24 clonotypes specific for Gag293

TRAV24 clonotypes obtained from 8 Controller cell lines, 8 treated patient cell lines, and 4 ex vivo controller samples are listed.
The V(D)J gene nomenclature is that of the IMGT database (www.imgt.org). Public clonotypes are in bold colored type.
Clonotypes tested functionally are marked by an asterisk and highlighted with an orange background.

HIC 1 DR15+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01, or TRAV24*02	TRAJ38*01	tgtgcccgtgacgaccgtaagctgatttgg	CARDDRKLIW	1	1.89	1.89	30
TRAV24*01	TRAJ34*01	tgtgcctctggtaacaccgacaagctcatcttt	CASGNTDKLIF	1	1.89	1.89	33
TRAV24*01	TRAJ39*01	tgtgccttttgtaatgcaggcaacatgctcaccttt	CAFCNAGNMLTF	1	1.89	1.89	
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaacttttt	**CAFKAAGNKLTF***	2	3.77	5.66	
TRAV24*01	TRAJ17*01	tgtgcctttaaggctgcaggcaacaagctaacttttt		1	1.89		
TRAV24*01	TRAJ17*01	tgtgcctttacggctgcaggcaacaagctaacttttt	CAFTAAGNKLTF	1	1.89	1.89	36
TRAV24*01	TRAJ17*01	tgtgccctagaaaatgcaggcaacaagctaacttttt	CALENAGNKLTF	1	1.89	1.89	
TRAV24*01	TRAJ39*01	tgtgccctcggtaatgcaggcaacatgctcaccttt	CALGNAGNMLTF	33	62.26	64.15	
TRAV24*01	TRAJ39*01	tgtgccctcggtaatgcaggcaacatgctcacgttt		1	1.89		
TRAV24*01	TRAJ57*01	tgctcgcctcagggcggatctgaaaagctggtcttt	CSPQGGSEKLVF	1	1.89	1.89	
TRAV24*01	TRAJ6*01	tgtgcctttatcccaggaggaagctacatacctacattt	CAFIPGGSYIPTF	1	1.89	1.89	
TRAV24*01	TRAJ42*01	tgtgcctctgatggaggaagccaaggcaatctcatcttt	CASDGGSQGNLIF	1	1.89	1.89	39
TRAV24*01	TRAJ32*02	tgtgcctcttatggtggtgctacaaacaagctcatcttt	**CASYGGATNKLIF**	8	15.09	15.09	
		Total	11	53	100.00	100.00	

HIC 2 DRB5+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaacttttt	**CAFKAAGNKLTF***	2	3.03	56.06	
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaacttttt		35	53.03		
TRAV24*01	TRAJ17*01	tgtgcctttaaggttgcaggcaacaagctaacttttt	CAFKVAGNKLTF	1	1.52	1.52	
TRAV24*01	TRAJ39*01	tgtgcctttaggatggcaggcaacatgctcaccttt	CAFRMAGNMLTF	1	1.52	1.52	
TRAV24*01	TRAJ39*01	tgtgcctttcgtaatgcaggcaacatgctcaccttt	**CAFRNAGNMLTF**	1	1.52	1.52	
TRAV24*01	TRAJ17*01	tgtgcccacaaagctgcaggcaacaagctaacttttt	**CAHKAAGNKLTF**	2	3.03	4.55	36
TRAV24*01	TRAJ17*01	tgtgcccataaagctgcaggcaacaagctaacttttt		1	1.52		
TRAV24*01	TRAJ39*01	tgtgcccctataaatgcaggcaacatgctcaccttt	CAPINAGNMLTF	6	9.09	9.09	
TRAV24*01	TRAJ17*01	tgtgcccgcaaagctgcaggcaacaagctaacttttt	CARKAAGNKLTF	1	1.52	1.52	
TRAV24*01	TRAJ17*01	tgtgcctctaaagctgcaggcaacaagctaacttttt	**CASKAAGNKLTF***	13	19.70	19.70	
TRAV24*01	TRAJ17*01	tgtgcctcacgaactgcaggcaacaagctaacttttt	CASRTAGNKLTF	3	4.55	4.55	
		Total	9	66	100.00	100.00	

HIC 3 DR11+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgctccaaagagcaggcaacaagctaacttt	CAPKSRQQANF	1	0.64	0.64	33
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaacttttt	**CAFKAAGNKLTF***	64	41.03	46.15	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaacttttt		8	5.13		
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgccttcagggctgcaggcaacaagctaacttttt	**CAFRAAGNKLTF**	2	1.28	1.28	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgccttgaaagctgcaggcaacaagctaacttttt	**CALKAAGNKLTF**	1	0.64	0.64	
TRAV24*01	TRAJ39*01	tgtgccttgaaacaagcaggcaacaagctcacttttt	CALKQAGNKLTF	1	0.64	0.64	
TRAV24*01	TRAJ39*01	tgtgccttgaggcaagcaggcaacatgctcaccttt	CALRQAGNMLTF	6	3.85	3.85	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgccatgaaagctgcaggcaacaagctaacttttt	CAMKAAGNKLTF	1	0.64	1.28	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgcgatgaaagctgcaggcaacaagctaacttttt		1	0.64		
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgccaacagagctgcaggcaacaagctaacttttt	CANRAAGNKLTF	1	0.64	0.64	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgcctccaaagctgcaggcaacaagctaacttttt	**CASKAAGNKLTF***	4	2.56	2.56	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtgcctacaaagctgcaggcaacaagctaacttttt	CAYKAAGNKLTF	1	0.64	0.64	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtggtttcaaagctgcaggcaacaagctaacttttt	CGFKAAGNKLTF	1	0.64	0.64	36
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtggttggaaagctgcaggcaacaagctaacttttt	CGWKAAGNKLTF	1	0.64	0.64	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtagtttgaaagctgcaggcaacaagctaacttttt	CSLKAAGNKLTF	2	1.28	1.28	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtagtttgagagctgcaggcaacaagctaacttttt	CSLRAAGNKLTF	1	0.64	0.64	
TRAV24*01	TRAJ17*01	tgtagtcggagggctgcaggcaacaagctaacttttt	**CSRRAAGNKLTF***	18	11.54	11.54	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtagttggaaagctgcaggcaacaagctaacttttt	CSWKAAGNKLTF	4	2.56	2.56	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtagttggagagctgcaggcaacaagctaacttttt	CSWRAAGNKLTF	1	0.64	1.28	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtagttggagggctgcaggcaacaagctaacttttt		1	0.64		
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtaccaagaaagctgcaggcaacaagctaacttttt	CTKKAAGNKLTF	1	0.64	21.15	
TRAV24*01	TRAJ17*01	tgtacgaagaaagctgcaggcaacaagctaacttttt		32	20.51		
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtaccttgaaagctgcaggcaacaagctaacttttt	CTLKAAGNKLTF	1	0.64	0.64	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtacgaacaaagctgcaggcaacaagctaacttttt	CTNKAAGNKLTF	1	0.64	0.64	
TRAV24*01, or TRAV24*02	TRAJ17*01	tgtactaggaaagctgcaggcaacaagctaacttttt	CTRKAAGNKLTF	1	0.64	0.64	
		Total	22	156	100.00	100.00	

HIC 4 DR15+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ39*01	tgtgccttccaaaatgcaggcaacatgctcaccttt	CAFQNAGNMLTF	6	9.23	9.23	
TRAV24*01	TRAJ17*01	tgtgcctttagagctgcaggcaacaagctaacttttt	**CAFRAAGNKLTF**	1	1.54	1.54	36
TRAV24*01	TRAJ39*01	tgtgcgacgcgccgtgcaggcaacatgctcaccttt	**CATRRAGNMLTF**	6	9.23	9.23	
TRAV24*01	TRAJ57*01	tgtgcctacgaggggggcatctgaaaagctggtcttt	**CAYEGASEKLVF**	3	4.62	4.62	
TRAV24*01	TRAJ32*02	tgtgccgaatatggtggtgctacaaacaagctcatcttt	**CAEYGGATNKLIF**	2	3.08	3.08	
TRAV24*01	TRAJ32*02	tgtgccccttatggtggtgctacaaacaagctcatcttt	**CAPYGGATNKLIF**	2	3.08	3.08	
TRAV24*01	TRAJ32*02	tgtgcccgttatggtggtgctgcaaacaagctcatcttt	CARYGGAANKLIF	1	1.54	1.54	
TRAV24*01	TRAJ32*02	tgtgcccgttatggtggtgctacaaacaagctcatcttt	**CARYGGATNKLIF**	10	15.38	16.92	
TRAV24*01	TRAJ32*02	tgtgctcgttatggtggtgctacaaacaagctcatcttt		1	1.54		
TRAV24*01, or TRAV24*02	TRAJ32*02	tgtgccgctatggtggtggtacaaacaagctcatttttt	CARYGGGTNKLIF	1	1.54	1.54	39
TRAV24*01	TRAJ54*01	tgtgcctccgagtccacgggagcccagaagctggtattt	**CASESTGAQKLVF**	3	4.62	4.62	
TRAV24*01	TRAJ32*02	tgtgcctcctatggtggtgctacaaacaagctcatcttt		25	38.46	43.08	
TRAV24*01	TRAJ32*02	tgtgcctcgtatggtggtgctacaaacaagctcatcttt	**CASYGGATNKLIF**	2	3.08		
TRAV24*01	TRAJ32*02	tgtgcctcttatggtggtgctacaaacaagctcatcttt		1	1.54		
TRAV24*01	TRAJ32*02	tgtgcctcctatgttggtgctacaaacaagctcatcttt	CASYVGATNKLIF	1	1.54	1.54	
		Total	12	65	100.00	100.00	

HIC 5 DR1+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*02	TRAJ38*01	tgtgccttcgacaaccgtaagctgatttgg	**CAFDNRKLIW**	31	51.67	55.00	30
TRAV24*01	TRAJ38*01	tgtgcctttgacaaccgtaagctgatttgg		2	3.33		

TRAV24*01	TRAJ17*01	tgtgcctttaaggctgcaggcaacaagctaactttt	CAFKAAGNKLTF*	1	1.67	1.67	
TRAV24*01	TRAJ17*01	tgtgcctttcgagctgcaggcaacaagctaactttt	CAFRAAGNKLTF	2	3.33	3.33	
TRAV24*01	TRAJ36*01	tgtgcctcagaaactggggcaaacaacctcttcttt	CASETGANNLFF	2	3.33	3.33	36
TRAV24*02	TRAJ39*01	tgtgcgacgcgccgtgcaggcaacatgctcaccttt	CATRRAGNMLTF	5	8.33	8.33	
TRAV24*01	TRAJ57*01	tgtgcctacgaggggggcatctgaaaagctggtcttt	CAYEGASEKLVF	1	1.67	1.67	
TRAV24*01	TRAJ32*02	tgtgccgaatatggtggtgctacaaacaagctcatcttt	CAEYGGATNKLIF	1	1.67	1.67	
TRAV24*01	TRAJ22*01	tgtgccttcgcttctggttctgcaaggcaactgaccttt	CAFASGSARQLTF	13	21.67	21.67	39
TRAV24*01	TRAJ54*01	tgtgcctccgagtccacgggagcccagaagctggtattt	CASESTGAQKLVF	1	1.67	1.67	
TRAV24*02	TRAJ38*01	tgtgccttttacccccctggcaacaaccgtaagctgatttgg	CAFYPPGNNRKLIW	1	1.67	1.67	42
		Total	10	60	100.00	100.00	

HIC 6 DR11+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgcatttaaagctgcaggcaacaagctaactttt		1	1.69	23.73	
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaactttt	CAFKAAGNKLTF*	2	3.39		
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaactttt		11	18.64		
TRAV24*01	TRAJ17*01	tgtgcctttaaagatgcaggcaacaagctaactttt	CAFKDAGNKLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgcctttcctaatgcaggcaacatgctcaccttt	CAFPNAGNMLTF	5	8.47	8.47	
TRAV24*01	TRAJ17*01	tgtgcctttagggctgcaggcaacaagctaactttt	CAFRAAGNKLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgcctttcggaatgcaggcaacatgctcaccttt	CAFRNAGNMLTF	1	1.69	1.69	
TRAV24*01	TRAJ17*01	tgtgctctaaaagctgcaggcaacaagctaactttt	CALKAAGNKLTF	6	10.17	10.17	36
TRAV24*01	TRAJ17*01	tgtgctctaaaagatgcaggcaacaagctaactttt	CALKDAGNKLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgccttaaaaaatgcaggcaacatgctcaccttt	CALKNAGNMLTF	4	6.78	6.78	
TRAV24*01	TRAJ39*01	tgtgccctcaataatgcaggcaacatgctcaccttt	CALNNAGNMLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgccctgcggaatgcaggcaacatgctcaccttt	CALRNAGNMLTF	3	5.08	5.08	
TRAV24*01	TRAJ17*01	tgtgcccccaaagctgcaggcaacaagctaactttt	CAPKAAGNKLTF	12	20.34	20.34	
TRAV24*01	TRAJ17*01	tgtgcccccaaagatgcaggcaacaagctaactttt	CAPKDAGNKLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgcctccaagaatgcaggcaacatgctcaccttt	CASKNAGNMLTF	1	1.69	1.69	
TRAV24*01	TRAJ39*01	tgtgcctccatgaatgcaggcaacatgctcaccttt	CASMNAGNMLTF	7	11.86	11.86	
TRAV24*01	TRAJ53*01	tgtgcctttaagggaggtggaggtagcaactataaactgacattt	CAFKGGGGSNYKLTF	1	1.69	1.69	45
		Total	15	59	100.00	100.00	

HIC 7 DRB5+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ20*01	tgtgcctttggcgactacaagctcagcttt	CAFGDYKLSF	2	3.64	3.64	30
TRAV24*01	TRAJ17*01	tgtgcctttcacgctgcaggcaacaagctaactttt	CAFHAAGNKLTF	1	1.82	1.82	
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaactttt	CAFKAAGNKLTF*	10	18.18	18.18	
TRAV24*01	TRAJ10*01	tgtgcctttaagggaggaggaaacaaactcaccttt	CAFKGGGNKLTF	1	1.82	1.82	
TRAV24*01	TRAJ17*01	tgtgcctttaacgctgcaggcaacaagctaactttt	CAFNAAGNKLTF	3	5.45	5.45	
TRAV24*01	TRAJ17*01	tgtgccttccaggctgcaggcaacaagctaactttt	CAFQAAGNKLTF	9	16.36	16.36	36
TRAV24*01	TRAJ10*01	tgtgcctttaggggaggaggaaacaaactcaccttt	CAFRGGGNKLTF	11	20.00	20.00	
TRAV24*01	TRAJ39*01	tgtgcctttcgaagagcaggcaacatgctcaccttt	CAFRRAGNMLTF	1	1.82	1.82	
TRAV24*01	TRAJ17*01	tgtgcccacaaagctgcaggcaacaagctaactttt	CAHKAAGNKLTF	3	5.45	5.45	
TRAV24*01	TRAJ17*01	tgtgcccacaaaggagcaggcaacaagctaactttt	CAHKGAGNKLTF	1	1.82	1.82	
TRAV24*01	TRAJ32*02	tgtgccgaatatggtggtgctacaaacaagctcatcttt	CAEYGGATNKLIF	3	5.45	5.45	
TRAV24*01	TRAJ32*01	tgtgccaactatggcggtgctacaaacaagctcatcttt	CANYGGATNKLIF	2	3.64	3.64	
TRAV24*01	TRAJ57*01	tgtgcccccgggggggggcggatctgaaaagctggtcttt	CAPGGGGSEKLVF	2	3.64	3.64	
TRAV24*01	TRAJ32*02	tgtgcccttatggtggtgctacaaacaagctcatcttt	CAPYGGATNKLIF	1	1.82	3.64	39
TRAV24*01	TRAJ32*01	tgtgctccttatggcggtgctacaaacaagctcatcttt		1	1.82		
TRAV24*01	TRAJ32*01	tgtgcctcctatggcggtgctacaaacaagctcatcttt		2	3.64	7.27	
TRAV24*01	TRAJ32*02	tgtgcctcctatggtggtgctacaaacaagctcatcttt	CASYGGATNKLIF	1	1.82		
TRAV24*01	TRAJ32*02	tgtgcctcttatggtggtgctacaaacaagctcatcttt		1	1.82		
		Total	15	55	100.00	100.00	

HIC 8 DR1+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ31*01	tgtgggggggataacaatgccagactcatgttt	CGGDNNARLMF	54	77.14	77.14	33
TRAV24*01	TRAJ31*01	tgtgggggggataacaatgccagactcacgttt	CGGDNNARLTF	1	1.43	1.43	
TRAV24*01	TRAJ34*01	tgtgcctctctataacaccgacaagctcatcttt	CASLYNTDKLIF	10	14.29	14.29	36
TRAV24*01	TRAJ32*01	tgtgccaactatggcggtgctacaaacaagctcatcttt	CANYGGATNKLIF	5	7.14	7.14	39
		Total	4	70	100.00	100.00	

HAART 1 DRB5+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ38*01	tgtgccttcgacaaccgtaagctgatttgg	CAFDNRKLIW	37	59.68	59.68	30
TRAV24*01	TRAJ5*01	tgtgcctttgacaggagagcacttactttt	CAFDRRALTF	25	40.32	40.32	
		Total	2	62	100.00	100.00	

