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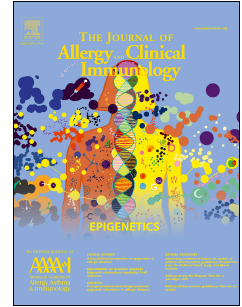
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Single cell transcriptomics reveal polyclonal memory T cell responses in abacavir patch test positive skin

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1 **Single cell transcriptomics reveal polyclonal memory T cell responses in abacavir patch test**  
2 **positive skin.**

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31 **Running head:** Ex vivo single cell profiling of abacavir-responsive T cells

32 **Conflicts of Interest:** The authors have no conflicts of interest relevant to this manuscript.  
33 However, EP receives consulting fees from Biocryst. EP and SM receive royalties from UpToDate  
34 and have equity in IIID Pty Ltd that holds a patent for HLA-B\*57:01 testing for abacavir  
35 hypersensitivity. EP, SM, KCK and AC have a patent pending for HLA-A\*32:01 testing for  
36 vancomycin drug reaction and eosinophilia and systemic symptoms.

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40 Research Council (Australia) and Australian Centre for HIV & Hepatitis Research (ACH2).

41

42 **Capsule Summary.** Single-cell responses in HLA-B\*57:01 abacavir patch test positive skin remote  
43 to the acute hypersensitivity reaction demonstrate polyclonal T-cell activation and proliferation  
44 characterized by a transcriptional and cellular response consistent with memory responses to  
45 altered peptides.

46

47 **Key words.** Abacavir, drug hypersensitivity, T cell, T-cell receptor, HLA, CD103

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60 **To the Editor**

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62 Abacavir is a guanosine analogue used as part of combination antiretroviral therapy for the  
63 treatment of HIV-1 infection. Abacavir hypersensitivity syndrome (AHS) was the major treatment-  
64 limiting toxicity of abacavir characterized by fever, malaise, gastrointestinal and respiratory  
65 symptoms, and a generalized rash that occurs later in 70% of cases. AHS requires carriage of HLA-  
66 B\*57:01, providing a 100% negative predictive value and a 55% positive predictive value(1-3). AHS  
67 is now a preventable disease that has been addressed by routine HLA-B\*57:01 screening prior to  
68 abacavir prescription. Research has shown that abacavir non-covalently binds to the floor of the  
69 peptide binding groove of HLA-B\*57:01, thus generating a vastly different immunopeptidome  
70 presented to CD8<sup>+</sup> T cells and the concurrent generation of CD8<sup>+</sup> T cells with multiple  
71 specificities(4, 5).

72

73 AHS is a CD8<sup>+</sup> T-cell cell dependent reaction and does not elicit an antibody response. Although  
74 the mechanism by which abacavir alters antigen presentation is understood, the nature of the  
75 specific T-cell responses is less well defined. Both CD8<sup>+</sup> and CD4<sup>+</sup> T cells are recruited to the skin in  
76 response to abacavir (6). Polyclonal HLA-B\*57:01-restricted CD8<sup>+</sup> T-cell responses to abacavir  
77 within the peripheral blood are a feature of AHS(4, 7). However, it is unknown if this polyclonal  
78 response is a feature of tissue responses to abacavir, or if a restricted subset of T cells is recruited  
79 to sites of inflammation. Although it is known that HLA-B\*57:01-restricted CD8<sup>+</sup> T cells produce  
80 interferon gamma (IFN $\gamma$ ) and tumour necrosis factor alpha (TNF $\alpha$ ) in response to abacavir (7), the  
81 full functionality of these cells has not been assessed. Here we combine single cell (sc) T-cell  
82 receptor (TCR) sequencing (scTCRseq) and scRNAseq to define the landscape of abacavir-specific T  
83 cells within a positive skin patch test to abacavir applied fourteen years after AHS.

84

85 A 67 year old HLA-B\*57:01 positive man had a history of AHS in February 2002 which was  
86 characterized by onset of headaches, arthralgia, myalgia, fever and nausea 11 days following  
87 commencement of a fixed dose combination of abacavir, lamivudine and zidovudine, and  
88 resolution within 48 hours of discontinuation of all drugs. In March 2002, he commenced and  
89 tolerated zidovudine, lamivudine and efavirenz. In March 2003, CD4+ T cell count was  $1080/\text{mm}^3$   
90 (40%) and viral load (VL) 80 copies/ml and abacavir patch tests to 1% and 10% abacavir in  
91 petrolatum were positive. In May 2004, he was changed to zidovudine, lamivudine, lopinavir and  
92 ritonavir due to efavirenz central nervous system side effects. In April 2005 he was changed to  
93 tenofovir, lamivudine atazanavir/ritonavir due to fat wasting. In November 2016 he was simplified  
94 to tenofovir, emtricitabine and dolutegravir. For the last 12 years he had remained stable with  
95 normal CD4+ T cell counts and undetectable viral load. In July 2017, after informed consent 1%  
96 and 10% abacavir and petrolatum control were applied to the flat surface of the back. The positive  
97 1% and 10% patch tests and unaffected skin distant to the patch tests were biopsied 96 hours  
98 later. At the time of sampling in July 2017, he remained on tenofovir, emtricitabine and  
99 dolutegravir and CD4+ T cell count was  $828/\text{mm}^3$  (42%); viral load <40 copies/ml. T cells were  
100 isolated by collagenase digestion from all biopsies. CD3<sup>+</sup> T cells were single cell sorted and  
101 subjected to immediate *ex vivo* primer-based scTCRseq and scRNAseq. In addition, T-cell lines  
102 created from the collagenase digested tissue or isolated by explant culture, were exposed to drug  
103 to confirm specificity to abacavir.

104

105 T cells within normal skin were predominantly of the effector memory T-cell ( $T_{EM}$ ) phenotype  
106 (CD45RO+CCR7-). In normal skin, CD4+ T cells were the major cell type expressing the skin homing  
107 marker C-C chemokine receptor 10 (CCR10) (52%), the residency marker CD103 (11%); few cells  
108 expressed CD69. In abacavir-exposed skin, 56% of CD3+ cells were CD4+ T cells. Of these, the  
109 majority (98%) were of the  $T_{EM}$  phenotype; 34% expressed CCR10 and the majority were negative

110 for CD103 and CD69 suggesting recent recruitment to the site. CD8 $\alpha$  was poorly expressed on  
111 CD3<sup>+</sup> T cells, possibly as a consequence of collagenase P digestion. CD4<sup>+</sup> and CD8<sup>+</sup> T cells were  
112 both present in explant cultures from 1% abacavir-exposed skin, *i.e.* those not exposed to  
113 collagenase digestion (Sup. Fig. 1).

