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Clonal selection in the human $V\delta 1$ T cell repertoire indicates $\gamma\delta$ TCR-dependent adaptive immune surveillance

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$\gamma\delta$ T cells are considered to be innate-like lymphocytes that respond rapidly to stress without clonal selection and differentiation. Here we use next-generation sequencing to probe how this paradigm relates to human $V\delta 2^{\text{neg}}$ T cells, implicated in responses to viral infection and cancer. The prevalent $V\delta 1$ T cell receptor (TCR) repertoire is private and initially unfocused in cord blood, typically becoming strongly focused on a few high-frequency clonotypes by adulthood. Clonal expansions have differentiated from a naive to effector phenotype associated with CD27 downregulation, retaining proliferative capacity and TCR sensitivity, displaying increased cytotoxic markers and altered homing capabilities, and remaining relatively stable over time. Contrastingly, $V\delta 2^+$ T cells express semi-invariant TCRs, which are present at birth and shared between individuals. Human $V\delta 1^+$ T cells have therefore evolved a distinct biology from the $V\delta 2^+$ subset, involving a central, personalized role for the $\gamma\delta$ TCR in directing a highly adaptive yet unconventional form of immune surveillance.

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$\gamma\delta$ T cells have been preserved alongside $\alpha\beta$ T cells and B cells over the last ~450 million years of vertebrate evolution¹, and are increasingly recognized as having important roles in immune responses to both microbial and non-microbial stress challenges². Although $\gamma\delta$ T cells recognize target cells in an MHC-independent fashion, consistent with a lack of surface CD4/CD8 $\alpha\beta$ co-receptor expression, the key paradigms underpinning their distinct immunobiology are unclear. Mouse studies have highlighted $\gamma\delta$ T cell subsets bearing semi-invariant TCRs^{1,3–5}, suggestive of an innate-like biology and a limited range of self-ligands. In humans the $V\delta 2^{+}$ repertoire predominant in peripheral blood arguably conforms to this paradigm. As for other unconventional lymphocyte populations in humans such as natural killer T (NKT) cells and mucosal-associated invariant T (MAIT) cells, $V\delta 2^{+}$ T cells feature a conserved chain pairing (in the case of $V\delta 2^{+}$ cells with $V\gamma 9$), restricted CDR3 region diversity, comprising motifs conserved between many individuals⁶, and is generated early in gestation⁷. Most importantly, there is strong evidence $V\delta 2^{+}$ cells share a conserved biology, as they display potent TCR-dependent reactivity to pyrophosphate antigens generated by many species of bacteria/mycobacteria, with the butyrophilin-like molecule BTN3A1 a central player in antigen recognition⁸.

The extent to which these ideas apply to the human $V\delta 2^{neg}$ repertoire, present in both blood and peripheral tissues, is unclear. Previous studies have highlighted a diverse variable (V) region usage for this subset, and a diverse range of ligands have also been proposed for $\gamma\delta$ TCRs³, although to what extent they represent physiological reactivities is uncertain. Moreover, some studies have highlighted the potential for TCR-independent effector functions^{9,10}. Nevertheless, $V\delta 2^{neg}$ $\gamma\delta$ T cells are implicated in immune responses to viral infection, particularly cytomegalovirus (CMV)^{11,12}, but also Epstein Barr virus^{13,14}, and can also recognize a broad range of cancer cells¹⁵. One possibility is that within a seemingly diverse $V\delta 2^{neg}$ subset there exist conserved innate-like populations; however, a distinct biology underpinning $V\delta 2^{neg}$ $\gamma\delta$ T cell stress responses might alternatively be involved. Characterizing the $V\delta 2^{neg}$ TCR repertoire would enhance our understanding of this area.

Here, we use next-generation sequencing (NGS) approaches to define the $V\delta 2^{neg}$ repertoire from human peripheral blood, focusing on the predominant $V\delta 1$ subset. By comparing neonates and healthy CMV-seropositive/CMV-seronegative adults, we show that the $V\delta 1$ TCR repertoire is private, initially unfocused, and subsequently shaped by TCR-dependent clonal selection, concurrent with differentiation. These findings suggest that a distinct mode of adaptive immune surveillance applies to the $V\delta 1$ subset, and raise further questions regarding the nature of the $\gamma\delta$ TCR-linked stress challenges driving evolution of these responses *in vivo*.

Results

$V\delta 2^{+}$ and $V\delta 2^{neg}$ T cell phenotype in human peripheral blood.