HAART 2 DRB5+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ39*01	tgtgcccgtcgtaatgcagacaacatgctcaccttt	CARRNADNMLTF	1	1.89	1.89	
TRAV24*01	TRAJ39*01	tgtgcccgtcgtaatgcaggcaacatgctcaccttt	CARRNAGNMLTF	42	79.25	79.25	36
TRAV24*01	TRAJ17*01	tgtagtcggagggctgcaggcaacaagctaactttt	CSRRAAGNKLTF*	10	18.87	18.87	
		Total	3	53	100.00	100.00	

HAART 3 DR1+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ36*01	tgtgcctatggagcaaacaacctcttcttt	CAYGANNLFF*	1	1.75	87.72	30
TRAV24*01	TRAJ36*01	tgtgcctatggggcaaacaacctcttcttt		49	85.96		
TRAV24*01	TRAJ58*01	tgtgccttaggcgggggagaaaccagtggctctaggttgaccttt	CALGGGETSGSRLTF	7	12.28	12.28	45
		Total	2	57	100.00	100.00	

HAART 4 DR11+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaactttt	CAFKAAGNKLTF*	1	1.14	68.18	
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaactttt		59	67.05		
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacatgctaactttt	CAFKAAGNMLTF	1	1.14	1.14	
TRAV24*01	TRAJ17*01	tgtgcctttaaaaatgcaggcaacaagctcactttt	CAFKNAGNKLTF	1	1.14	1.14	
TRAV24*01	TRAJ17*01	tgtgcctttcaagctgcaggcaacatgctcactttt	CAFQAAGNMLTF	1	1.14	1.14	

TRAV24*01	TRAJ39*01	tgtgcctttaggaatgcaggcaacatgctcaccttt	CAFRNAGNMLTF	4	4.55	4.55	
TRAV24*01	TRAJ17*01	tgtgcctttagaactgcaggcaacaagctaacttttt	CAFRTAGNKLTF	2	2.27	2.27	36
TRAV24*01	TRAJ17*01	tgtgccttaaaagctgcaggcaacaagctaacttttt	CALKAAGNKLTF	1	1.14	1.14	
TRAV24*01	TRAJ17*01	tgtgccttaaaaaatgcaggcaacaagctcacttttt	CALKNAGNKLTF	1	1.14	1.14	
TRAV24*01	TRAJ39*01	tgtgccttacaaaatgcaggcaacatgctcaccttt	CALQNAGNMLTF	1	1.14	2.27	
TRAV24*01	TRAJ39*01	tgtgccttacaaaatgcaggcaacatgctcacttttt		1	1.14		
TRAV24*01	TRAJ39*01	tgtgccttaagaaatgcaggcaacatgctcaccttt	CALRNAGNMLTF	1	1.14	14.77	
TRAV24*01	TRAJ39*01	tgtgccttacgaaatgcaggcaacatgctcaccttt		12	13.64		
TRAV24*01	TRAJ37*02	tgtgccctgcctcatggctctagcaacacaggcaaactaatcttt	CALPHGSSNTGKLIF	2	2.27	2.27	45
		Total	11	88	100.00	100.00	

HAART 5 DR1+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ38*01	tgtgcccataatgctggcaacaaccgtaagctgatttgg	CAHNAGNNRKLIW	25	36.76	36.76	39
TRAV24*01	TRAJ3*01	tgtgcctccctgtacagcagtgcttccaagataatcttt	CASLYSSASKIIF	18	26.47	26.47	
TRAV24*01	TRAJ27*01	tgtgcctttaatcctcccaccaatgcaggcaaatcaaccttt	CAFNPPTNAGKSTF	25	36.76	36.76	42
		Total	3	68	100.00	100.00	

HAART 6 DR1+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgcctttcgagctgcaggcaacaagctaacttttt	CAFRAAGNKLTF	3	5.45	5.45	36
TRAV24*01	TRAJ39*01	tgtgccttaaataatgcaggcaacatgctcaccttt	CALNNAGNMLTF	24	43.64	43.64	
TRAV24*01	TRAJ42*01	tgtgcctccgattatggaggaagccaaggaaatctcatcttt	CASDYGGSQGNLIF*	28	50.91	50.91	42
		Total	3	55	100.00	100.00	

HAART 7 DR11+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaacttttt	CAFKAAGNKLTF*	37	61.67	61.67	
TRAV24*01	TRAJ39*01	tgtgcctttagaaatgcaggcaacatgctcaccttt	CAFRNAGNMLTF	10	16.67	16.67	36
TRAV24*01	TRAJ17*01	tgtgcctccccagctgcaggcaacaagctaacttttt	CASPAAGNKLTF	5	8.33	8.33	
TRAV24*01	TRAJ39*01	tgtgcctccccgcgggggcaggcaacatgctcaccttt	CASPRGAGNMLTF	8	13.33	13.33	39
		Total	4	60	100.00	100.00	

HAART 8 DRB5+

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgcctttgaagctgcaggcaacaagctaacttttt	CAFEAAGNKLTF	11	20.75	20.75	36
TRAV24*01	TRAJ17*01	tgtgccccccagactgcaggcaacaagctaacttttt	CAPQTAGNKLTF	9	16.98	16.98	
TRAV24*01	TRAJ32*02	tgtgctcattatggtggtgctacaaacaagctcatcttt	CAHYGGATNKLIF	6	11.32	11.32	
TRAV24*01	TRAJ32*02	tgtgccccgtatggtggtgctacaaacaagctcatcttt	CAPYGGATNKLIF	1	1.89	1.89	39
TRAV24*01	TRAJ32*02	tgtgctcggtatggtggtgctacaaacaagctcatcttt	CARYGGATNKLIF	26	49.06	49.06	
		Total	5	53	100.00	100.00	

HIC 1 DRB5+ ex vivo

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ38*01	tgtgcccgtgacgaccgtaagctgatttgg	CARDDRKLIW	4	3.36	4.20	30
TRAV24*01	TRAJ38*01	tgtgctcgtgacgaccgtaagctgatttgg		1	0.84		
TRAV24*01	TRAJ17*01	tgtgcctttacggctgcaggcaacaagctaacttttt	CAFTAAGNKLTF	10	8.40	8.40	36
TRAV24*01	TRAJ39*01	tgtgccctcggtaatgcaggcaacatgctcaccttt	CALGNAGNMLTF	33	27.73	27.73	
TRAV24*01	TRAJ6*01	tgtgcctttatcccaggaggaagctacatacctacattt	CAFIPGGSYIPTF	4	3.36	3.36	
TRAV24*01	TRAJ32*02	tgtgcctcgtatggtggtgctacaaacaagctcatcttt	CASYGGATNKLIF	15	12.61	21.85	39
TRAV24*01	TRAJ32*02	tgtgcctcttatggtggtgctacaaacaagctcatcttt		11	9.24		
TRAV24*01	TRAJ45*01	tgtgctctcgattcaggaggaggtgctgacggactcaccttt	CALDSGGGADGLTF	40	33.61	34.45	42
TRAV24*01	TRAJ45*01	tgtgctctcgattcgggaggaggtgctgacggactcaccttt		1	0.84		
		Total	6	119	100.00	100.00	

HIC 2 DRB5+ ex vivo

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgccttaaagctgcaggcaacaagctaacttttt	CAFKAAGNKLTF*	10	17.86	17.86	
TRAV24*01	TRAJ39*01	tgtgccaggcgtaatgcaggcaacatgctcaccttt	CARRNAGNMLTF	7	12.50	12.50	36
TRAV24*01	TRAJ17*01	tgtgcctctaaagctgcaggcaacaagctaacttttt	CASKAAGNKLTF*	39	69.64	69.64	
		Total	3	56	100.00	100.00	

HIC 3 DRB5+ ex vivo

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ17*01	tgtgctctcaaagctgcaggcaacaagctaacttttt	CALKAAGNKLTF	4	5.26	6.58	
TRAV24*01	TRAJ17*01	tgtgctctcaaagctgctggcaacaagctaacttttt		1	1.32		36
TRAV24*01	TRAJ39*01	tgtgccttgaggcaagcaggcaacatgctcaccttt	CALRQAGNMLTF	69	90.79	93.42	
TRAV24*01	TRAJ39*01	tgtgccttgaggcaagcgggcaacatgctcaccttt		2	2.63		
		Total	2	76	100.00	100.00	

HIC 7 DRB5+ ex vivo

V-GENE	J-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRAV24*01	TRAJ13*02	tgtgcccctgggggttaccagaaagttaccttt	CAPGGYQKVTF	5	4.72	4.72	33
TRAV24*01	TRAJ22*01	tgtgcctgggggttctgcaaggcaactgaccttt	CAWGSARQLTF	5	4.72	4.72	
TRAV24*01	TRAJ17*01	tgtgccttcaaagctgcaggcaacaagctaacttttt	CAFKAAGNKLTF*	19	17.92	54.72	
TRAV24*01	TRAJ17*01	tgtgcctttaaagctgcaggcaacaagctaacttttt		39	36.79		36
TRAV24*01	TRAJ17*01	tgtgcctttaacgctgcaggcaacaagctaacttttt	CAFNAAGNKLTF	6	5.66	5.66	
TRAV24*01	TRAJ26*01	tgtgcctttgtagctgctggtcagaattttgtcttt	CAFVAAGQNFVF	5	4.72	4.72	
TRAV24*01	TRAJ32*02	tgtgccgaatatggtggtgctacaaacaagctcatcttt	CAEYGGATNKLIF	4	3.77	3.77	
TRAV24*01	TRAJ32*01	tgtgccaactatggcggtgctacaaacaagctcatcttt	CANYGGATNKLIF	7	6.60	6.60	39
TRAV24*01	TRAJ32*02	tgtgcctcgtatggtggtgctacaaacaagctcatcttt	CASYGGATNKLIF	1	0.94	0.94	
TRAV24*01	TRAJ24*02	tgtgccttaatgacaactgacagctgggggaaattgcagttt	CALMTTDSWGKLQF	15	14.15	14.15	42
		Total	9	106	100.00	100.00	

Supplemental Table S3: List of TRBV2 clonotypes specific for Gag293

TRBV2 clonotypes obtained from 8 Controller cell lines, 8 treated patient cell lines, and 4 ex vivo controller samples are listed.
The V(D)J gene nomenclature is that of the IMGT database (www.imgt.org). Public clonotypes are in bold colored type.
Clonotypes tested functionally are marked by an asterisk and highlighted with an orange background.

HIC 1 DR15+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01	TRBJ2-7*01	TRBD1*01	tgtgccagcttagggcccctacggcacgagcagtacttc	CASLGPLRHEQYF	2	3.33	3.33	39
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcaaaccactagttagcacagatacgcagtatttt	CASKPLVSTDTQYF	1	1.67	1.67	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagccttgaaaggactagcgggggtgagcagttcttc	CASLERTSGGEQFF	1	1.67	1.67	42
TRBV2*01	TRBJ2-1*01	TRBD1*01	tgtgccagcacccgggacaggacaaagaatgagcagttcttc	CASTRDRTKNEQFF	1	1.67	1.67	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcgttggctagcgggggagatgagcagttcttc	CASSALASGGDEQFF	1	1.67	1.67	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcgttagctagcggtacagatacgcagtatttt	**CASSALASGTDTQYF**	1	1.67	1.67	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgaactgacctctagaacctacgagcagtacttc	CASSELTSRTYEQYF	1	1.67	1.67	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD2*01	tgtgccagcagtgaacgggtttcgggcaatcagccccagcatttt	CASSERVSGNQPQHF	2	3.33	3.33	45
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagccctatggctagcgggggggatgagcagttcttc	CASSPMASGGDEQFF	1	1.67	1.67	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagccgtaggactagcgggacttacgagcagtacttc	**CASSRRTSGTYEQYF**	1	1.67	1.67	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgtgatggctagccgtgggaatgagcagttcttc	CASSVMASRGNEQFF	1	1.67	1.67	
TRBV2*01	TRBJ1-5*01	TRBD2*01	tgtgccagccaaaggggggctcgggggggcaatcagccccagcatttt	CASQRGARGGNQPQHF	1	1.67	1.67	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-4*01	TRBD1*01	tgtgccagcagggctcgaacaggggcaactaatgaaaaactgttttt	CASRARTGATNEKLFF	1	1.67	1.67	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaagactagcgggggctcagatacgcagtatttt	CASSAKTSGGSDTQYF	1	1.67	1.67	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgccctggctagcgggggccgggatacgcagtatttt	CASSALASGGRDTQYF	1	1.67	1.67	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcccggactagcgggggactcgatgagcagttcttc	CASSARTSGGLDEQFF	1	1.67	1.67	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggctcggatacgcagtatttt	**CASSARTSGGSDTQYF**	1	1.67	1.67	48
TRBV2*01, or TRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagtaagagggctagcgggggcacagatacgcagtatttt	CASSKRASGGTDTQYF	2	3.33	3.33	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcctaaggactagcgggggttcagatacgcagtatttt	**CASSLRTSGGSDTQYF**	1	1.67	1.67	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagccgcttgacgagcgggggcggaatgagcagttcttc	CASSRLTSGGRNEQFF	2	3.33	3.33	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagttctaagactagcgggggccacagatacgcagtatttt	CASSSKTSGGTDTQYF	1	1.67	1.67	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagttcaaggactagcgggggccaagatgagcagttcttc	CASSSRTSGGQDEQFF	1	1.67	1.67	
TRBV2*01	TRBJ1-5*01	TRBD2*01	tgtgccacctccagaggagcgcggggaagcaatcagccccagcatttt	CATSRGARGSNQPQHF	34	56.67	56.67	
			Total	23	60	100.00	100.00	

HIC 2 DRB5+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcgccaggacaggggcgttggctacaccttc	CASARTGGVGYTF	1	0.94	0.94	39
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcaggactagcgggacctacgagcagtacttc	CASRTSGTYEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD1*01	tgtgccagcaaagcaaaaacggtaacctacaagcagtacttc	CASKAKTVTYKQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcaaaccaaaagcggtaacctacgagcagtacttc	CASKPKAVTYEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-3*01	TRBD1*01	tgtgccagcagagggacagcgactggaaacaccatatatttt	CASRGTATGNTIYF	1	0.94	0.94	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-4*01	TRBD1*01	tgtgccagcagaccgacagcaactaatgaaaaactgttttt	CASRPTATNEKLFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgaatatgcgactagcaatgagcagttcttc	CASSEYATSNEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-1*01	TRBD1*01	tgtgccagcagtcgtggacagcggcacagatacgcagtattt	CASSRGQRHRYAVF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccatctcgcgtctagcgggaggcatggacgagcagtacttc	CAISRLAGGMDEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcggccgactagcatcgggcacagatacgcagtatttt	CASGRLASGTDTQYF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagcaggaggggggactagcggcaccggggagctgtttttt	CASRRGTSGTGELFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgatggggctagcggggtgggagagcagtacttc	CASSDGASGVGEQYF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-6*02	TRBD1*01	tgtgccagcagtgaagctgccaggggtaattcacccctccacttt	CASSEAARGNSPLHF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgaaggggctagcgggctcggggagcagtacttc	CASSEGASGLGEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgaactggctagcgggataagtgagcagttcttc	CASSELASGISEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgaacttgctagcgggctcgcagagcagttcttc	CASSELASGLAEQFF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgaactggctagcgggacgggtgagcagttcttc	CASSELASGTGEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagtgaacgggctagcgggaccgacgagcagtacttc	CASSERASGTDEQYF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagcagtgaaagggctagcggggtcggggagctgtttttt	CASSERASGVGELFF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcggactggctagcggcacagatacgcagtatttt	CASSGLASGTDTQYF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagttcgggactagcgtcgggcaccggggagctgtttttt	CASSGLASGTGELFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagcgggatgactagccgatcctacgagcagtacttc	CASSGMTSRSYEQYF	3	2.83	2.83	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagcagcccgggactagccggcaccggggagctgtttttt	CASSPGLAGTGELFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtccgttgactagcggaacagatacgcagtatttt	**CASSPLTSGTDTQYF**	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtcctcgggccaggggggaatcagccccagcatttt	CASSPRARGNQPQHF	2	1.89	1.89	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagccctcggactagcggtccctacgagcagtacttc	CASSPRTSGPYEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagtcctcggactagcgggagttacgagcagtacttc	CASSPRTSGSYEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagcagccaagggctagcgggcaccgggggagctgtttttt	CASSQGLAGTGELFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcaattagctaggggcacagatacgcagtatttt	CASSQLARGTDTQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD1*01	tgtgccagcagtcaacttgtatcgctgaggggggagcagtacttc	CASSQLVSLRGEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagtcaacggactagcgggagcgacgagcagtacttc	CASSQRTSGSDEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccaagttgcgggggggtacagctacgcagtatttt	CASSQVAGGTATQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD2*01	tgtgccagctcccgggggggctcggggcaatcagccccagcatttt	CASSRGARGNQPQHF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagccgactagcgggaggtttaggtgagcagttcttc	CASSRLAGGLGEQFF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagccgactagcgggagggatggatgagcagttcttc	**CASSRLAGGMDEQFF***	11	10.38	10.38	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagccgactagcgggagggacggatgagcagttcttc	CASSRLAGGTDEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgtctgactagcggcacagatacgcagtatttt	CASSRLTSGTDTQYF	2	1.89	1.89	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagccgagtgacgggagggatggatgagcagttcttc	CASSRVTGGMDEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcaccaaactagcgggggtacatctgagcagttcttc	CASTKLAGGTSEQFF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcaccaaactagcgtggggcacatatacgcagtatttt	CASTKLAWGTYTQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccaccaccccgggggctagcgggataagtgagcagttcttc	CATTPGASGISEQFF*	35	33.02	33.96	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccaccaccccgggggctagtgggataagtgagcagttcttc		1	0.94		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD1*01	tgtgccagcagtgaaaggggacaggggggcgcggtacgagcagtacttc	CASSERGQGARYEQYF	1	0.94	0.94	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgtatgactggcgggggcacagatacgcagtatttt	CASSRMTGGGTDTQYF	1	0.94	0.94	48
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgtaggactagcgggggcacagatacgcagtatttt	**CASSRRTSGGTDTQYF***	6	5.66	5.66	
			Total	44	106	100.00	100.00	