114

115 Direct *ex vivo* single cell sorting and sequencing was employed to map TCR usage and measure the  
116 clonality of abacavir-responsive T cells. Similar to responses that have been previously  
117 demonstrated to abacavir in the peripheral blood (Sup. Fig. 2), T-cell responses to abacavir in a  
118 positive patch test remote to the acute AHS were highly polyclonal (Fig. 1). Circos plots show  
119 variable T-cell receptor alpha variable (TRAV) and T-cell receptor beta variable (TRBV) gene  
120 expression, with associated joining (TRAJ or TAJ) chain usage for each TCR V alpha and V beta  
121 gene (Fig. 1). TRAV-26.1, -38, -12.2 and -9.2 were the most common TCR V alpha genes used by T  
122 cells in abacavir-exposed skin, with TRBV20.1 the most common V beta gene. In normal skin  
123 TRAV30 and TRBV20.1 were the most common V alpha and V beta genes, respectively.

124

125 T cells isolated from the skin of normal and abacavir-exposed skin by collagenase digestion were  
126 used to create T-cell lines using two rounds of non-specific stimulation (phytohemagglutinin P  
127 followed by anti-CD3 treatment). These lines were tested for specificity to abacavir by IFN $\gamma$   
128 enzyme-linked immunospot (ELISpot) assay. T-cell lines from 1% and 10% abacavir-exposed skin  
129 but not those from normal skin produced IFN $\gamma$  when exposed to 35  $\mu$ M of drug (Sup. Fig. 3A).  
130 Similar to what we had demonstrated in non-expanded T-cell populations, bulk TCR sequencing of  
131 the T-cell line from the 1% abacavir-exposed skin showed a highly diverse TCR repertoire (Sup. Fig  
132 3B). Explant cultured T cells isolated from 1% abacavir-exposed, but not normal skin, proliferated  
133 in culture without additional exogenous stimulation. This spontaneously expanded line was also  
134 tested for specificity to abacavir. Following stimulation of the T-cell line with abacavir, CD8<sup>+</sup> T cells

135 up-regulated both CD69 and CD137, indicating continued specificity for the drug in culture. This T-  
136 cell line expressed a more restricted, but still, polyclonal TCR repertoire. (Sup. Fig. 1).

137

138 Single cell transcriptional profiling was used to assess the phenotype of T cells in normal versus  
139 abacavir-exposed skin directly *ex vivo* (Fig. 2). T cells derived from skin exposed to 1% or 10%  
140 abacavir demonstrated a common transcriptional signature (Fig. 2A) and these data were  
141 therefore pooled for subsequent analysis. The top 20 differentially regulated genes in abacavir-  
142 exposed and non-exposed skin-derived T cells are shown in Figure 2B (see also Sup. Fig. 4).  
143 Differentially expressed genes fall into several categories. T cells in normal skin were marked by  
144 genes known to be enriched or suppressed in T<sub>RM</sub> cells and included those that either regulate T-  
145 cell migration or commitment to tissue residency such as S1PR1, SELL (L-selectin), CD44 and  
146 DUSP1 (8) . Genes significantly elevated in T cells from abacavir-exposed skin compared to  
147 abacavir-unexposed, unaffected skin included those involved in T-cell metabolism such as LAT1 (9)  
148 and those involved in T-cell activation and effector function such as superoxide dismutase 2,  
149 interferon-induced transmembrane genes 1 and 2. The latter two genes regulate immunity to  
150 RNA viruses, including HIV. A Broad Institute gene set enrichment analysis (GSEA) identified  
151 several hallmark gene sets that were differentially expressed in T cells derived from normal versus  
152 abacavir-exposed skin. The IFN $\gamma$  response pathway ( $p=1.06 \times 10^{-11}$ ) and the IFN $\alpha$  response  
153 pathway ( $p=1.03 \times 10^{-8}$ ), were significantly up-regulated in T cells from abacavir-exposed skin. In  
154 contrast, in T cells derived from normal skin the TNF $\alpha$  signalling via NF $\kappa$ b pathway ( $p=9.57 \times 10^{-17}$ )  
155 and the UV response - down pathway ( $p=2.76 \times 10^{-8}$ ) were significantly up-regulated.

156

157 Our findings in abacavir-exposed patch test-positive skin in a patient 14 years following acute AHS  
158 are consistent with the altered peptide model of hypersensitivity. We propose that in keeping



159 with this model, as applied to the skin patch test, abacavir is taken up by dendritic cells (DC) in the  
160 epidermis and presented to T<sub>RM</sub> cells. This interaction leads to endothelial activation and  
161 recruitment of polyclonal T<sub>EM</sub> to the site of abacavir exposure. It is also likely that migratory DC  
162 present the antigen to T<sub>EM</sub> cells in skin- draining lymph nodes and that these T<sub>EM</sub> lead to additional  
163 populations of polyclonal T<sub>EM</sub> cells that home to the skin. Collectively these T<sub>EM</sub> recognize the  
164 complex of HLA-B\*57:01 plus abacavir complexed with self-antigens to form novel structures.  
165 Altered peptide presentation leads to T-cell activation and proliferation and the expression of a  
166 transcriptional profile consistent with memory responses to viral pathogens.

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201 **Figure 1. TCR usage in normal or abacavir exposed skin.** A patient with a prior history of abacavir  
202 hypersensitivity was patch tested with 1 or 10% abacavir for 96 hours. Each 4 mm punch biopsy, 1 from  
203 normal skin, 1 from 1% abacavir exposed skin and 2 from 10% abacavir exposed skin was digested with  
204 collagenase P. CD3<sup>+</sup> cells were single cell sorted and subjected to TCR sequencing. Shown are TCR variable  
205 and joining chains making up each CDR3 region. Data are from normal skin and combined data from 1 and  
206 10% abacavir exposed skin.