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V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagtcaccggacatacacagatacgcagtatttt	CASHRTYTDTQYF	2	1.60	1.60	39
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-1*01	TRBD1*01	tgtgccagctcaggacagacgaacactgaagctttcttt	**CASSGQTNTEAFF**	10	8.00	8.00	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcagatggacagcaacctcttatggctacaccttc	CASRWTATSGYGTF	15	12.00	12.00	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcagtcccacaacgacagggtatggctacaccttc	CASSPTTTGYGYTF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD1*01	tgtgcctcccacgaaggggccgggggctacggggagctgtttttt	CASHEGAGGFGELFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD1*01	tgtgcctcccacgaaggggccgggggctacggggagctgtttttt	CASHEGAGGYGELFF	2	1.60	1.60	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgccggaactagaggggtgggggagcagttcttc	CASSAGTRGVGEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgctttggctagcggcacagatacgcagtatttt	**CASSALASGTDTQYF**	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgacgcggctagcggtgtgggcgagcagtacttc	CASSDAASGVGEQYF	6	4.80	4.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgatctggctagcgggacgaatgagcagttcttc	CASSDLASGTNEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgaccgggctagcggggtcggggagcagttcttc	CASSDRASGVGEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgacaggactagcggtccccatgagcagttcttc	CASSDRTSGPHEQFF	6	4.80	4.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcggactagcgggaggaatggatgagcagttcttc	CASSGLAGGMDEQFF*	7	5.60	5.60	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagccccgggggcgagaggaattgatgagcagttcttc	CASSPGARGIDEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgcaagcagccccgggactagcggagttggtgagcagttcttc	**CASSPGTSGVGEQFF***	15	12.00	12.80	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgcaagcagccccgggactagcggagttggtgagcagtttttc		1	0.80		

TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgcaagcagccccgggacgagcggagttggtaagcagtttttc	CASSPGTSGVGKQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagccccaggactagcgggggaggcgagcagtacttc	CASSPRTSGGGEQYF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtcccagtgctcgcggcaatcagccccagcatttt	CASSPSARGNQPQHF	2	1.60	1.60	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagcccgacgactagcgggagaggcgagcagtacttc	CASSPTTSGRGEQYF	2	1.60	1.60	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagttccgggactagcgggccgggggagcagttcttc	CASSSGTSGAGEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagttccgggactagcggagttggtgagcagttcttc	CASSSGTSGVGEQFF	1	0.80	27.20	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagttccgggactagcggggtcggggagcagttcttc	CASSSGTSGVGEQFF	33	26.40		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgtcgggactagcggggtgggcgagcagtacttc	CASSVGTSGVGEQYF	11	8.80	8.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagttacggggctagcggggtgggggagcagttcttc	CASSYGASGVGEQFF	1	0.80	0.80	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagttacaggactagcgggccccgggagcagttcttc	CASSYRTSGPREQFF	1	0.80	0.80	
			Total	24	125	100.00	100.00	

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V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD2*01	tgtgccagcaggaaagaaggatctaggctacacctc	CASRKEGSRLHL	1	0.66	0.66	36
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcagtgacagaacgacatgtggctacaccttc	CASSDRTTCGYTF	1	0.66	0.66	39
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcagtgaaagaaggatctatggctacaccttc	CASSERRIYGYTF	5	3.29	3.29	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagagccctagcgtcgggggtgagcagttcttc	CASRALASGGEQFF	5	3.29	3.29	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgctttagctagcggagataagcagtatttt	CASSALASGDKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgctttggctagcggagatacgcagtatttt	CASSALASGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgacgacagggtcggcgatgagcagttcttc	CASSDDRVGDEQFF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagcaaactagcgtctggagatgagcagttcttc	CASSKLASGDEQFF	4	2.63	2.63	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgttttacctggaggcaatgatccgctcttc	CASSVLPGGNDPLF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgttttacctggtcgcaatgagccgttcttc	CASSVLPGRNEPFF	1	0.66	0.66	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgcgccagcagtgttttacgtggtggcaatgagcagtttttc	CASSVLRGGNEQFF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgttttacgtggtcgcaatgagccgttcttc	CASSVLRGRNEPFF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01		tgtgccagcagtgttttacgtggtcgcaatgagcagttcttc	CASSVLRGRNEQFF	8	5.26	5.26	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgtttcacgaggtggcaataagcagtttttc	CASSVSRGGNKQFF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagtgtattaatgaggacgaacaatgagcagttcttc	CASVLMRTNNEQFF	9	5.92	5.92	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgctccagcagagctagagggtgcgcgggtaagcagtatttc	CSSRARGCAGKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgccctgactagcgggggcgatgagcagttcttc	CASSALTSGGDEQFF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcaaggactagcgggggatccgagcagttcttc	CASSARTSGGSEQFF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagtgctaggactagcgggagtgacgagcagtacttc	CASSARTSGSDEQYF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtgacagggcctcaggcggggatacgcagtatttt	CASSDRASGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgatcgggctagcgggggggatacgcagtatttt	CASSDRASGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtgatcgggctacagggggggatacgcagtatttt	CASSDRATGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgaaaaggctagcgggggggatacgcagtatttt	CASSEKASGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgaattggctagcgggggggatgagcagttcttc	CASSELASGGDEQFF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcacaaggcttcaggggggggataagcagtatttt	CASSHKASGGDKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagctctcacatggcctcaggcggcgatacgcagtatttt	CASSHMASGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcacagggcctcaggcggggctactccgtatttt	CASSHRASGGATPYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcaccgggcctcaggtggggatactccgcatttt	CASSHRASGGDTPHF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcacagggcctcaggcggggatacgcagtatttt	CASSHRASGGDTQYF	31	20.39	20.39	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagctcaaaactggctagcgggccgacgagcagtacttc	CASSKLASGADEQYF	6	3.95	4.61	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagctcaaaactggctagcgggccgacgagcagtatttc		1	0.66		
TRBV2*01, or TRBV2*02	TRBJ2-7*01	TRBD1*01	tgtgccagctcaaaacttactaggggcgcagataagcagtatttc	CASSKLTRGADKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtaagaggactagcggtacctacgagcagtacttc	CASSKRTSGTYEQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagcctccggactagcggctcctacgagcagtacttc	CASSLRTSGSYEQYF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtccccggactagcggtacctacgagcagtacttc	CASSPRTSGTYEQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagctcgccgcgagtcttctctgtcggggagctgtttttt	CASSPRVFSVGELFF	4	2.63	2.63	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagccaaagggctagcgggggggacgagcagttcttc	CASSQRASGGDEQFF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgtgccagcagtagacggactagcgggacctacgagcagtacttc	CASSRRTSGTYEQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagcgtccggactagcgggtcctacgagcagtacttc	CASSVRTSGSYEQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*02	tgcaccagcagtggtaggactagcgggagggataagcagtatttc	CTSSGRTSGRDKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtaccagcagtcacagggcctcaggcggggatacgcagtatttt	CTSSHRASGGDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgccaggattagcgggggctcaacgagcagtacttc	CASSARISGGLNEQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcaaggactagcgggggggccgatacgcagtatttt	CASSARTSGGADTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggggcttgacgagcagtacttc	CASSARTSGGLDEQYF	19	12.50	12.50	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgctcggactagcgggggggtcagatacgcagtatttt	CASSARTSGGSDTQYF	3	1.97	1.97	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtaaaaggactagcgggggggccgatacgcagtatttt	CASSKRTSGGADTQYF	2	1.32	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcttaggactagcgggggcacagatacgcagtatttt	CASSLRTSGGTDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccccaggactagcgggggcacagatacgcagtatttt	CASSPRTSGGTDTQYF	5	3.29	3.29	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagctcacgacgggcttccgggggcactactccgcattatttt	CASSRRASGGTTPHYF	1	0.66	0.66	48
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgacggactagcgggggcacagatacgcagtatttt	CASSRRTSGGTDTQYF*	1	0.66	1.32	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagctcacgacggactagcgggggcacagatacgcagtatttt		1	0.66		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*02	tgtgccagcagtcgtcggactagcgggagggcggatacgcagtatttt	CASSRRTSGRADTQYF	4	2.63	2.63	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*02	tgtgccagcagtcgtaggactagcgggagtctagatacgcagtatttt	CASSRRTSGSLDTQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD1*01	tgtgccagcagcaccaggattagaggggcacagatagcagtatttt	CASSTRIRGGTDKQYF	1	0.66	0.66	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgttaggactagcgggggcacagatacgcagtatttt	CASSVRTSGGTDTQYF	1	0.66	0.66	
			Total	52	152	100.00	100.00	

HIC 5 DR1+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01	TRBJ1-2*01	TRBD1*01	tgtgccagcagagacagtaactatggctacaccttc	CASRDSNYGYTF	1	1.61	1.61	36
TRBV2*02	TRBJ2-5*01	TRBD1*01	tgtgccagcagtcgacggacggagacccagtacttc	CASSRRTETQYF	3	4.84	4.84	
TRBV2*02	TRBJ2-4*01	TRBD1*01	tgtgccagcagtgaaaccagggccaacattcagtacttc	CASSETRANIQYF	1	1.61	1.61	39
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagcggactagcggcgaatgagcagttcttc	CASSGLAANEQFF	1	1.61	1.61	
TRBV2*01, or TRBV2*02	TRBJ1-1*01	TRBD1*01	tgtgcctcaagggcagggtcggtggccactgaagctttcttt	CASRAGSVATEAFF	1	1.61	1.61	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgggaggactagcggcaatgagcagttcttc	CASSGRTSGNEQFF	2	3.23	3.23	42
TRBV2*02	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgtcgtgggcagttacaatgagcagttcttc	CASSVVGSYNEQFF	34	54.84	54.84	
TRBV2*01	TRBJ2-1*01	TRBD1*01	tgtgccagtgtattaatgaggacgaacaatgagcagttcttc	CASVLMRTNNEQFF	4	6.45	6.45	
TRBV2*02	TRBJ2-2*01	TRBD1*01	tgtgccagcagggccgggacctcgggcaccggggagctgtttttt	CASRAGTSGTGELFF	1	1.61	1.61	
TRBV2*01, or TRBV2*02	TRBJ2-7*01	TRBD2*02	tgtgccagcaggaaggggactagcgggagtggcaagcagtacttc	CASRKGTSGSGKQYF	2	3.23	3.23	
TRBV2*02	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgaaaaggctagcgggtggatgagcagttcttc	CASSEKASGVDEQFF	1	1.61	1.61	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgaaaggctagcgggcacgatacgcagtatttt	CASSERASGHDTQYF	1	1.61	1.61	45
TRBV2*01	TRBJ2-3*01	TRBD1*01	tgtgccagcagtcacagggcctcaggcggggatacgcagtatttt	CASSHRASGGDTQYF	1	1.61	1.61	
TRBV2*01, or TRBV2*02	TRBJ2-7*01	TRBD2*01	tgtgccagctcaaaactggctagcgggccgacgagcagtacttc	CASSKLASGADEQYF	1	1.61	1.61	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtaaacaggctagcgggggcgacgagcagtacttc	CASSKQASGGDEQYF	8	12.90	12.90	
			Total	15	62	100.00	100.00	

HIC 6 DR11+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagagaatacgcgactagcaacgagcagtacttc	CASREYATSNEQYF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD2*01	tgtgccagcagtgaaatggcgaccgggttgcgctacaccttc	CASSEMATGLRYTF	1	1.52	1.52	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccagcagtgaaacggcgacagggttgcgctacaccttc	CASSETATGLRYTF	4	6.06	6.06	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-6*02	TRBD2*01	tgtgccagcacgctaacacgggttaattcacccctccacttt	CASTLTRVNSPLHF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcaatcaacggactagcgggccttacgagcagtacttc	CASNQRTSGPYEQYF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgatttggctagcggcacaggggagcagttcttc	CASSDLASGTGEQFF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgaagctgcaggggctacggtgagcagttcttc	CASSEAAGGYGEQFF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtgaatttgccaggggcaatcagccccagcatttt	CASSEFARGNQPQHF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtgaattcgtaagggacaatcagccccagcatttt	CASSEFVRDNQPQHF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtgaattcgtaaggggcaatcagccccagcatttt	CASSEFVRGNQPQHF	4	6.06	6.06	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtgaaggggcggctggcaatcagccccagcatttt	CASSEGAAGNQPQHF	1	1.52	1.52	

TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgaaggagctaggggcgtgggggagcagttcttc	CASSEGARGVGEQFF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-5*01	TRBD2*01	tgtgccagcagtgaagggggctagcggtacgggggcccagtacttc	CASSEGASGTGAQYF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD1*01	tgtgccagcagtgaaggcgctagtggcgtaggggagcagttcttc	CASSEGASGVGEQFF	1	1.52	1.52	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgagggtactagcacctttcgtgagcagttcttc	CASSEGTSTFREQFF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-2*01	TRBD2*01	tgtgccagcagtgaattagcgagcggcaccgggggagctgtttttt	CASSELASGTGELFF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD2*02	tgtgccagcagtggggcagcgaggggcaatcagccccagcatttt	CASSGAARGNQPQHF	5	7.58	7.58	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagcaaactgactagcgggggatacgagcagtacttc	CASSKLTSGGYEQYF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcccgggactagcggggttggtgagcagttcttc	CASSPGTSGVGEQFF*	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcgtctagcgggggtttcgatgagcagttcttc	CASSRLAGGFDEQFF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgactagcgggggggcacagatacgcagtatttt	CASSRLAGGTDTQYF	2	3.03	3.03	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtagactagcgtctggcacagatacgcagtatttt	CASSRLASGTDTQYF	5	7.58	7.58	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgtattggctagcgggctgggtgagcagtacttc	CASSVLASGLGEQYF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagacaggggggcgaggggaggcaatcagccccagcatttt	CASRQGARGGNQPQHF	6	9.09	9.09	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagctcacaggggggcgcgggggggaaatcagccccagcatttt	CASSQGARGGNQPQHF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtcgattagcgggggggagctcctacgagcagtacttc	CASSRLAGGSSYEQYF	2	3.03	3.03	48
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgcctgactagcgggggggcagatacgcagtatttt	CASSRLTSGGADTQYF	1	1.52	1.52	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgccggactagcgggggcacagatacgcagtatttt	CASSRRTSGGTDTQYF*	12	18.18	18.18	
			Total	28	66	100.00	100.00	

HIC 7 DRB5+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtcctcgggcctcgggggagagcagtacttc	CASSPRASGGEQYF	3	3.85	3.85	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-4*01	TRBD2*01	tgtgccagcagtgtgcggcggaataatgaaaaactgttttt	CASSVRRNNEKLFF	3	3.85	3.85	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcaaccgaaggactagcggaacctacgagcagtacttc	CASNRRTSGTYEQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgcactagcgtccgggggagatacgcagtatttt	CASSALASGGDTQYF	3	3.85	3.85	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcacgggctagcgggggggatgagcagttcttc	CASSARASGGDEQFF	3	3.85	5.13	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcacgggctagcgggggggatgagcagtttttc		1	1.28		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtgcccggacgagtgggggtcagccccagcatttt	CASSARTSGGQPQHF	4	5.13	5.13	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagcgcccggacatcgggcaatcagccccagcatttt	CASSARTSGNQPQHF	11	14.10	14.10	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgaactggctagcgggatcaatgagcagttcttc	CASSELASGINEQFF	5	6.41	6.41	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgagttgactagcgggggggatgagcagttcttc	CASSELTSGGDEQFF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*02	tgtgccagcagtaagaggacctctggaggagatacgcagtatttt	CASSKRTSGGDTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagcctaaggactagcgggggggatgagcagtacttc	CASSLRTSGGDEQYF	3	3.85	3.85	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcccccgactagcgccacagatacgcagtatttt	CASSPLTSATDTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcctcgggctagcgggggcgatgagcagttcttc	CASSPRASGGDEQFF	5	6.41	6.41	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagtccccggactagcgggggcgacgagcagtacttc	CASSPRTSGGDEQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcaggctccggactagcgggggtacagatacgcagtatttt	CASRLRTSGGTDTQYF	2	2.56	2.56	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagacgactagcgggtttatggcagatacgcagtatttt	CASRRLAGFMADTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcacggactagcgcgggcacagatacgcagtatttt	CASSARTSAGTDTQYF	1	1.28	7.69	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcacggactagcgctggcacagatacgcagtatttt		5	6.41		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggggcagatacgcatatttt	CASSARTSGGADTHYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggggcagatacgcagtatttt	CASSARTSGGADTQYF	1	1.28	2.56	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtctaggactagcgggggggcagatacgcagtatttt		1	1.28		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgcccggactagcgggggtcagatacgcagtatttt	CASSARTSGGSDTQYF	1	1.28	3.85	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcccaggactagcgggggtcagatacgcagtatttt		2	2.56		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcggaggcacagatacgcagtatttt	CASSARTSGGTDTQYF	2	2.56	3.85	48
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgctaggactagcgggggcacagatacgcagtatttt		1	1.28		
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgaacggactagcgggggacgcgatacgcagtatttt	CASSERTSGGRDTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcggtaggactagcgggggatcggatacgcagtatttt	CASSGRTSGGSDTQYF	3	3.85	3.85	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcttagggctagcgggggggtcagatacgcagtatttt	CASSLRASGGSDTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtctgaggactagcgggggggcagatacgcagtatttt	CASSLRTSGGADTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccaacggactagcgggggggcagatacgcagtatttt	CASSQRTSGGADTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgactgactagcgggggatcagatacgcagtatttt	CASSRLTSGGSDTQYF	4	5.13	5.13	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcgccggactagcgggggtctagatacgcagtatttt	CASSRRTSGGLDTQYF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcggcggactagcgggggcccaatgagcagttcttc	CASSRRTSGGPNEQFF	1	1.28	1.28	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcggaggactagcgggggcacagatacgcagtatttt	CASSRRTSGGTDTQYF*	1	1.28	1.28	
			Total	30	78	100.00	100.00	