207

208 **Figure 2. Single cell transcriptional analysis. A.** tSNE plot comparing transcriptional profile of T cells  
209 isolated from normal skin and 1% and 10% abacavir exposed skin. **B.** Top 20 differentially expressed genes  
210 in abacavir exposed and normal skin. Abacavir exposed skin data are combined single cell data from 1%  
211 and 10% abacavir exposed T cells.

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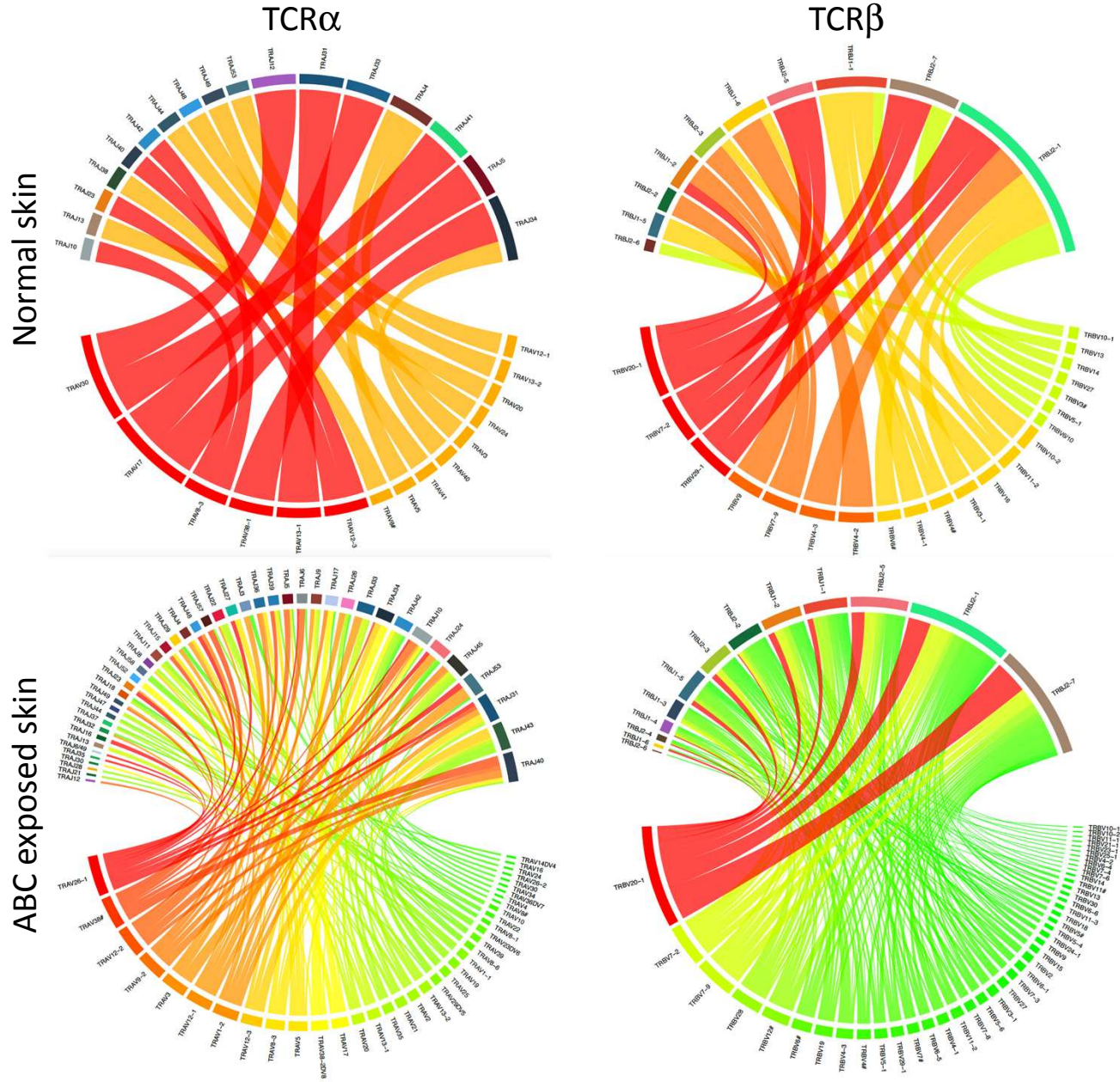
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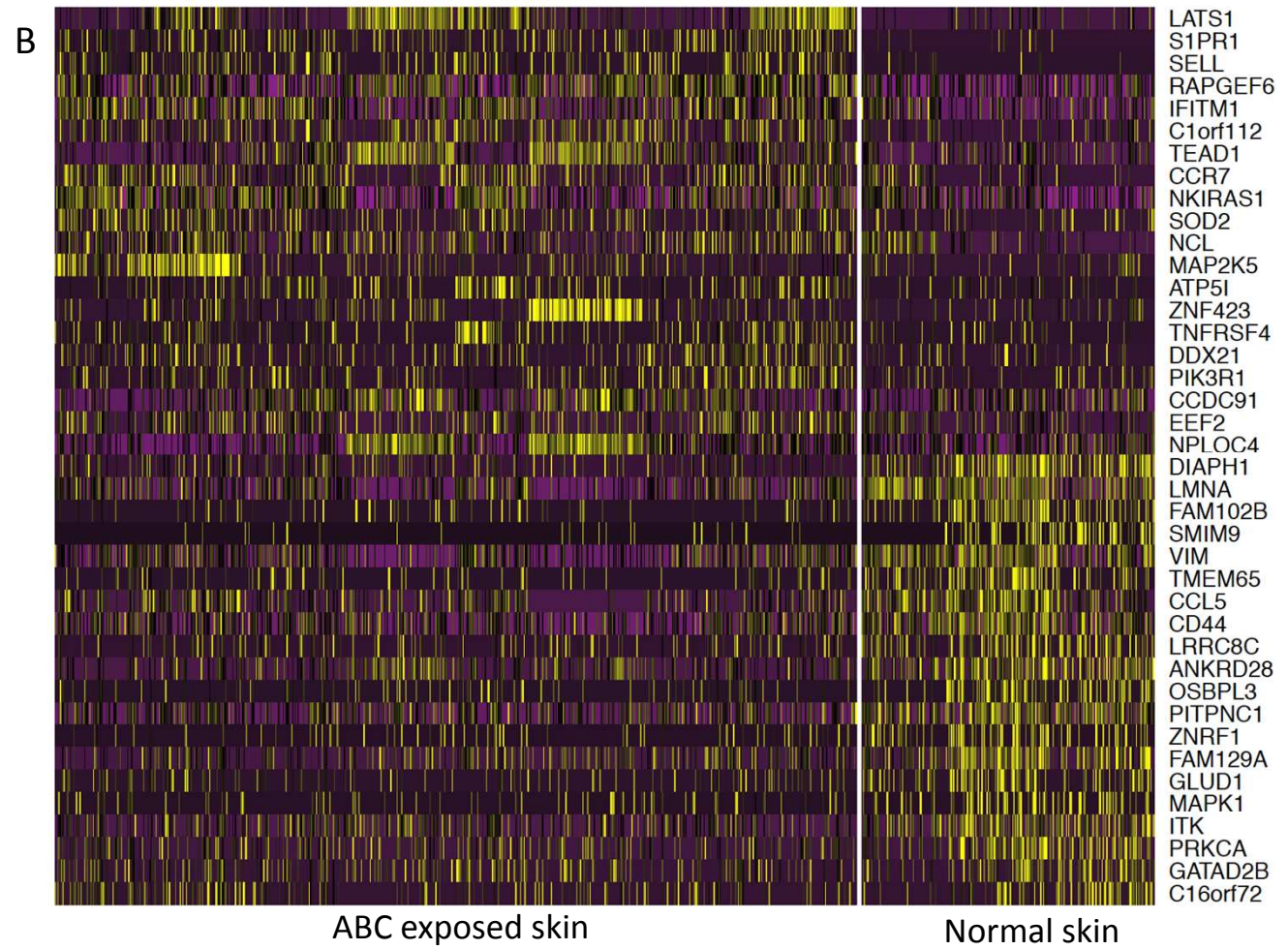
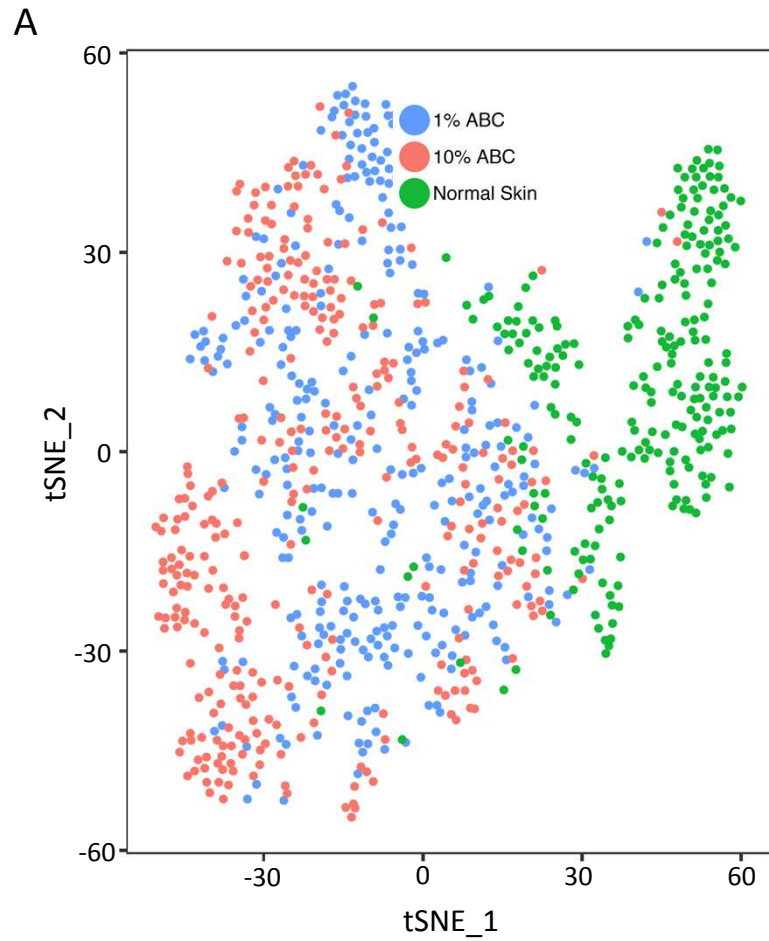
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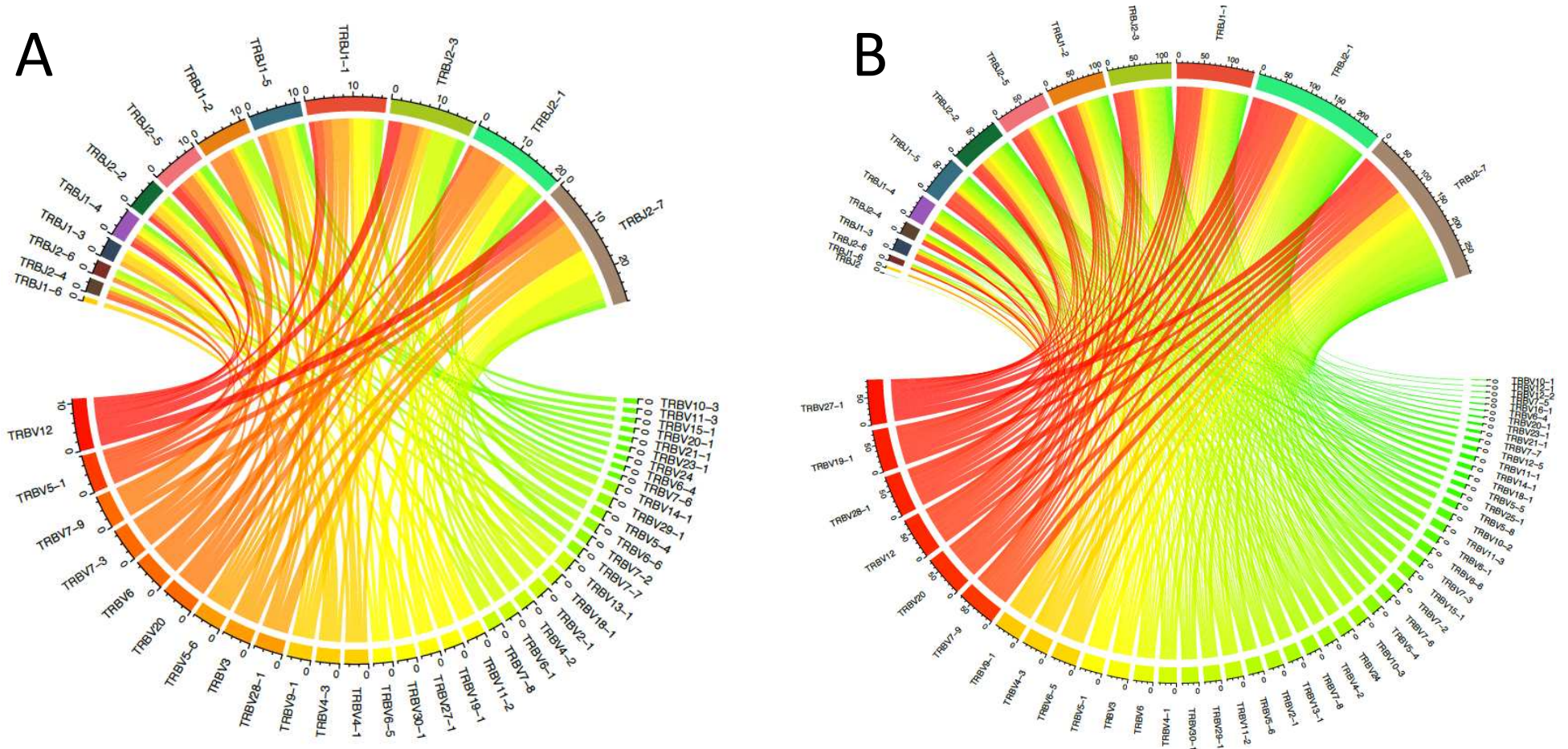