HIC 8 DR1+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-7*01	TRBD1*01	tgtgccagcagtgaagggtgggaaccctacgagcagtacttc	CASSEGWEPYEQYF	1	1.49	1.49	42
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgagttgactagcgggggggatgagcagttcttc	CASSELTSGGDEQFF	63	94.03	94.03	45
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgagttgactagcgggggggatgagcagttgttc	CASSELTSGGDEQLF	1	1.49	1.49	
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcggaggcacagatacgcagtatttt	CASSARTSGGTDTQYF	1	1.49	1.49	48
TRBV2*01, or TRBV2*02 or TRBV2*03	TRBJ1-2*01	TRBD1*01	tgtgccaccaccgccgccgggacaggggtagacggaaactatggctacaccttc	CATTAAGTGVDGNYGYTF	1	1.49	1.49	54
			Total	5	67	100	100	

HAART 1 DRB5+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcaaacccgccagggccaatgagcagttcttc	CASKPARANEQFF	57	86.36	86.36	39
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcaaacccaccagggccaatgagcagttcttc	CASKPTRANEQFF	1	1.52	1.52	
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtgagagccacactgctgggtatggctacaccttc	CASSESHTAGYGYTF	8	12.12	12.12	45
			Total	3	66	100.00	100.00	

HAART 2 DRB5+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtgaactcgctgcgggcacagatacgcagtatttt	CASSELAAGTDTQYF	2	2.86	2.86	
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtgtactaaggacggtcaacactgaagctttcttt	CASSVLRTVNTEAFF	13	18.57	18.57	45
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcaccctcttgactagcggcaccggggagctgtttttt	CASTLLTSGTGELFF	17	24.29	24.29	
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtcggtcgtcgggaggcgcctacaatgagcagttcttc	CASSRSSGGAYNEQFF	38	54.29	54.29	48
			Total	4	70	100.00	100.00	

HAART 3 DR1+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagagtccgggctcaaggctacaccttc	CASRVRAQGYTF	2	3.39	3.39	36
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgtcagggctcaaggctacaccttc	CASSVRAQGYTF	30	50.85	50.85	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagccgcttcgggacatcgggcggggagctgtttttt	CASRFGTSGGELFF	1	1.69	1.69	42
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagaccctccacagcgtctacgagcagtacttc	CASRPLHSVYEQYF*	26	44.07	44.07	
			Total	4	59	100.00	100.00	

HAART 4 DR11+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgcaggactagcccgagatacgcagtatttt	CASSAGLARDTQYF	3	4.05	4.05	42
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtcccttagcggtgcaagagacccagtacttc	CASSPLAVQETQYF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagaggcaccgtactcgggggaaacaccatatatttt	CASRGTVLGGNTIYF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagaagactagccgggggaaccggggagctgtttttt	CASRRLAGGTGELFF	7	9.46	9.46	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgccctggctagtggcacagatacgcagtatttt	CASSALASGTDTQYF	2	2.70	2.70	

Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgacctcgctagcggaacagatacgcagtatttt	CASSDLASGTDTQYF	2	2.70	2.70	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaagcggcctcaggggtcggcgagcagtacttc	CASSEAASGVGEQYF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagcgaggggggcggcgggcaatcagccccagcatttt	CASSEGAAGNQPQHF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaaggtgcgaggggaagtcagccccagcatttt	CASSEGARGSQPQHF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaattagcatcgggcacagatacgcagtatttt	CASSELASGTDTQYF	3	4.05	4.05	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaattggcctccggtgtcaatgagcagttcttc	CASSELASGVNEQFF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaattaactagcggggtgagtgagcagtacttc	CASSELTSGVSEQYF	4	5.41	5.41	45
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgagcggactagcggggtcggtgagcagttcttc	CASSERTSGVGEQFF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgggatggctagcggaacagatacgcagtatttt	CASSGMASGTDTQYF	12	16.22	16.22	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtttactagcgggggggcatggatgagcagttcttc	CASSLLAGGMDEQFF	4	5.41	5.41	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagcctaaccactagcgggactggcgagcagtacttc	CASSLTTSGTGEQYF	5	6.76	6.76	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtccgggggcctcgggggtcggggagctgttttttt	CASSPGASGVGELFF	4	5.41	5.41	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtccattgactagcggcacagatacgcagtatttt	CASSPLTSGTDTQYF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtccagtggcggtgagcaatcagccccagcatttt	CASSPVAVSNQPQHF	2	2.70	2.70	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagccaactaacctctggcacagatacgcagtatttt	CASSQLTSGTDTQYF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtagactagcgggggggaatggacgagcagtacttc	CASSRLAGGMDEQYF	11	14.86	14.86	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagttcccgggcaaggggcaatcagccccagcatttt	CASSSRARGNQPQHF	1	1.35	1.35	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcctgagatcgactagcggggttatcgatgagcagttcttc	CASLRSTSGVIDEQFF	4	5.41	5.41	48
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcaggccgggactagcgggagggcttcaagagacccagtacttc	CASRPGLAGGLQETQYF	1	1.35	1.35	51
			Total	24	74	100.00	100.00	

HAART 5 DR1+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcactgagacagggtacggagctttcttt	CASTETGYGAFF	1	1.67	1.67	36
Homsap TRBV2*01	Homsap TRBJ2-6*01		tgtgccagcagtgaagtctctgggggccaacgtcctgactttc	CASSEVSGANVLTF	35	58.33	58.33	
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtgagtggggagagttgaacgagcagtacttc	CASSEWGELNEQYF	11	18.33	18.33	42
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagccggacaggggggcgcggagacccagtacttc	CASSRTGGAETQYF	6	10.00	10.00	
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtggcaggggctcaactaatgaaaaactgttttttt	CASSGRGSTNEKLFF	2	3.33	3.33	45
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagagcgccgggactagctttccaagagacccagtacttc	CASRAPGLAFQETQYF	1	1.67	1.67	48
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagagcgccgggactagctttccaagggacccagtacttc	CASRAPGLAFQGTQYF	4	6.67	6.67	
			Total	7	60	100.00	100.00	

HAART 6 DR1+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgcgccagcagtgaatttaggacaaggggctacaccttc	CASSEFRTRGYTF*	1	1.41	87.32	39
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaatttaggacaaggggctacaccttc		61	85.92		
Homsap TRBV2*01	Homsap TRB	Homsap TR	tgtgccagcagtgaaggacccggggtaagaaatggctacaccttc	CASSEGPGVRNGYTF	3	4.23	4.23	45
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcacccccactgtggcgcactcctacaatgagcagttcttc	CASTPTVAHSYNEQFF	4	5.63	5.63	48
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcatagtccgaactagcggggcgtcctacaatgagcagttcttc	CASIVRTSGASYNEQFF	2	2.82	2.82	51
			Total	4	71	100.00	100.00	

HAART 7 DR11+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TRBJ2-3*01	tgtgccagcagcgctcccgttaccgatacgcagtatttt	CASSAPVTDTQYF	4	5.00	5.00	39
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagctcaggacagacgaacactgaagctttcttt	CASSGQTNTEAFF	2	2.50	2.50	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcttgggacaggcgaacaccggggagctgttttttt	CASLGQANTGELFF	2	2.50	2.50	42
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TRBJ1-4*01	tgtgccagcaggcctttgcaactaatgaaaaactgttttttt	CASRPFATNEKLFF	35	43.75	43.75	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcggagtcctagcgtcgggcaccggggagctgttttttt	CASGVLASGTGELFF	12	15.00	15.00	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagccccggggctagcggtgtctacgagcagtacttc	CASSPGASGVYEQYF	1	1.25	1.25	45
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtcaggggactagcggggttggggagcagttcttc	CASSQGTSGVGEQFF	1	1.25	1.25	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaagggctgggggttcggtcagccccagcatttt	CASSEGAGGFGQPQHF	21	26.25	26.25	48
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgtttcgacaggggcattctggaaaaactgttttttt	CASSVSTGGILEKLFF	2	2.50	2.50	
			Total	9	80	100.00	100.00	

HAART 8 DRB5+

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgatggaggaatctatggctacaccttc	CASSDGGIYGYTF	2	2.35	2.35	39
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgatcgacgaatctatggctacaccttc	CASSDRRIYGYTF	18	21.18	21.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagatccctagtgagcaccggggagctgttttttt	CASRSLVSTGELFF	30	35.29	35.29	42
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgtcagcagatccctagtgagcaccggggagctgttttttt	CVSRSLVSTGELFF	1	1.18	1.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtgaatgggctaggggttccggggagctgttttttt	CASSEWARGSGELFF	7	8.24	8.24	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagccccccggactagcggggcagatacgcagtatttt	CASSPRTSGADTQYF	2	2.35	2.35	45
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagccccccggactagcgggggggacgagcagtacttc	CASSPRTSGGDEQYF	1	1.18	1.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtcctaggactagcggaacctacgagcagtacttc	CASSPRTSGTYEQYF	1	1.18	1.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtattcggactagcgggggaacagatacgcagtatttt	CASSIRTSGGTDTQYF	11	12.94	12.94	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagccttaggactagcgggggttcagatacgcagtatttt	CASSLRTSGGSDTQYF	1	1.18	1.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtctccggactagcgggggcacagatacgcagtatttt	CASSLRTSGGTDTQYF	2	2.35	3.53	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtcttcggactagcgggggaacagatacgcagtatttt		1	1.18		48
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtctccggactagcgggggtgtagatacgcaggatttt	CASSLRTSGGVDTQDF	1	1.18	1.18	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtctccggactagcgggggtgtagatacgcagtatttt	CASSLRTSGGVDTQYF	3	3.53	3.53	
Homsap TRBV2*01, orTRBV2*02 orTRE	Homsap TRB	Homsap TR	tgtgccagcagtccccggactagcgggggtcagatacgcagtatttt	CASSPRTSGGSDTQYF	4	4.71	4.71	
			Total	14	85	100.00	100.00	

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V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagccagcggggaaattcctacaatgagcagttcttc	CASQRGNSYNEQFF	2	4.17	4.17	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagaatccggactagcgggggggagcagtacttc	CASRIRTSGGEQYF	11	22.92	22.92	42
TRBV2*01	TRBJ2-1*01	TRBD1*01	tgtgccagcacccgggacaggacaaagaatgagcagttcttc	CASTRDRTKNEQFF	1	2.08	2.08	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcgttggctagcgggggagatgagcagttcttc	CASSALASGGDEQFF	1	2.08	2.08	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtctccggactagcgggggagatgagcagttcttc	CASSLRTSGGDEQFF	2	4.17	4.17	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagccctatggctagcgggggggatgagcagttcttc	CASSPMASGGDEQFF	2	4.17	4.17	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagccccccggactagcggcacagatacgcagtatttt	CASSPRTSGTDTQYF	2	4.17	4.17	45
TRBV2*01	TRBJ2-7*01	TRBD2*02	tgtgccagcagccgtaggactagcgggacttacgagcagtacttc	CASSRRTSGTYEQYF	1	2.08	2.08	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgtgatggctagccgtgggaatgagcagttcttc	CASSVMASRGNEQFF	1	2.08	2.08	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgtcagcagtgcgttggctagcgggggagatgagcagttcttc	CVSSALASGGDEQFF	1	2.08	2.08	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcaataaattgactagcgggggccgggatacgcagtatttt	CASNKLTSGGRDTQYF	4	8.33	8.33	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggctcggatacgcagtatttt	CASSARTSGGSDTQYF	4	8.33	8.33	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagcaaaaggactagcgggggcgactgatgagcagttcttc	CASSKRTSGATDEQFF	2	4.17	4.17	
TRBV2*01	TRBJ2-5*01	TRBD2*01	tgtgccagcagtttgttgactagcgggggacgggagacccagtacttc	CASSLLTSGGRETQYF	6	12.50	12.50	48
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagccgcttgacgagcgggggggcggaatgagcagttcttc	CASSRLTSGGRNEQFF	2	4.17	4.17	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagctccaggactagcgggggcacagatacgcagtatttt	CASSSRTSGGTDTQYF	3	6.25	6.25	
TRBV2*01	TRBJ1-5*01	TRBD2*01	tgtgccacctccagaggagcgcggggaagcaatcagccccagcatttt	CATSRGARGSNQPQHF	3	6.25	6.25	
			Total	17	48	100.00	100.00	

HIC 2 DRB5+ ex vivo

V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-2*01	TRBD1*01	tgtgccagcagagacggcctcggggagctgtttttt	CASRDGLGELFF	1	2.00	2.00	36
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ1-1*01	TRBD1*01	tgtgccagctcaggacagacgaacactgaagctttcttt	CASSGQTNTEAFF	3	6.00	6.00	39
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgcactggctagcggaacagatacgcagtatttt	CASSALASGTDTQYF	1	2.00	2.00	
TRBV2*01	TRBJ2-5*01	TRBD2*01	tgtgccagcagtgaattggctagcgggcagggatcccagtacttc	CASSELASGQGSQYF	5	10.00	10.00	
TRBV2*01	TRBJ2-7*01	TRBD2*02	tgtgccagcagtgaactggctagcgggagctacgagcagtacttc	CASSELASGSYEQYF	3	6.00	6.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtgaactggctagcgggacgggtgagcagttcttc	CASSELASGTGEQFF	1	2.00	2.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagccctcggactagcggtccctacgagcagtacttc	CASSPRTSGPYEQYF	3	6.00	6.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccaattgactagcggcacagatacgcagtatttt	CASSQLTSGTDTQYF	2	4.00	4.00	45
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*02	tgtgccagcagtcgactagcgggaggatttgatgagcagttcttc	CASSRLAGGFDEQFF	1	2.00	2.00	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcggttggctagcggcacagatacgcagtatttt	CASSRLASGTDTQYF	4	8.00	8.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagtcggacagtctcgggcaatcagccccagcatttt	CASSRTVSGNQPQHF	1	2.00	2.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagcagttcgttggctagcagaccctacgagcagtacttc	CASSSLASRPYEQYF	1	2.00	2.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcacgaagggcgctagcgggtcgggtgagcagttcttc	CASTKGASGSGEQFF	2	4.00	4.00	
TRBV2*01	TRBJ2-1*01	TRBD2*02	tgtgccaccacccccggggctagcgggataagtgagcagttcttc	CATTPGASGISEQFF*	14	28.00	28.00	
TRBV2*01	TRBJ2-7*01	TRBD1*01	tgtgccagcagtgaaaggggacaggggggcgcggtacgagcagtacttc	CASSERGQGARYEQYF	5	10.00	10.00	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgaaggactagcggaggcacagatacgcagtatttt	CASSRRTSGGTDTQYF*	2	4.00	6.00	48
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgaaggactagcggaggtacagatacgcagtatttt		1	2.00		
			Total	16	50	100.00	100.00	