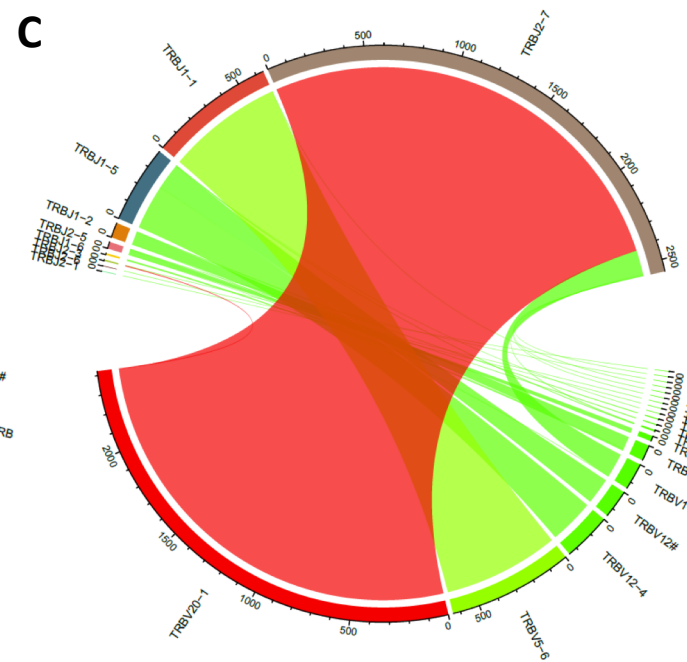
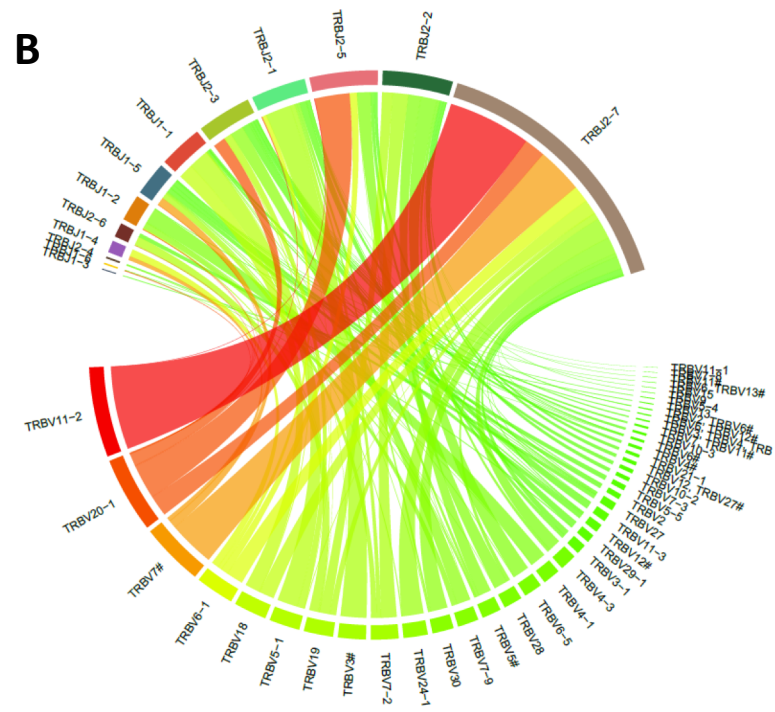
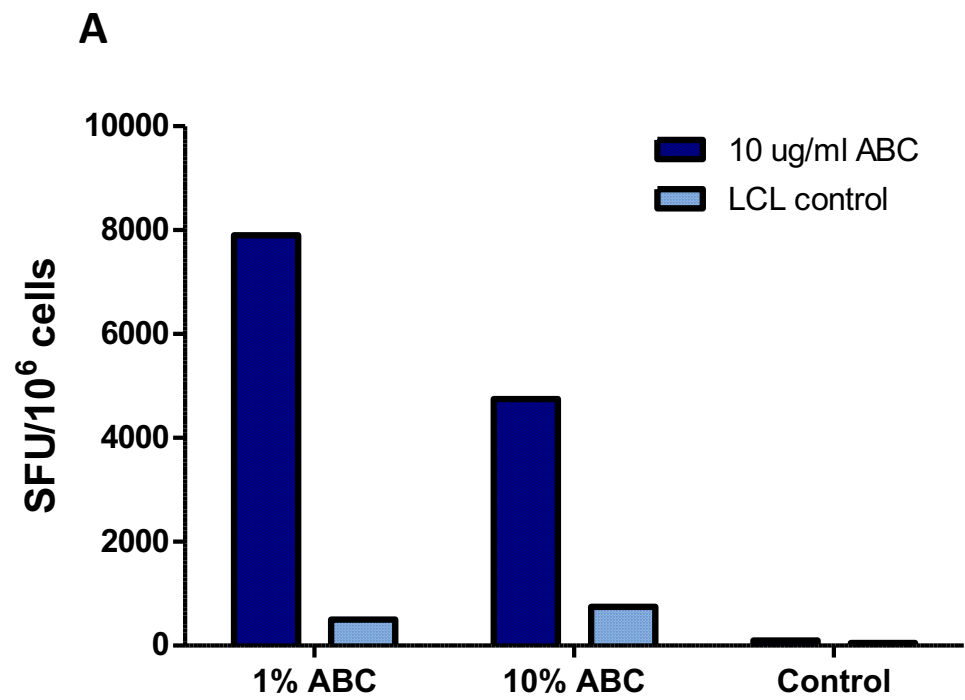


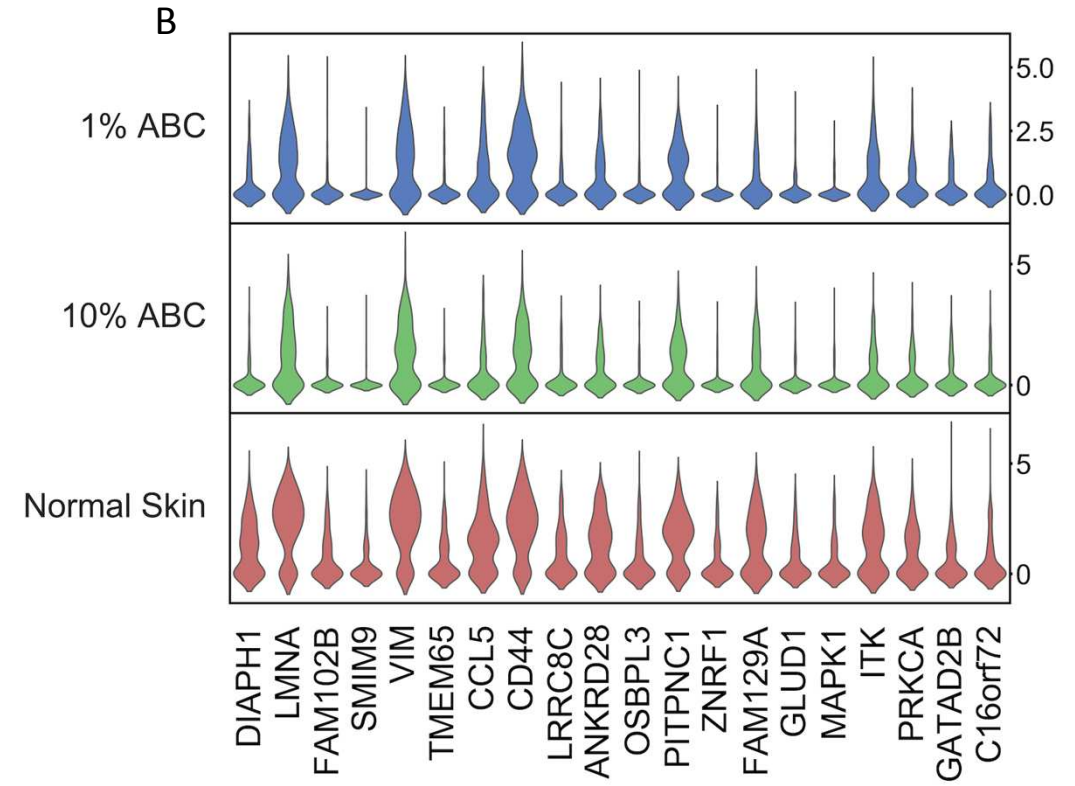
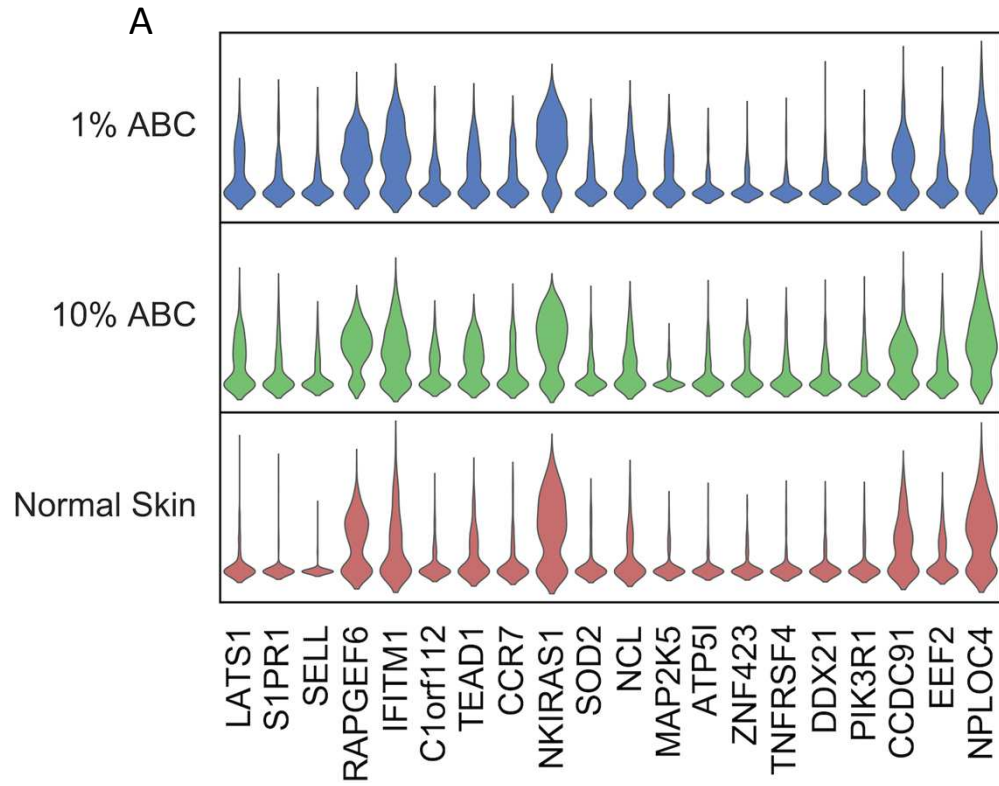