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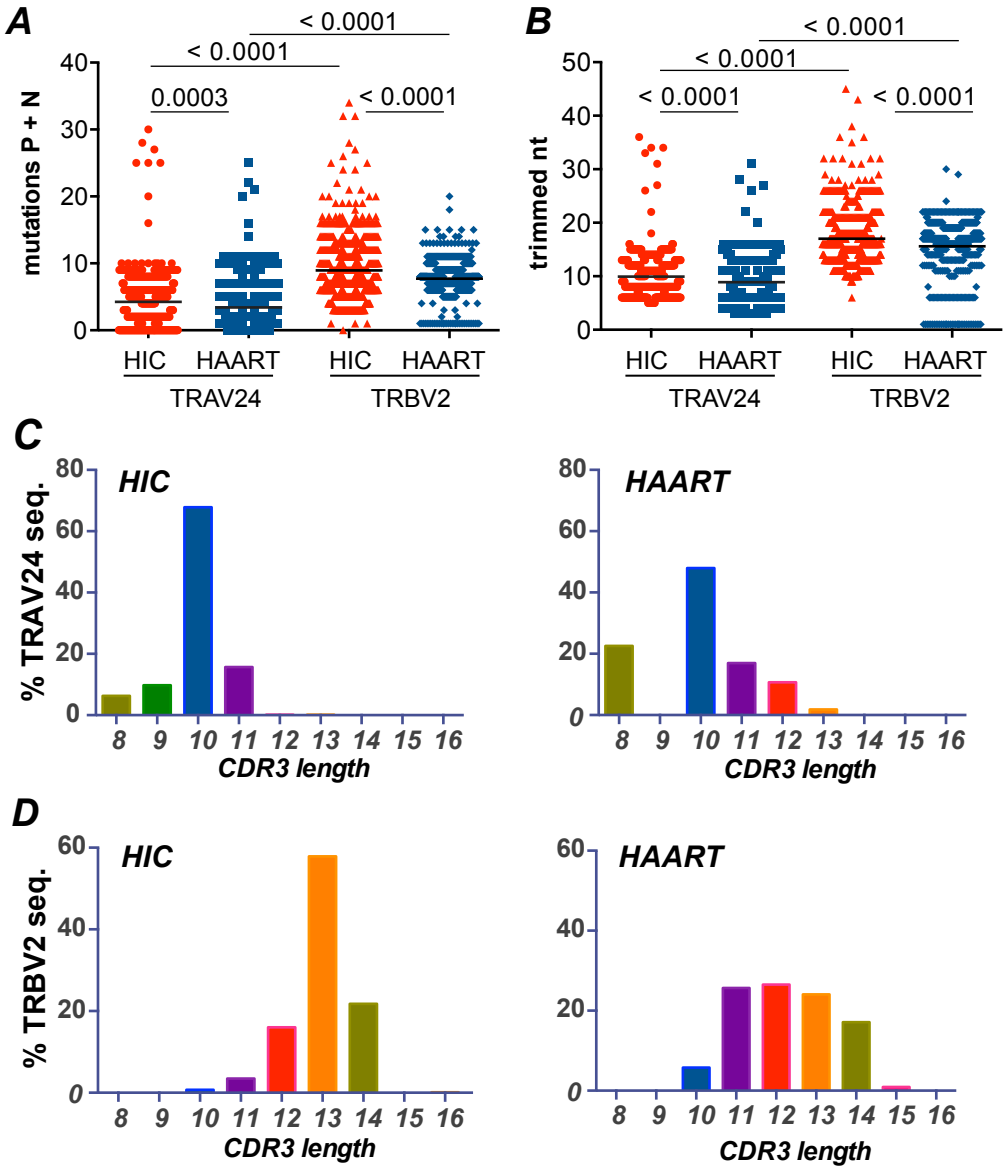
V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01	TRBJ2-1*01	TRBD2*02	tgtgccagcgcccgactagcgggaggtaccgatgagcagttcttc	CASARLAGGTDEQFF	1	4.00	4.00	
TRBV2*01	TRBJ1-5*01	TRBD2*01	tgtgccagcagcgcgaaggcccgcgggaatcagccccagcatttt	CASSAKARGNQPQHF	2	8.00	8.00	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgcactagcgggggggaacagatacgcagtatttt	CASSALAGGTDTQYF	3	12.00	12.00	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtctttggctagcggcacagatacgcagtatttt	CASSALASGTDTQYF	5	20.00	20.00	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgacgcggctagcggtgtgggcgagcagtacttc	CASSDAASGVGEQYF	4	16.00	16.00	45
TRBV2*01	TRBJ1-5*01	TRBD1*01	tgtgccagcagcggacaggcgaggggcaatcagccccagcatttt	CASSGQARGNQPQHF	4	16.00	16.00	
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgcaagcagccccgggactagcggagttggtgagcagttcttc	CASSPGTSGVGEQFF*	4	16.00	16.00	
TRBV2*01	TRBJ1-5*01	TRBD1*01	tgtgccagcagtcccagtgctcgcggcaatcagccccagcatttt	CASSPSARGNQPQHF	1	4.00	4.00	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtgtcgggactagcggggtgggcgagcagtacttc	CASSVGTSGVGEQYF	1	4.00	4.00	
			Total	9	25	100.00	100.00	

HIC 7 DRB5+ ex vivo

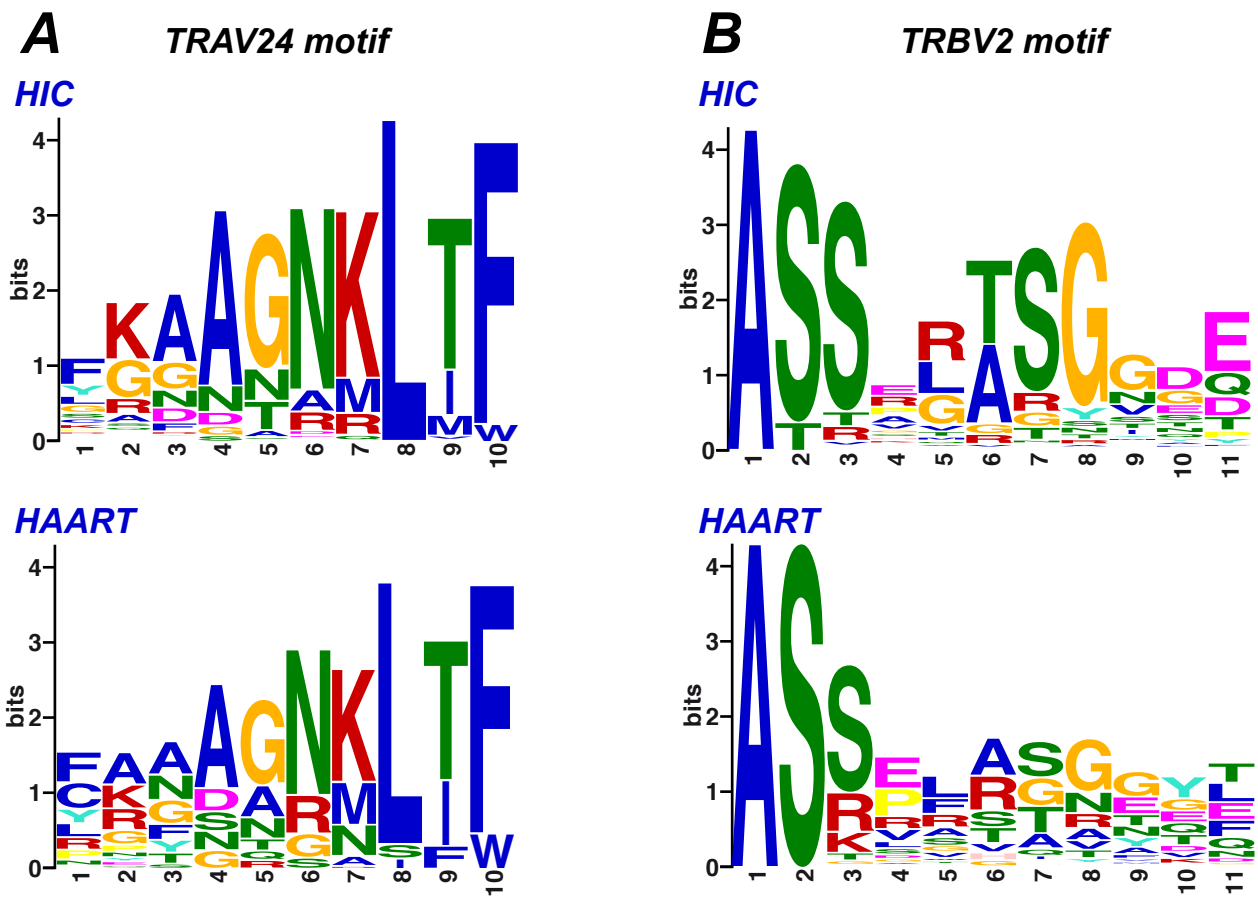
V-GENE	J-GENE	D-GENE	JUNCTION	JUNCTION (AA)	frequency	% nt seq	% AA seq	JUNCTION nt number
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagccaggcaagcggccgatcctacgagcagtacttc	CASQASGRSYEQYF	4	3.67	3.67	
TRBV2*01	TRBJ2-5*01	TRBD1*01	tgtgccagcagtgaatttgggggcaagagacccagtacttc	CASSEFWGQETQYF	1	0.92	0.92	42
TRBV2*01	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgagctggctagcggggatgagcagttcttc	CASSELASGDEQFF	9	8.26	8.26	
TRBV2*01	TRBJ2-7*01	TRBD1*01	tgtgccagcagtgtatcgcaggggagcgacgagcagtacttc	CASSVSQGSDEQYF	1	0.92	0.92	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-7*01	TRBD2*01	tgtgccagctgtcccatggctagccgatcctacgagcagtacttc	CASCPMASRSYEQYF	1	0.92	0.92	
TRBV2*01	TRBJ1-2*01	TRBD1*01	tgtgccagcattatcggttcccaaggggcctatggctacaccttc	CASIIGSQGAYGYTF	1	0.92	0.92	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgcactagcgtccgggggagatacgcagtatttt	CASSALASGGDTQYF	6	5.50	5.50	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtgcacgggctagcgggggggatgagcagttcttc	CASSARASGGDEQFF	4	3.67	3.67	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ1-5*01	TRBD1*01	tgtgccagcagcgcccggacatcgggcaatcagccccagcatttt	CASSARTSGNQPQHF	5	4.59	4.59	
TRBV2*01, orTRBV2*02	TRBJ1-1*01	TRBD1*01	tgtgccagcagtgaacgcgggacagccaacactgaagctttcttt	CASSERGTANTEAFF	1	0.92	0.92	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcttcaggactagcgggggtgatacgcagtatttt	CASSFRTSGGDTQYF	2	1.83	1.83	45
TRBV2*01, orTRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagtaagcgggctagcgggggagatacgcagtatttt	CASSKRASGGDTQYF	2	1.83	1.83	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcctcgggctagcgggggcgatgagcagttcttc	CASSPRASGGDEQFF	3	2.75	2.75	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtccccgggactagcgggggcgacgagcagtacttc	CASSPRTSGGDEQYF	7	6.42	6.42	
TRBV2*01, orTRBV2*02	TRBJ2-7*01	TRBD2*02	tgtgccagcagccccaggactagcgggacctacgagcagtacttc	CASSPRTSGTYEQYF	1	0.92	15.60	
TRBV2*01	TRBJ2-7*01	TRBD2*02	tgtgccagcagtcctcggactagcgggacctacgagcagtacttc		16	14.68		
TRBV2*01	TRBJ2-7*01	TRBD1*01	tgtgccagcagccccgtggccaggggccttacgagcagtacttc	CASSPVARGPYEQYF	1	0.92	0.92	
TRBV2*01	TRBJ2-7*01	TRBD2*01	tgtgccagcagtcaactgactagcagaacctacgagcagtacttc	CASSQLTSRTYEQYF	1	0.92	0.92	
TRBV2*01, orTRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcgggggtcagatacgcagtatttt	CASSARTSGGSDTQYF	6	5.50	5.50	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagcgcccggactagcgggggcacagatacgcagtatttt	CASSARTSGGTDTQYF	1	0.92	11.01	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgccaggactagcggaggcacagatacgcagtatttt		11	10.09		
TRBV2*01, orTRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagcggtaggactagcgggggatcggatacgcagtatttt	CASSGRTSGGSDTQYF	4	3.67	3.67	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtctgaggactagcgggggggcagatacgcagtatttt	CASSLRTSGGADTQYF	1	0.92	0.92	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtctcaggactagcgggggttcagatacgcagtatttt	CASSLRTSGGSDTQYF	2	1.83	1.83	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcctctgactagcgggggcacagatacgcagtatttt	CASSPLTSGGTDTQYF	1	0.92	0.92	
TRBV2*01, orTRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagtcggaggactagcggggcctcagatacgcagtatttt	CASSRRTSGASDTQYF	1	0.92	0.92	
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagtcgacgtactagcgggggggccgatgagcagttcttc	CASSRRTSGGADEQFF	1	0.92	0.92	48
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-3*01	TRBD2*01	tgtgccagcagccgacggactagcgggggggacggatacgcagtatttt		2	1.83	5.50	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagccggcggactagcgggggcacagatacgcagtatttt	CASSRRTSGGTDTQYF*	2	1.83		
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtagaaggactagcggtggcacagatacgcagtatttt		1	0.92		
TRBV2*01, orTRBV2*02	TRBJ2-3*01	TRBD2*01	tgtgccagcagtagacggactagcgggggggacagatacgcagtatttt		1	0.92		
TRBV2*01, orTRBV2*02 orTRBV2*03	TRBJ2-1*01	TRBD2*01	tgtgccagcagacgaactagcgggggatacgatgagcagttcttc	CASSRRTSGGYDEQFF	2	1.83	1.83	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtagccggactagcgggggatcagatacgcagtatttt	CASSSRTSGGSDTQYF	5	4.59	4.59	
TRBV2*01	TRBJ2-3*01	TRBD2*01	tgtgccagcagtgttcggactagcgggggggtcagatacgcagtatttt	CASSVRTSGGSDTQYF	1	0.92	0.92	
TRBV2*01	TRBJ2-7*01	TRBD1*01	tgtgccagcagtataagtttacccgggacactttattacgagcagtacttc	CASSISLPGTLYYEQYF	1	0.92	0.92	51
			Total	30	109	100.00	100.00	



Supplemental Figure S4: Analysis of mutations and CDR3 lengths in Gag293-specific clonotypes

(A) The number of mutations (P + N) inserted in Gag293-specific clonotypes compared to TRAV24-containing (left) or TRBV2-containing (right) germline sequences is reported.
(B) The number of germline nucleotides trimmed during V(D)J recombination to generate the observed Gag293-speific TRAV24-containing (left) and TRBV2-containing (right) clonotypes is reported.
(A and B): The numbers of mutations and trimmed nucleotides were computed in the IMGT/HighV-QUEST program, using the IMGT database of human germline TRAV and TRBV alleles as a reference (www.imgt.org). Significant differences between means (P<0.05) obtained by the unpaired student t-test are reported.

(C): the distribution of CDR3 lengths were compared for TRAV24 between the sets of HIV controller sequences (HIC, n=584) and treated patient sequences (HAART, n=496). CDR3 lengths are reported in number of a.a.
(D): the distribution of CDR3 lengths were compared for TRBV2 between the sets of HIV controller sequences (HIC, n=716) and treated patient sequences (HAART, n=566).
The CDR3 length was computed by counting the number of residues comprised between but not including the conserved cysteine (C104) and the conserved phenylalanine or tryptophan (F/W 118) that define the boundaries of this hypervariable TCR region. For TRAV24 sequences, CDR3 length peaked at 10 a.a., consistent with the Immunoscope data (A). The 10 a.a. peak represented 68% and 48% of HIC and HAART TRAV24 sequences, respectively, pointing to more homogenous CDR3 lengths in Controller sequences (P=5.61e-11; kurtosis: 7.35 for HIC vs 2.91 for HAART). For TRBV2 sequences (B), CDR3 lengths showed a peak at 13 a.a. in HIC sequences, while CDR3 lengths were more evenly distributed in HAART sequences (P<2.2e-16; kurtosis: 4.82 for HIC vs -2.16 for HAART). Thus, CDR3 lengths were more narrowly distributed in the HIC than in the HAART group.



Supplemental Figure S5:

Identification of prevalent amino acid motifs in Gag293-specific clonotypes

The Meme motif discovery program (meme-suite.org) was used to identify the most prevalent a.a. motifs in HIV controller (HIC) and treated patients (HAART) clonotypes. The Meme program was used in normal mode with the «one ocurrence per sequence» option, to take all clonotypes into account. The relative sizes of the letters in the logo are proportional to their frequencies, while the total height of the letters indicates the information content of the position, in bits.

(A) Most prevalent motif in TRAV24 clonotypes from the HIC (top; n=584) and HAART (bottom; n=496) groups.

(B) Most prevalent motif in TRBV2 clonotypes from the HIC (top; n=716) and HAART (bottom; n=566) groups.