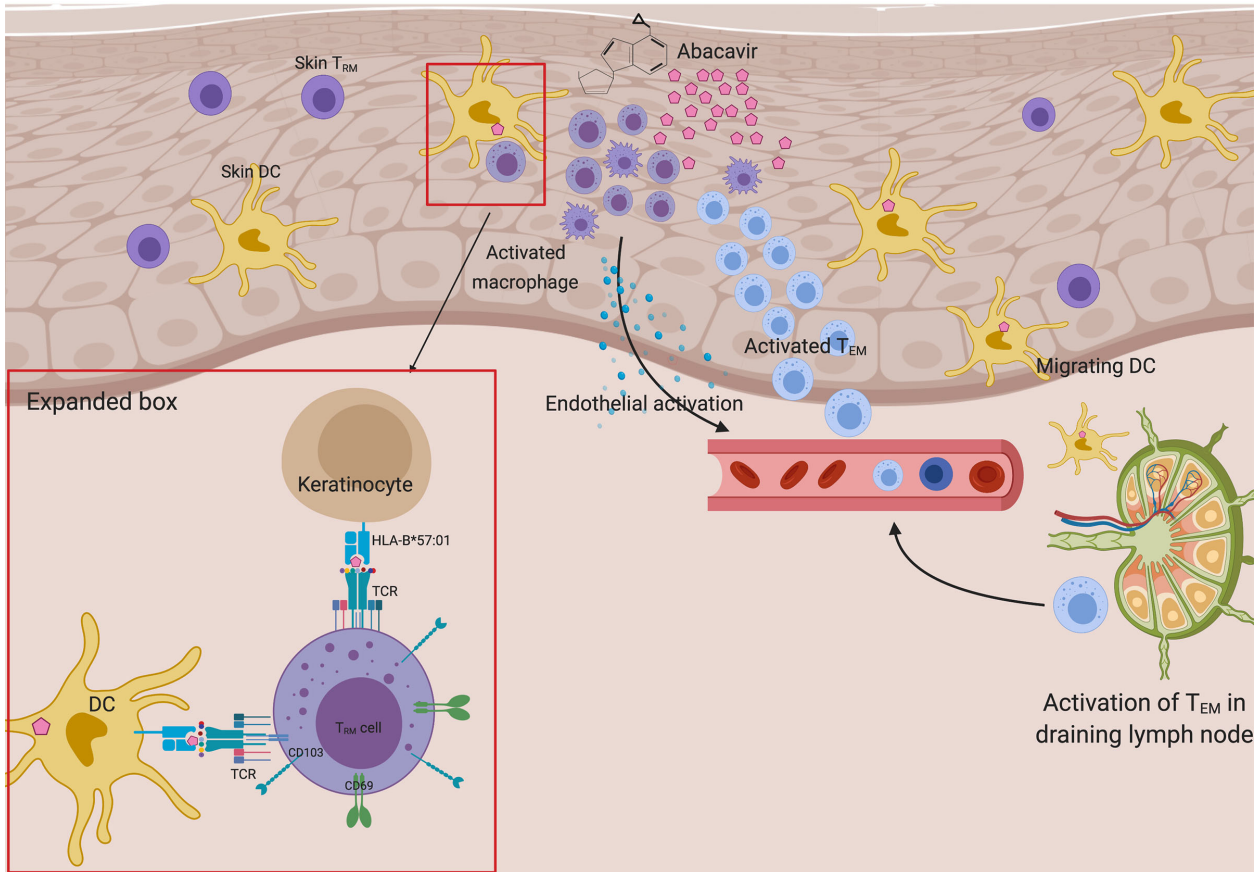












**Supplementary Materials and Methods**

**Patch testing and biopsy.** Skin patch tests were prepared and applied in duplicate according to the procedure previously reported by Phillips et al. 2002 (1) and were adapted to use 1% and 10% concentrations of abacavir and excipient and petrolatum controls (Oxford compounding Pty Ltd). Test results were read and recorded at 48 h after application and then, because of the large time interval between last patch test exposure to ABC, 14 years, were re-applied for a further 48 hours. Two biopsies were taken from 1% and 10% ABC patch test skin and one biopsy was taken from control patch test, normal skin.

**T cell isolation.** Two 4 mm biopsies from each of the 1% and 10% ABC patch test skin and one biopsy from normal skin were collected directly into RPMI plus 10% fetal calf serum (FCS) and processed within 30 minutes of collection. Biopsies were finely minced in 1 ml of PBS and then added to 5 ml of 50% T-cell media (TCM, Iscove's Modified Dulbecco's Medium, 20% FCS, 2mM L-glutamine, 100 Units/ml penicillin, 100 ug/ml of streptomycin and 3.4 uM beta 2-mercaptoethanol).

For enzymatic digestion cells in T-cell media were incubated with 1 mg/ml of collagenase P and placed a rotator for 90 minutes at 37°C. DNA was digested by the addition of 200 Kuntz units/ml of DNase I for 15 minutes at 37°C before the cells were strained through a 70 uM filter and washed with 25 ml of Hank's buffered salt solution (HBSS)/HEPES/10 mM EDTA at 4°C. Cells were centrifuged at 400 x g and washed with a further 10 ml of PBS. Skin derived T cells were then stained immediately for single cell sorting.

For the isolation of T cells via explant culture, one 1% abacavir skin biopsy was minced and placed in TCM plus 100 units/ml of rIL-2 on a cellfoam matrix grid (Nohla Therapeutics, Australia, CY-903) for 2 weeks. T cells that migrated into the media proliferated without the

addition of additional stimulation and were frozen as a T cell line. This line was used to assess specificity for abacavir. 200,000 T cells were cultured overnight in TCM, TCM plus 20,000 autologous LCLs or TCM plus 20,000 autologous LCLs (lymphoblastoid cell line) and 10 µg/ml of abacavir. Cells were stained for CD3 (BD, AF700, clone UCHT1), CD4 (BD, PerCP-Cy5.5, clone OKT4), CD8a (Biolegend, APC Fire 750, clone RPA-T8), CD137 (PE, clone 4B4-1), CD69 (BD, APC, clone FN50), CD103 (BD, PE/Cy7 clone Ber-ACT8), CCR7 (BV421, clone 150503), CD45RO (BV510, clone UCHL1) and CCR10 (BB515, clone 1B5). Flow cytometry was employed to determine specificity by assessing up-regulation of CD137 and CD69.