A- TRAV24 Public Clonotypes

			HIC1 DR15	HIC2 DRB5	HIC3 DR11	HIC4 DR15	HIC5 DR1	HIC6 DR11	HIC7 DRB5	HIC8 DR1	HAA1 DRB5	HAA2 DRB5	HAA3 DR1	HAA4 DR11	HAA5 DR1	HAA6 DR1	HAA7 DR11	HAA8 DRB5	Nb of HIC	Nb of HAART
TRAJ17	CAFKAAGNKLTF	tgtgcctttaaagctgcaggcaacaagctaacttttt	2	35	8			11						59			37		6	2
		tgtgcctttaaggctgcaggcaacaagctaacttttt	1				1													
		tgtgccttcaaagctgcaggcaacaagctaacttttt		2	64			2	10					1						
		tgtgcatttaaagctgcaggcaacaagctaacttttt						1												
	CAFRAAGNKLTF	tgtgccttcagggctgcaggcaacaagctaacttttt			2														4	1
		tgtgcctttagagctgcaggcaacaagctaacttttt				1														
		tgtgcctttcgagctgcaggcaacaagctaacttttt					2									3				
		tgtgcctttagggctgcaggcaacaagctaacttttt						1												
	CAHKAAGNKLTF	tgtgcccacaaagctgcaggcaacaagctaactttt		2					3										2	0
		tgtgcccataaagctgcaggcaacaagctaacttttt		1																
	CALKAAGNKLTF	tgtgccttgaaagctgcaggcaacaagctaacttttt			1														2	1
		tgtgccttaaaagctgcaggcaacaagctaacttttt												1						
		tgtgctctaaaagctgcaggcaacaagctaacttttt						6												
	CASKAAGNKLTF	tgtgcctctaaagctgcaggcaacaagctaacttttt		13															2	0
		tgtgcctccaaagctgcaggcaacaagctaacttttt			4															
	CSRRAAGNKLTF	tgtagtcggagggctgcaggcaacaagctaacttttt			18							10							1	1
TRAJ32	CAEYGGATNKLIF	tgtgccgaatatggtggtgctacaaacaagctcatctttt				2	1		3										3	0
	CANYGGATNKLIF	tgtgccaactatggcggtgctacaaacaagctcatctttt							2	5									2	0
	CAPYGGATNKLIF	tgtgcccctatggtggtgctacaaacaagctcatctttt				2			1										2	1
		tgtgctcctatggcggtgctacaaacaagctcatctttt							1											
		tgtgccccgtatggtggtgctacaaacaagctcatctttt																1		
	CARYGGATNKLIF	tgtgcccgttatggtggtgctacaaacaagctcatctttt				10													1	1
		tgtgctcgttatggtggtgctacaaacaagctcatctttt				1														
		tgtgctcggtatggtggtgctacaaacaagctcatctttt																26		
	CASYGGATNKLIF	tgtgcctcttatggtggtgctacaaacaagctcatctttt	8			1			1										3	0
		tgtgcctcctatggtggtgctacaaacaagctcatctttt				25			1											
		tgtgcctcgtatggtggtgctacaaacaagctcatctttt				2														
		tgtgcctcctatggcggtgctacaaacaagctcatctttt							2											
TRAJ38	CAFDNRKLIW	tgtgccttcgacaaccgtaagctgatttgg					31				37								1	1
		tgtgcctttgacaaccgtaagctgatttgg					2													
TRAJ39	CAFRNAGNMLTF	tgtgcctttcgtaatgcaggcaacatgctcacctttt		1															2	2
		tgtgccttcggaatgcaggcaacatgctcacctttt						1												
		tgtgccttaggaatgcaggcaacatgctcacctttt												4						
		tgtgccttagaaatgcaggcaacatgctcacctttt															10			
	CALNNAGNMLTF	tgtgccctcaataatgcaggcaacatgctcacctttt						1											1	1
		tgtgccttaaataatgcaggcaacatgctcacctttt														24				
	CALRNAGNMLTF	tgtgccctgcggaatgcaggcaacatgctcacctttt						3											1	1
		tgtgccttaagaaatgcaggcaacatgctcacctttt												1						
		tgtgccttacgaaatgcaggcaacatgctcacctttt												12						
	CATRRAGNMLTF	tgtgcgacgcgccgtgcaggcaacatgctcacctttt				6	5												2	0
TRAJ54	CASESTGAQKLVF	tgtgcctccgagtccacgggagcccagaagctggtattt				3	1												2	0
TRAJ57	CAYEGASEKLVF	tgtgcctacgaggggcatctgaaaagctggtcttt				3	1												2	0

B- TRBV2 Public Clonotypes

			HIC1 DR15	HIC2 DRB5	HIC3 DR11	HIC4 DR15	HIC5 DR1	HIC6 DR11	HIC7 DRB5	HIC8 DR1	HAA1 DRB5	HAA2 DRB5	HAA3 DR1	HAA4 DR11	HAA5 DR1	HAA6 DR1	HAA7 DR11	HAA8 DRB5	Nb of HIC	Nb of HAART
TRBJ1-1	CASSGQTNTEAFF	tgtgccagctcaggacagacgaacactgaagctttcttt			10												2		1	1
TRBJ1-5	CASSEGAAGNQPQHF	tgtgccagcagtgaagggcggctggcaatcagccccagcatttt						1											1	1
		tgtgccagcagcgaggggggcggcgggcaatcagccccagcatttt												1						
TRBJ2-1	CASSELTSGGDEQFF	tgtgccagcagtgagttgactagcgggggggatgagcagttcttc							1	63									2	0
	CASSPGTSGVGEQFF	tgtgcaagcagccccgggactagcggagttggtgagcagttcttc			15														2	0
		tgtgcaagcagccccgggactagcggagttggtgagcagttttc			1															
		tgtgccagcagtcccgggactagcggggttggtgagcagttcttc						2												
	CASVLMRTNNEQFF	tgtgccagtgtattaatgaggacgaacaatgagcagttcttc				9	4												2	0
TRBJ2-3	CASSALASGTDTQYF	tgtgccagcagtgcgttagctagcggtacagatacgcagtatttt	1																2	1
		tgtgccagcagtgctttggctagcggcacagatacgcagtatttt			1															
		tgtgccagcagtgccctggctagtggcacagatacgcagtatttt												2						
	CASSARTSGGADTQYF	tgtgccagcagtgcaaggactagcgggggggccgatacgcagtatttt				1													2	0
		tgtgccagcagtgccaggactagcgggggggcagatacgcagtatttt							1											
		tgtgccagcagtgctaggactagcgggggggcagatacgcagtatttt							1											
	CASSARTSGGSDTQYF	tgtgccagcagtgccaggactagcgggggctcggatacgcagtatttt	1																3	0
		tgtgccagcagtgctcggactagcgggggtcagatacgcagtatttt				3														
		tgtgccagcagcgcccggactagcgggggtcagatacgcagtatttt							1											
		tgtgccagcagtgccaggactagcgggggtcagatacgcagtatttt							2											
	CASSARTSGGTDTQYF	tgtgccagcagtgccaggactagcggaggcacagatacgcagtatttt							2	1									2	0
		tgtgccagcagtgctaggactagcgggggcacagatacgcagtatttt							1											
	CASSHRASGGDTQYF	tgtgccagcagtcacagggcctcaggcggggatacgcagtatttt				31	1												2	0
	CASSLRTSGGSDTQYF	tgtgccagcagcctaaggactagcgggggttcagatacgcagtatttt	1																1	1
		tgtgccagcagccttaggactagcgggggttcagatacgcagtatttt																1		
	CASSLRTSGGTDTQYF	tgtgccagcagtcttaggactagcgggggcacagatacgcagtatttt				1													1	1
		tgtgccagcagtctccggactagcgggggcacagatacgcagtatttt																2		
		tgtgccagcagtcttcggactagcgggggaacagatacgcagtatttt																1		
	CASSPLTSGTDTQYF	tgtgccagcagtccgttgactagcggaacagatacgcagtatttt		1															1	1
		tgtgccagcagtccattgactagcggcacagatacgcagtatttt												1						
	CASSRRTSGGTDTQYF	tgtgccagcagtcgtaggactagcgggggcacagatacgcagtatttt		6															4	0
		tgtgccagcagtcgacggactagcgggggcacagatacgcagtatttt				1														
		tgtgccagctcacgacggactagcgggggcacagatacgcagtatttt				1														
		tgtgccagcagccgccggactagcgggggcacagatacgcagtatttt						12												
		tgtgccagcagtcggaggactagcgggggcacagatacgcagtatttt							1											
TRBJ2-7	CASSKLASGADEQYF	tgtgccagctcaaaactggctagcgggggccgacgagcagtacttc				6	1												2	0
		tgtgccagctcaaaactggctagcgggggccgacgagcagtatttc				1														
	CASSPRTSGGDEQYF	tgtgccagcagtccccggactagcgggggcgacgagcagtacttc							1										1	1
		tgtgccagcagccccccggactagcgggggggacgagcagtacttc																1		
	CASSPRTSGTYEQYF	tgtgccagcagtccccggactagcggtacctacgagcagtacttc				1													1	1
		tgtgccagcagtcctaggactagcggaacctacgagcagtacttc																1		
	CASSRRTSGTYEQYF	tgtgccagcagccgtaggactagcgggacttacgagcagtacttc	1																2	0
		tgtgccagcagtagacggactagcgggacctacgagcagtacttc				1														

Supplemental Figure S6: Distribution of Gag293-specific public clonotypes

The number of nucleotide sequences coding for a TRAV24 (A) or TRBV2 (B) public clonotype is reported for each patient studied. The number of HIC and HAART patients sharing a given public clonotype is reported in the last two columns. HIC: HIV controler; HAART or HAA: patient receiving highly active antiretroviral therapy. The tetramer used for sorting (DR1, DR11, DR15, or DRB5) is reported below each patient code.

Seq.	V name	3'V-region	P	N	5'J-REGION	J name	N	trim	%
1	TRAV24*01	tgtgccttta			......aagctgcaggcaacaagctaactttt	TRAJ17*01	0	6	64.9 %
2	TRAV24*01	tgtgccttta		ag	........gctgcaggcaacaagctaactttt	TRAJ17*01	2	8	0.9 %
3	TRAV24*01	tgtgcctt..			....caaagctgcaggcaacaagctaactttt	TRAJ17*01	0	6	33.8 %
4	TRAV24*01	tgtgc.....		attt	.....aaagctgcaggcaacaagctaactttt	TRAJ17*01	4	10	0.4 %

Supplemental Table S7: Structure of the CDR3 junction coding for the most prevalent public clonotype TRAV24-F.

The 4 nucleotide sequences coding for the CDR3 junction CAFKAAGNKLTF, which corresponds to the most prevalent public clonotype TRAV24-F, are reported with gene segments indicated according to the IMGT nomenclature. No P mutations (P) were detected in these sequences. The number of N mutations (N), the number of trimmed nucleotides (trim), and the respective frequencies of the 4 nucleotide sequences coding for the public clonotype TRAV24-F (%) are reported in the rightmost columns.

Supplemental Table S8: Intrapatient comparison of Gag293-specific clonotypic repertoires obtained with different MHC II tetramers

The Gag293-specific repertoire was compared in two cell lines obtained from the same patient but sorted with two distinct MHC II tetramers.
The TRAV24 clonotypes (A) and TRBV2 clonotypes (B) shared between the two tetramer+ samples are highlighted in orange.
Comparisons are shown for 3 HIV controllers. Public clonotypes are in bold colored type. Clonotypes tested functionally are marked by an asterisk.

A- TRAV24 clonotypes

HIC 1 DR15+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ38*01	CARDDRKLIW	1.89
TRAV24	TRAJ34*01	CASGNTDKLIF	1.89
TRAV24	TRAJ39*01	CAFCNAGNMLTF	1.89
TRAV24	TRAJ17*01	**CAFKAAGNKLTF***	5.66
TRAV24	TRAJ17*01	CAFTAAGNKLTF	1.89
TRAV24	TRAJ17*01	CALENAGNKLTF	1.89
TRAV24	TRAJ39*01	CALGNAGNMLTF	64.15
TRAV24	TRAJ57*01	CSPQGGSEKLVF	1.89
TRAV24	TRAJ6*01	CAFIPGGSYIPTF	1.89
TRAV24	TRAJ42*01	CASDGGSQGNLIF	1.89
TRAV24	TRAJ32*02	**CASYGGATNKLIF**	15.09
Total		11	100.00

HIC1 DRB5+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ34*01	CAFDNTDKLIF	6.82
TRAV24	TRAJ17*01	**CAFKAAGNKLTF***	11.36
TRAV24	TRAJ39*01	CALGNAGNMLTF	4.55
TRAV24	TRAJ17*01	CSFKAAGNKLTF	2.27
TRAV24	TRAJ17*01	CSFKGAGNKLIF	2.27
TRAV24	TRAJ57*01	CSPQGGCEKLVF	2.27
TRAV24	TRAJ6*01	CAFIPGGSYIPTF	2.27
TRAV24	TRAJ32*02	CALYGGATNKLIF	2.27
TRAV24	TRAJ32*02	CASYGGAPHDLIF	2.27
TRAV24	TRAJ32*02	CASYGGATKILFV	2.27
TRAV24	TRAJ32*02	**CASYGGATNKLIF**	61.37
Total		11	100.00

HIC 3 DR11+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ17*01	CAPKSRQQANF	0.64
TRAV24	TRAJ17*01	**CAFKAAGNKLTF***	46.16
TRAV24	TRAJ17*01	**CAFRAAGNKLTF**	1.28
TRAV24	TRAJ17*01	**CALKAAGNKLTF**	0.64
TRAV24	TRAJ39*01	CALKQAGNKLTF	0.64
TRAV24	TRAJ39*01	CALRQAGNMLTF	3.85
TRAV24	TRAJ17*01	CAMKAAGNKLTF	1.28
TRAV24	TRAJ17*01	CANRAAGNKLTF	0.64
TRAV24	TRAJ17*01	**CASKAAGNKLTF***	2.56
TRAV24	TRAJ17*01	CAYKAAGNKLTF	0.64
TRAV24	TRAJ17*01	CGFKAAGNKLTF	0.64
TRAV24	TRAJ17*01	CGWKAAGNKLTF	0.64
TRAV24	TRAJ17*01	CSLKAAGNKLTF	1.28
TRAV24	TRAJ17*01	CSLRAAGNKLTF	0.64
TRAV24	TRAJ17*01	**CSRRAAGNKLTF***	11.54
TRAV24	TRAJ17*01	CSWKAAGNKLTF	2.56
TRAV24	TRAJ17*01	CSWRAAGNKLTF	1.28
TRAV24	TRAJ17*01	CTKKAAGNKLTF	21.15
TRAV24	TRAJ17*01	CTLKAAGNKLTF	0.64
TRAV24	TRAJ17*01	CTNKAAGNKLTF	0.64
TRAV24	TRAJ17*01	CTRKAAGNKLTF	0.64
Total		22	100.00

HIC 3 DRB5+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ17*01	**CALKAAGNKLTF**	1.79
TRAV24	TRAJ17*01	CALRAAGNKLTF	1.79
TRAV24	TRAJ17*01	CALRAAGNMLTF	3.58
TRAV24	TRAJ39*01	CALRQAGNMLTF	62.50
TRAV24	TRAJ17*01	CASQAAGNKLTF	1.79
TRAV24	TRAJ17*01	**CSRRAAGNKLTF***	28.57
Total		6	100.00

HIC 7 DRB5+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ20*01	CAFGDYKLSF	3.64
TRAV24	TRAJ17*01	CAFHAAGNKLTF	1.82
TRAV24	TRAJ17*01	**CAFKAAGNKLTF***	18.18
TRAV24	TRAJ10*01	CAFKGGGNKLTF	1.82
TRAV24	TRAJ17*01	CAFNAAGNKLTF	5.45
TRAV24	TRAJ17*01	CAFQAAGNKLTF	16.36
TRAV24	TRAJ10*01	CAFRGGGNKLTF	20.00
TRAV24	TRAJ39*01	CAFRRAGNMLTF	1.82
TRAV24	TRAJ17*01	**CAHKAAGNKLTF**	5.45
TRAV24	TRAJ17*01	CAHKGAGNKLTF	1.82
TRAV24	TRAJ32*02	**CAEYGGATNKLIF**	5.45
TRAV24	TRAJ32*01	**CANYGGATNKLIF**	3.64
TRAV24	TRAJ57*01	CAPGGGGSEKLVF	3.64
TRAV24	TRAJ32*02	**CAPYGGATNKLIF**	3.64
TRAV24	TRAJ32*01	**CASYGGATNKLIF**	7.28
Total		15	100.00

HIC 7 DR1502+

V-GENE	J-GENE	JUNCTION (AA)	% nt seq
TRAV24	TRAJ31*01	CAFDNARLMF	1.03
TRAV24	TRAJ31*01	CASYGAALMF	1.03
TRAV24	TRAJ36*01	CAYGANNLFF	1.03
TRAV24	TRAJ34*01	CAFDNADKLIF	1.03
TRAV24	TRAJ34*01	CAFDNTDKLIF	2.06
TRAV24	TRAJ39*01	CAFCNAGNMLTF	1.03
TRAV24	TRAJ17*01	**CAFKAAGNKLTF***	21.65
TRAV24	TRAJ39*01	CALGNAGNMLTF	5.15
TRAV24	TRAJ17*01	**CALKAAGNKLTF**	2.06
TRAV24	TRAJ17*01	**CASKAAGNKLTF***	40.21
TRAV24	TRAJ57*01	CSPQGGSEKLVF	2.06
TRAV24	TRAJ36*01	CVFQTGGNNLFF	1.03
TRAV24	TRAJ32*02	CACYGGATNKLIF	1.03
TRAV24	TRAJ15*01	CAFDNQAANNLIF	1.03
TRAV24	TRAJ15*01	CAFDNQAGTALIF	3.09
TRAV24	TRAJ32*02	**CASYGGATNKLIF**	12.37
TRAV24	TRAJ42*01	CAYCGGSPNNLIF	1.03
TRAV24	TRAJ42*01	CASDYGGSQGNLIF	1.03
TRAV24	TRAJ42*01	CASYDGGTQGNLIV	1.03
Total		19	100.00

B- TRBV2 clonotypes

HIC 1 DR15+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ2-7*01	TRBD1*01	CASLGPLRHEQYF	3.33
TRBJ2-3*01	TRBD2*01	CASKPLVSTDTQYF	1.67
TRBJ2-1*01	TRBD2*01	CASLERTSGGEQFF	1.67
TRBJ2-1*01	TRBD1*01	CASTRDRTKNEQFF	1.67
TRBJ2-1*01	TRBD2*01	CASSALASGGDEQFF	1.67
TRBJ2-3*01	TRBD2*01	**CASSALASGTDTQYF**	1.67
TRBJ2-7*01	TRBD2*01	CASSELTSRTYEQYF	1.67
TRBJ1-5*01	TRBD2*01	CASSERVSGNQPQHF	3.33
TRBJ2-1*01	TRBD2*01	CASSPMASGGDEQFF	1.67
TRBJ2-7*01	TRBD2*02	**CASSRRTSGTYEQYF**	1.67
TRBJ2-1*01	TRBD2*01	CASSVMASRGNEQFF	1.67
TRBJ1-5*01	TRBD2*01	CASQRGARGGNQPQHF	1.67
TRBJ1-4*01	TRBD1*01	CASRARTGATNEKLFF	1.67
TRBJ2-3*01	TRBD2*01	CASSAKTSGGSDTQYF	1.67
TRBJ2-3*01	TRBD2*01	CASSALASGGRDTQYF	1.67
TRBJ2-1*01	TRBD2*01	CASSARTSGGLDEQFF	1.67
TRBJ2-3*01	TRBD2*01	**CASSARTSGGSDTQYF**	1.67
TRBJ2-3*01	TRBD2*01	CASSKRASGGTDTQYF	3.33
TRBJ2-3*01	TRBD2*01	CASSLRTSGGSDTQYF	1.67
TRBJ2-1*01	TRBD2*01	CASSRLTSGGRNEQFF	3.33
TRBJ2-3*01	TRBD2*01	CASSSKTSGGTDTQYF	1.67
TRBJ2-1*01	TRBD2*01	CASSSRTSGGQDEQFF	1.67
TRBJ1-5*01	TRBD2*01	CATSRGARGSNQPQHF	56.67
Total		23	100.00

HIC 1 DRB5+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ2-7*01	TRBD2*01	CACRIRTSGGEQYF	1.92
TRBJ2-4*01	TRBD2*02	CASARERTKNIQYF	3.85
TRBJ2-1*01	TRBD2*01	CASIPRTSGGLQFF	1.92
TRBJ2-3*01	TRBD2*01	CASKALVSTDTQYF	1.92
TRBJ2-3*01	TRBD2*01	CASKDRTSGDTQYF	1.92
TRBJ2-7*01	TRBD2*01	CASRIRTSGGEQYF	5.77
TRBJ2-5*01	TRBD2*01	CASRLLVSQETQYF	1.92
TRBJ2-7*01	TRBD2*01	CASSALAGVNEQFF	1.92
TRBJ2-3*01	TRBD2*01	CASSELVSGGLHRY	1.92
TRBJ2-7*01	TRBD1*01	CASSPTVNTYEQYF	3.85
TRBJ2-3*01	TRBD1*01	CASQLLVQHTDTQYF	3.85
TRBJ2-3*01	TRBD2*01	**CASSALASGTDTQYF**	3.85
TRBJ2-1*01	TRBD2*01	CASSPMASGGDEQFF	1.92
TRBJ2-7*01	TRBD2*01	**CASSPRTSGTYEQYF**	5.77
TRBJ2-7*01	TRBD2*01	CASSPWARGGDEQFF	3.85
TRBJ2-1*01	TRBD2*01	CASSRWASGGDEQFF	3.85
TRBJ2-1*01	TRBD2*01	CASSVMASRGNEQFF	5.77
TRBJ2-3*01	TRBD2*01	CASSARTSGGGDTQYF	17.31
TRBJ2-1*01	TRBD2*01	CASSARTSGGQDEQFF	1.92
TRBJ2-3*01	TRBD2*01	CASSARTSGGRDTQYF	1.92
TRBJ2-3*01	TRBD2*01	**CASSARTSGGSDTQYF**	1.92
TRBJ2-5*01	TRBD2*01	CASSLLTSGGRETQYF	15.38
TRBJ2-1*01	TRBD2*01	CASSRLTSGGRNEQFF	1.92
TRBJ2-3*01	TRBD2*01	CASSRRTSGGSDTQYF	1.92
TRBJ2-3*01	TRBD2*01	CASSSKTSGGTDTQYF	1.92
Total		25	100.00

HIC 3 DR11+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ2-3*01	TRBD1*01	CASHRTYTDTQYF	1.60
TRBJ1-1*01	TRBD1*01	CASSGQTNTEAFF	8.00
TRBJ1-2*01	TRBD1*01	CASRWTATSYGYTF	12.00
TRBJ1-2*01	TRBD1*01	CASSPTTTGYGYTF	0.80
TRBJ2-2*01	TRBD1*01	CASHEGAGGFGELFF	0.80
TRBJ2-2*01	TRBD1*01	CASHEGAGGYGELFF	1.60
TRBJ2-1*01	TRBD1*01	CASSAGTRGVGEQFF	0.80
TRBJ2-3*01	TRBD2*01	**CASSALASGTDTQYF**	0.80
TRBJ2-7*01	TRBD2*01	CASSDAASGVGEQYF	4.80
TRBJ2-1*01	TRBD2*02	CASSDLASGTNEQFF	0.80
TRBJ2-1*01	TRBD2*01	CASSDRASGVGEQFF	0.80
TRBJ2-1*01	TRBD2*01	CASSDRTSGPHEQFF	4.80
TRBJ2-1*01	TRBD2*02	CASSGLAGGMDEQFF*	5.60
TRBJ2-1*01	TRBD1*01	CASSPGARGIDEQFF	0.80
TRBJ2-1*01	TRBD2*01	CASSPGTSGVGEQFF*	12.80
TRBJ2-1*01	TRBD1*01	CASSPGTSGVGKQFF	0.80
TRBJ2-7*01	TRBD2*01	CASSPRTSGGGEQYF	0.80
TRBJ1-5*01	TRBD1*01	CASSPSARGNQPQHF	1.60
TRBJ2-7*01	TRBD2*02	CASSPTTSGRGEQYF	1.60
TRBJ2-1*01	TRBD2*01	CASSSGTSGAGEQFF	0.80
TRBJ2-1*01	TRBD2*01	CASSSGTSGVGEQFF	27.20
TRBJ2-7*01	TRBD2*01	CASSVGTSGVGEQYF	8.80
TRBJ2-7*01	TRBD2*01	CASSYGASGVGEQFF	0.80
TRBJ2-1*01	TRBD2*01	CASSYRTSGPREQFF	0.80
Total		24	100.00

HIC 3 DRB5+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ1-1*01	TRBD1*01	CASSGQTNTEAFF	1.69
TRBJ2-1*01	TRBD2*02	CASARLAGGTDEQFF	35.59
TRBJ2-3*01	TRBD2*01	CASSAMASGSDTQYF	3.39
TRBJ2-3*01	TRBD2*01	CASSELASGTDTQYF	1.69
TRBJ2-1*01	TRBD2*01	CASSPGTSGVGEQFF*	45.76
TRBJ1-5*01	TRBD1*01	CASSPSARGNQPQHF	5.08
TRBJ2-7*01	TRBD2*01	CASSVGTSGVGEQYF	6.78
Total		7	100.00

HIC 7 DRB5+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ2-7*01	TRBD2*01	CASSPRASGGEQYF	3.85
TRBJ1-4*01	TRBD2*01	CASSVRRNNEKLFF	3.85
TRBJ2-7*01	TRBD2*01	CASNRRTSGTYEQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSALASGGDTQYF	3.85
TRBJ2-1*01	TRBD2*01	CASSARASGGDEQFF	5.13
TRBJ1-5*01	TRBD1*01	CASSARTSGGQPQHF	5.13
TRBJ1-5*01	TRBD1*01	CASSARTSGNQPQHF	14.10
TRBJ2-1*01	TRBD2*02	CASSELASGINEQFF	6.41
TRBJ2-1*01	TRBD2*01	CASSELTSGGDEQFF	1.28
TRBJ2-3*01	TRBD2*02	CASSKRTSGGDTQYF	1.28
TRBJ2-7*01	TRBD2*01	CASSLRTSGGDEQYF	3.85
TRBJ2-3*01	TRBD2*01	CASSPLTSATDTQYF	1.28
TRBJ2-1*01	TRBD2*01	CASSPRASGGDEQFF	6.41
TRBJ2-7*01	TRBD2*01	CASSPRTSGGDEQYF	1.28
TRBJ2-3*01	TRBD2*01	CASRLRTSGGTDTQYF	2.56
TRBJ2-3*01	TRBD2*01	CASRRLAGFMADTQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSARTSAGTDTQYF	7.69
TRBJ2-3*01	TRBD2*01	CASSARTSGGADTHYF	1.28
TRBJ2-3*01	TRBD2*01	**CASSARTSGGADTQYF**	2.56
TRBJ2-3*01	TRBD2*01	**CASSARTSGGSDTQYF**	3.84
TRBJ2-3*01	TRBD2*01	CASSARTSGGTDTQYF	3.84
TRBJ2-3*01	TRBD2*01	CASSERTSGGRDTQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSGRTSGGSDTQYF	3.85
TRBJ2-3*01	TRBD2*01	CASSLRASGGSDTQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSLRTSGGADTQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSQRTSGGADTQYF	1.28
TRBJ2-3*01	TRBD2*01	CASSRLTSGGSDTQYF	5.13
TRBJ2-3*01	TRBD2*01	CASSRRTSGGLDTQYF	1.28
TRBJ2-1*01	TRBD2*01	CASSRRTSGGPNEQFF	1.28
TRBJ2-3*01	TRBD2*01	**CASSRRTSGGTDTQYF***	1.28
Total		30	100.00

HIC 7 DR1502+

J-GENE	D-GENE	JUNCTION (AA)	% nt seq
TRBJ2-3*01	TRBD2*01	CASSALASGGDTQYF	20.83
TRBJ2-1*01	TRBD2*02	**CASSRLAGGMDEQFF***	56.94
TRBJ2-3*01	TRBD2*01	**CASSRRTSGGTDTQYF***	22.22
Total		3	100.00

Supplemental Table S9 : Intrapatient comparisons of Gag293-specific clonotypic repertoires obtained with different MHC II tetramers - Summary

A

Patient	Tetramers used	% shared TRAV24 clonotypes AA[a]	% shared TRAV24 sequences[b]	% public in shared TRAV24 clonotypes AA[c]
HIC1	DRB1*1501 / DRB5*0101	22.22	83.51	50
HIC3	DRB1*1101 / DRB5*0101	7.69	16.98	100
HIC7	DRB5*0101 / DRB1*1502	6.25	30.92	100
Mean		**12.05**	**43.80**	**83.33**

B

Patient	Tetramers used	% shared TRBV2 clonotypes AA[a]	% shared TRBV2 sequences[b]	% public in shared TRBV2 clonotypes AA[c]
HIC1	DRB1*1501 / DRB5*0101	11.63	12.5	40
HIC3	DRB1*1101 / DRB5*0101	14.81	40.22	50
HIC7	DRB5*0101 / DRB1*1502	6.45	28.57	50
Mean		**10.96**	**27.10**	**46.67**

Legend: The degree of overlap of the Gag293-specific clonotypic repertoires restricted by two distinct HLA DR alleles in a same patient was evaluated. This intrapatient comparison was done for 3 HIV controllers (HIC1, HIC3, HIC7), for whom two cell lines sorted with different tetramers (DR15/DRB5, or DR11/DRB5) were analyzed in parallel.

(a) The % of shared clonotypes AA is obtained from the number of shared clonotypes AA divided by the total number of clonotypes AA obtained for the two tetramer+ samples. Clonotype AA: unique CDR3 sequence, in amino acids.

(b) The % of shared sequences is obtained from the number of nt sequences corresponding to shared clonotypes AA divided by the total number of sequences obtained for the two tetramer+ samples.

(c) The % of public clonotypes is computed among the shared clonotypes AA.

A consistent but moderate degree of clonotypic repertoire overlap was observed, with a mean of 12% TRAV24 clonotypes (A) and 11% of TRBV2 clonotypes (B) shared between the two Tet+ samples. However, the shared clonotypes were highly expressed, as they represented a mean of 43.8% TRAV24 sequences (A) and 27.1% TRBV2 sequences (B) analyzed. Public clonotypes were disproportionately represented among shared clonotypes, with a mean of 83.3% of shared TRAV24 clonotypes (A) and 46.7% of shared TRBV2 clonotypes (B). Thus, while the majority of Gag293-specific clonotypes did not show cross-restriction, the subset of clonotypes restricted by multiple HLA DR alleles appeared dominant and more frequently public.

Supplemental Table S10: Ex vivo analysis of the Gag293-specific TCR repertoire

HIC1 DRB5+ ex vivo (n=119 seq.)

J-GENE	JUNCTION (AA)	% ex vivo	% in cell line
TRAJ38*01	CARDDRKLIW	4.20	-
TRAJ17*01	CAFTAAGNKLTF	8.40	-
TRAJ39*01	CALGNAGNMLTF	27.73	4.65
TRAJ6*01	CAFIPGGSYIPTF	3.36	2.33
TRAJ32*02	**CASYGGATNKLIF**	21.85	62.79
TRAJ45*01	CALDSGGGADGLTF	34.45	-

HIC2 DRB5+ ex vivo (n=56 seq.)

J-GENE	JUNCTION (AA)	% ex vivo	% in cell line
TRAJ17*01	**CAFKAAGNKLTF**	17.86	56.06
TRAJ39*01	CARRNAGNMLTF	12.50	-
TRAJ17*01	**CASKAAGNKLTF**	69.64	19.70

HIC3 DRB5+ ex vivo (n=76 seq.)

J-GENE	JUNCTION (AA)	% ex vivo	% in cell line
TRAJ17*01	**CALKAAGNKLTF**	6.58	1.79
TRAJ39*01	CALRQAGNMLTF	93.42	62.50

HIC7 DRB5+ ex vivo (n=106 seq)

J-GENE	JUNCTION (AA)	% ex vivo	% in cell line
TRAJ13*02	CAPGGYQKVTF	4.72	-
TRAJ22*01	CAWGSARQLTF	4.72	-
TRAJ17*01	**CAFKAAGNKLTF**	54.72	18.18
TRAJ17*01	CAFNAAGNKLTF	5.66	5.45
TRAJ26*01	CAFVAAGQNFVF	4.72	-
TRAJ32*02	**CAEYGGATNKLIF**	3.77	5.45
TRAJ32*01	**CANYGGATNKLIF**	6.60	3.64
TRAJ32*02	**CASYGGATNKLIF**	0.94	7.27
TRAJ24*02	CALMTTDSWGKLQF	14.15	-

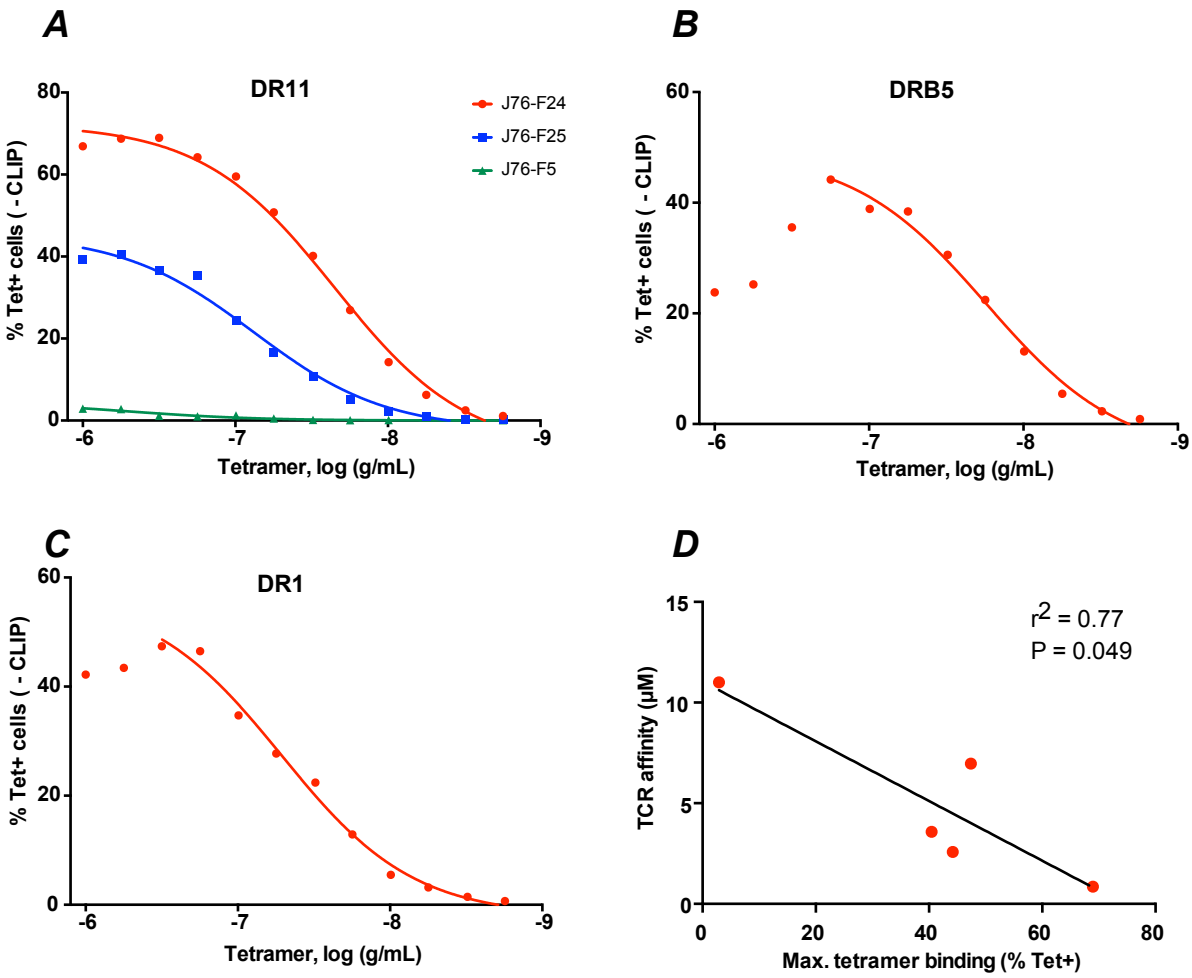
Listing of TRAV24 clonotypes found in Gag293-specific CD4+ T cells sorted ex vivo.