**T-cell expansion.** For cloning of enzymatically extracted T cells, tissues were re-extracted as described above for an additional 90 minutes. Cells extracted from normal and abacavir exposed tissues were non-specifically expanded as described previously (2). Briefly, in a single U bottomed well of a 96 well plate, washed T cells were provided with 150,000 irradiated allo-feeder cells (PBMCs) and cultured in T-cell cloning medium (RPMI, 5% human serum (Sigma-Aldrich), 5% FCS, 2mM L-glutamine, 100 Units/ml penicillin and 100 µg/ml of streptomycin) plus PHA to a final concentration of 1.6 µg/ml. Two days later, and then every 2-3 days, cells were supplemented with 10% natural IL-2 (ZeptoMetrix, USA). Two weeks later 50,000 T cells were further expanded by the addition of anti-CD3 (30 ng/ml of OKT3 plus  $5 \times 10^6$  irradiated (8000 Rad) autologous LCLs and  $50 \times 10^6$  irradiated (3300 Rad) autologous PBMCs in a total volume of 25 ml. Two days later T cells were provided with 100 units/ml of rIL-2. Cells were washed on day 4 to remove anti-CD3 and expanded for an additional 10 days with the rIL-2 being replaced every 2-3 days. T cells were frozen until required.

**Single cell sorting.** Collagenase P purified T cells were stained with CD3 (BD, AF700, clone UCHT1), CD4 (BD, PerCPCy5.5, clone OKT4), CD8 (Biolegend, APC Fire 750, clone RPA-T8), CD137 (PE, clone 4B4-1), CD69 (BD, APC, clone FN50), CD103 (BD, PE/Cy7 clone Ber-ACT8), CCR7 (BV421, clone 150503), CD45RO (BV510, clone UCHL1) and CCR10 (BB515, clone 1B5). All antibodies were obtained from Becton Dickinson (BD), Australia, unless otherwise stated. Dead cells were excluded with the use of the fixable viable Stain, FVS620 (BD). Single cells were index sorted into 96 well plates on a FACS Aria III (Telethon Kids Institute, Perth, Australia) directly into 3 ul of reverse transcriptase buffer. Immediately following sorting cells were frozen on dry ice and then plates were stored at -80°C until required.

**Single cell TCR sequencing.** Using our novel TCR/RNAseq platform single cells undergo oligodT-primed reverse transcription during which, individual well's (cell's) cDNA products were barcoded and generically tagged with both 3' oligo-dT and 5' biotin labelled template switching oligonucleotides (TSO). Subsequent amplification of the cDNA derived from a single cell was amplified using the generic tags. Specific transcripts were targeted with a combination of nested generic tags and suitable gene specific primers (e.g. TCR alpha or beta conserved regions). The transcriptome was analysed using a modified Nextera transposon-mediated tagging-and-fragmentation ("tagmentation") with subsequent amplification of the 5' and 3' ends of the transcripts between the introduced Nextera-tag and the generic tags from cDNA conversion. Samples were multiplexed for next generation library preparation and sequencing - single cell sequences are bioinformatically separated.

**IFN $\gamma$ ELISpot.** ELISpot were performed as previously described (3). Briefly, 96 well ELISpot plates (MultiScreen-IP Filter Plate, Millipore) were coated with 100 ul/well of anti-IFN $\gamma$  (1-DIK, 2 $\mu$ g/mL - Mabtech) overnight at 4°C. Coating antibody was removed by 6x washes in

200 ul of PBS and the wells blocked with 100 ul of RPMI plus 10% FCS (R10) for 30-180 minutes at room temperature (RT). 10, 000 to 20, 000 T cells were added to each well in a total volume of 100 ul of R10 (RPMI, 10% FCS, 2mM L-glutamine, 100 Units/ml penicillin and 100 ug/ml of streptomycin). Autologous LCLs were incubated for 24 hours with 35 uM abacavir and then washed 3 times before adding them to T cells. Cloned skin derived T cells were incubated in T cell cloning media plus 10 units/ml of rIL-2 with abacavir pulsed LCLs overnight. Controls (anti-CD3-positive control, 100 ul of R10-negative control and pulsed LCLs negative control) were treated similarly. Plates were washed as described and incubated with 100 ul/well of diluted (1/1000 in PBS/0.5% FCS) biotinylated anti-IFN $\gamma$  (7-B6, Mabtech) at RT for 2 hrs. Plates were washed as described and incubated with 100 ul/well of streptavidin horseradish peroxidase (1/1000 in PBS/0.5% FCS) for one hour at RT in the dark. Plates were washed as described and developed with 100 ul/well of TMB for 12 minutes in the dark. Colour reaction was stopped by 6 washes in water and the plates air dried for 24 hrs and read on a plate reader (AID).

**Bioinformatics.** 3' and 5' RNA libraries were sequenced using the 2 x 75 bp paired end Illumina NextSeq. Reads for the individual single-cells were demultiplexed using plate id (30 nt), and cell barcode (6 nt) from either Read 1 or Read 2. The other read was further demultiplexed as either 3' or 5' using primer sequence (30 nt) and the remainder 45 nt sequences were aligned with CLC Bio (v.2018), using the GRCh38 human reference genome (Ensembl rel. 92). Gene-specific read counts were calculated using HTSeq-count using latest Gencode annotations and the 3' and 5' counts were summed. Cells with less than 200 genes and more than 5% mitochondrial content were removed. Furthermore, genes with > 0 counts in fewer than three cells were also removed. Downstream analyses (normalization,



PCA, differential expression and visualization) were performed in Seurat v.2.3.4 R package and Scanpy. TSNE analysis was performed using following settings: theta=0, max\_iter=10000, perplexity=100. Differential expression analysis was performed using the Wilcoxon rank-sum test. The P values were adjusted for multiple testing using the False Discovery Rate (FDR) correction. Pathway analysis was done using MSigDB.

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