The representation of each clonotype in the TRAV24 sequence set obtained ex vivo (3rd column) and in the corresponding cell line (4th column) is reported.

TCR name	TRA CDR3 Junction	TRA motif	CDR3 length	TRB CDR3 Junction	TRB motif	CDR3 length	DR11 EC50	DR15 EC50	DRB5 EC50	DR1 EC50	DR7 EC50	DR4 EC50	DR3 EC50
F24	**CAFKAAGNKLTF**	AV24-1	10	**CASSRLAGGMDEQFF**	BV2-1	14	4.15E-07	2.17E-06	4.46E-06	2.53E-06	8.69E-06	-	-
F25	**CAFKAAGNKLTF**	AV24-1	10	CATTPGASGISEQF	-	13	7.48E-07	8.91E-06	2.36E-05	3.48E-05	-	-	-
F5	**CAFKAAGNKLTF**	AV24-1	10	CASSGLAGGMDEQFF	BV2-1	14	2.12E-06	1.60E-05	-	-	-	-	-
S24	**CASKAAGNKLTF**	AV24-1	10	**CASSRLAGGMDEQFF**	BV2-1	14	6.19E-07	3.57E-06	9.23E-06	9.98E-06	-	-	-
S25	**CASKAAGNKLTF**	AV24-1	10	CATTPGASGISEQF	-	13	3.79E-06	-	-	-	-	-	-
RR5	**CSRRAAGNKLTF**	AV24-1	10	CASSGLAGGMDEQFF	BV2-1	14	1.25E-06	8.46E-06	1.10E-05	1.11E-05	-	-	-
F4	**CAFKAAGNKLTF**	AV24-1	10	**CASSPGTSGVGEQFF**	BV2-1	13	1.39E-06	6.78E-05	8.42E-06	-	-	-	-
F13	**CAFKAAGNKLTF**	AV24-1	10	**CASSRRTSGGTDTQYF**	BV2-2	14	7.54E-07	2.61E-06	4.10E-06	-	-	-	-
HD5	CASDYGGSQGNLIF	-	12	CASSEFRTRGYTF	-	11	-	8.26E-06	5.86E-06	1.08E-05	-	-	-
HY9	CAYGANNLFF	-	8	CASRPLHSVYEQYF	-	12	-	1.99E-06	3.84E-06	3.04E-06	-	-	-

Supplemental Table S11: Antigen sensitivity of the TCRs tested by transduction in J76 cells.

The EC50 value for CD69 induction in J76 transduced with 10 different TCRs is reported.
Each TCR was tested with a panel of 7 L cell transfectants used as APC. Each L cell line expressed a single human HLA-DR allele.
The EC50 corresponds to the Gag293 peptide concentration (in M) at which half maximal CD69 induction was observed.
Responses too low for EC50 determination are indicated by a dash.
The CDR3 junction sequence is reported for the TRA and TRB chains of each TCR tested. Sequences in bold correspond to public clonotypes.



E

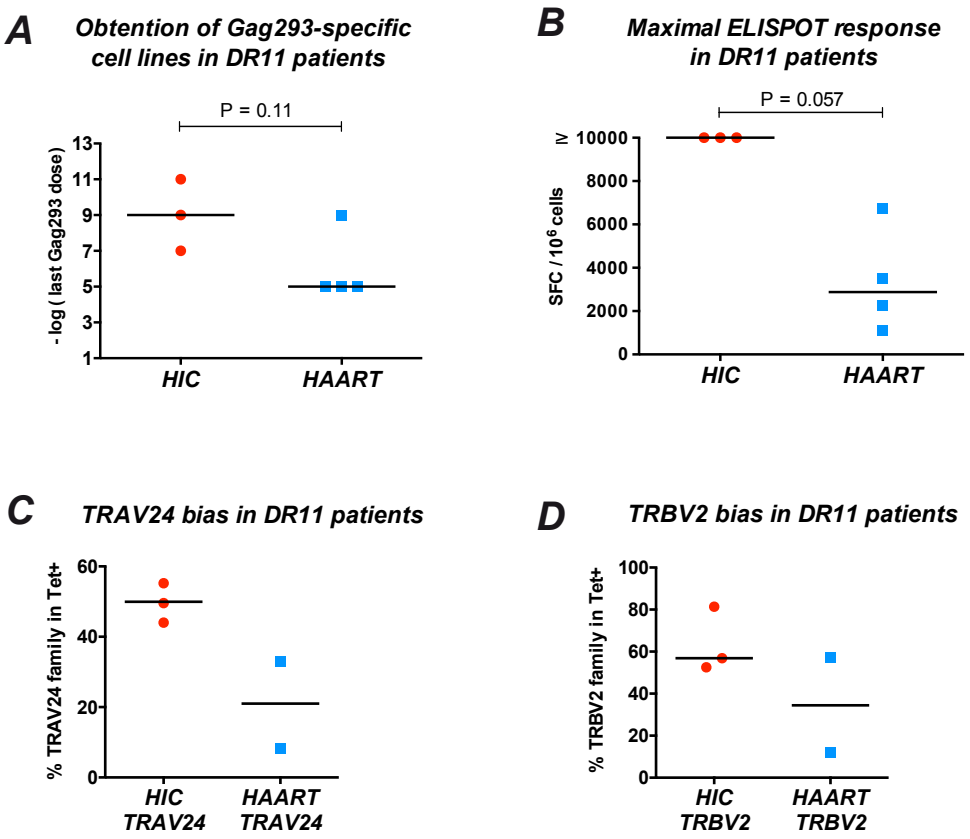
TCRs	DR11 EC50 (g/mL)	DRB5 EC50 (g/mL)	DR1 EC50 (g/mL)
F24	2.24E-08	1.73E-08	5.17E-08
F25	7.58E-08	ND	ND
F5	ND	ND	ND

Supplemental Figure S12: Analysis of TCR avidity by MHC II tetramer titration

(A) Gag293-DR11 tetramer titration: J76 cells transduced with the TCRs F24, F25, or F5 were incubated with decreasing concentrations of HLA-DR11 tetramer loaded with the Gag293 peptide. The percentage of Gag293-specific tetramer+ (Tet+) cells minus the percentage of cells labeled with a contol CLIP-loaded tetramer is reported. (B and C) Gag293-DRB5 tetramer (B) and Gag293-DR1 tetramer (C) titration on F24-transduced cells. The dip in binding curves at high tetramer concentrations likely reflects competition effects between multivalent ligands. EC50 computation was based on the sigmoidal part of the response curve.

(D) Linear correlation between the maximum % of tetramer+ cells and TCR affinity determined by SPR.

(E) The half-maximal tetramer binding values (EC50) are reported. ND: not detectable, i.e. tetramer binding was too low to evaluate the EC50 value.



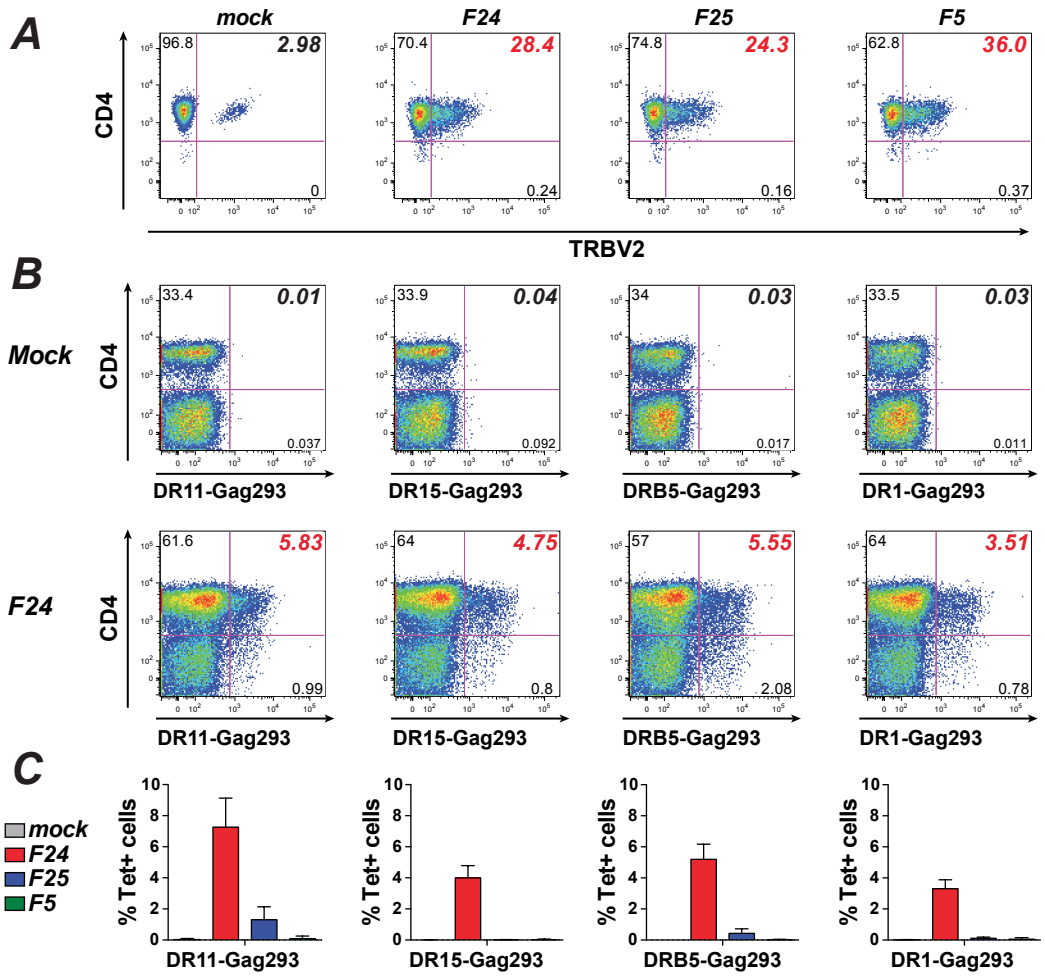
Supplemental Figure S13:

Analysis of Gag293-specific CD4+ T cell responses in DR11 patients

(A) Comparison of antigen sensitivity in HIV controllers (HIC) and treated patients (HAART) carrying at least one DR11 allele. Antigen sensitivity was measured by the last Gag293 peptide dilution (in M) that yielded a specific CD4+ T cell line.

(B) Comparison of the maximal ELIPOT response to Gag293 in DR11 patients. CD4+ T cell lines generated with a 10^{-5} M Gag293 peptide dose were restimulated with the same high peptide dose and analyzed by IFN-γ ELISpot assay. The number of spot forming cells (SFC) per 10^6 cells is reported. Values >10^4 SFC / 10^6 cells reached saturation and are reported as equal to 10^4 SFC / 10^6 cells. (A and B) P values obtained by the Mann-Whitney U test are reported.

(C and D) Comparison of TRAV24 (C) and TRBV2 (D) expression in Gag293-specific cells of DR11 patients. The percentage of TRAV24 or TRBV2 expression among tetramer-positive (Tet+) cells is reported.

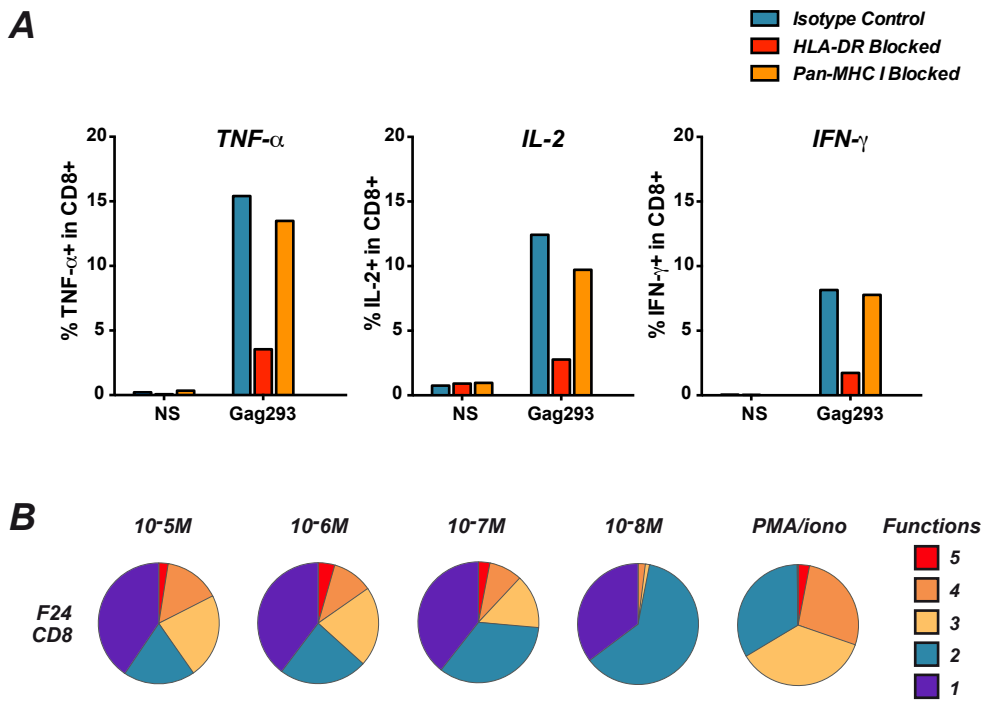


Supplemental Figure S14: TCR transfer in primary T cells from healthy donors confers Gag293-MHC II tetramer recognition

(A) Example of TCR transduction in primary CD4+ T cells from a healthy donor. PBMCs were mock transduced, or transduced to express the F24, F25, or F5 TCRs, and stained with anti-TRBV2 mAb.

(B) MHC II tetramer staining in CD4+ T cells transduced with the F24 TCR (second row), or mock transduced (first row). The percentage of CD4+ T cells stained with Gag293-loaded HLA-DR tetramers (DR11, DR15, DRB5, and DR1) is reported in red. For these experiments, the DR15 tetramer used corresponded to the HLA DRB1*1502 rather than the HLA DRB1*1501 allele.

(C) Quantification of MHC II tetramer staining in TCR-transduced primary CD4+ T cells. For each tetramer, the mean percentage of tetramer-positive (Tet+) CD4+ T cells obtained from 4 independent experiments is shown. The percentage of Gag293-specific Tet+ cells was computed by subtracting the percentage of CLIP-Tet+ cells from that of Gag293-Tet+ cells. Light grey bars: mock-transduced; red bars: F24-transduced; dark blue bars: F25-transduced; green bars: F5-transduced.



Supplemental Figure S15:

Analysis of cytokine production in CD8+ T cells transduced with the F24 TCR.

(A) Blocking of the cytokine response in CD8+ T cells with anti-HLA antibodies.
Cytokine induction was measured in CD8+ T cells transduced with the F24 TCR after stimulation with 10^{-5} M Gag293 peptide or in non-stimulated cells (NS). Cells were pretreated with an isotypic IgG2a control antibody (blue bars), an HLA-DR blocking antibody (red bars) or a pan-MHC I blocking antibody (orange bars) at 10 µg/ml prior to peptide stimulation. >75% of the response was blocked by HLA-DR antibody treatment for each cytokine tested, indicating that F24-expressing CD8+ T cells were predominantly restricted by MHC II.

(B) Analysis of the polyfunctionality of CD8+ T cells transduced with the Gag293-specific TCR F24. Polyfunctionality was defined as the capacity for specific cells to co-express at least 3 markers among the 5 studied (TNF-α, MIP-1β, IL-2, IFN-γ, and CD107a) after Gag293 peptide stimulation. The number of markers co-expressed defines the number of functions reported in legend. Polyfunctionality is visualized with pie charts in which each slice represents a functional category: red, 5 functions; orange, 4 functions; yellow, 3 functions; blue, 2 functions; and violet, 1 function. Polyfunctionality was assessed after stimulation at different peptide doses ranging from 10^{-5} M to 10^{-8} M. Stimulation with PMA and ionomycin was used as a positive control to induce a highly polyfunctional response (right pie).