We first characterized $V\delta 2^{neg}$ T cells in the peripheral blood of healthy adult donors selected for subsequent repertoire analyses. To account for possible effects of CMV status on phenotype^{12,16} we compared 10 CMV-seropositive and 10 CMV-seronegative donors, selecting individuals of a similar age (18–30 years), as previous studies have highlighted age-related changes in the CMV-specific $\alpha\beta$ T-cell repertoire^{17,18} and the $\gamma\delta$ T-cell repertoire in general^{19,20}. In all individuals we detected $V\delta 2^{+}$ and $V\delta 2^{neg}$ $\gamma\delta$ T-cell populations (Fig. 1a), the latter dominated by $V\delta 1^{+}$ cells (Fig. 1a,b). Consistent with previous studies, we observed a modestly increased proportion of $V\delta 1^{+}$ cells in

CMV⁺ individuals (Fig. 1c). Furthermore, we noted the presence of a $V\gamma 9/V\delta 1$ chain pairing in all individuals to varying degrees (Fig. 1d). Both $V\delta 2^{neg}$ T cells and the $V\delta 1^{+}$ subsets of $\gamma\delta$ T cells displayed a mixed CD27⁺/CD45RA⁺ or CD27⁺/CD45RA⁺ phenotype in most individuals (Supplementary Fig. 1A,B), as previously described¹⁶. In comparison, $V\delta 2^{+}$ T cells were predominantly CD27⁺ CD45RA⁻ (Supplementary Fig. 1A,B), consistent with previous studies²¹.

The $V\delta 1$ TCR repertoire is focused on dominant clonotypes.

We used amplicon rescued multiplex (ARM)-PCR and NGS methods to analyse the $V\delta 2^{neg}$ TCR repertoire in healthy adults, focusing initially on the dominant $V\delta 1$ subset. We achieved a mean sequencing depth of 346,371 ± 27,993 reads with an average of 2,742 ± 432 unique CDR3 sequences for TCR δ and 384,182 ± 31,547 reads with an average of 1,261 ± 170 unique CDR3 sequences for TCR γ (Supplementary Table 1), with no correlation observed between sequencing depth and numbers of unique CDR3 assigned (Supplementary Fig. 2A). Consistent with successful purification of $V\delta 1$ T cells, nearly all TCR δ sequences obtained used $V\delta 1$ (Fig. 2a); for TCR γ , consistent with flow cytometry (Fig. 1a,d), $V\gamma 9$ sequences were commonly prevalent (Fig. 2a) and correlated with $V\gamma 9$ antibody staining (Supplementary Fig. 2B), although clonotypes using other functional $V\gamma$ gene segments were detected in all donors (Fig. 2a; Supplementary Fig. 2C,D).

Strikingly, in most individuals (8/10 CMV⁺ and 5/10 CMV^{neg} adults), remarkably strong focusing of the $V\delta 1^{+}$ response was observed towards a small number of individual clonotypes (Fig. 2b; Supplementary Fig. 2E). This was evident for both TCR γ and TCR δ chains, and the majority of total error-corrected reads could be accounted for by a small number of the most prevalent clonotypes (≤ 10) (Fig. 2b). TCR δ D75 values (the percentage of unique sequences required to account for 75% of total reads) were <6% in this grouping (mean 2.23 ± s.e.m. 0.53%), emphasising extreme skewing (Fig. 2c). In addition, the $V\gamma 9/V\delta 1$ populations consistently present were often highly clonally focused. To address whether this extreme clonotypic focusing was restricted to $V\delta 1$ sequences, we developed a negative selection strategy enabling analysis of the broader $V\delta 2^{neg}$ population (Supplementary Fig. 3A,B), in four individuals. A more diverse range of $V\delta$ sequences were observed in these analyses, including chiefly $V\delta 3$ and $V\delta 8$, with evidence of moderate clonotypic focusing in some individuals for $V\delta 2^{neg}$, $V\delta 1^{neg}$ $V\delta$ chains (Supplementary Fig. 3C), although these $V\delta$ regions were used in a small percentage of clonotypes in these donors.

In contrast with this ‘focused adult’ subgroup, dramatically less focused repertoires were observed in seven individuals (TCR δ D75 mean 14.95 ± s.e.m. 2.74%; in most cases the top 10 sequences represented <20% of the total error-corrected reads detected) and used a varied set of $V\gamma$ gene segments (Fig. 2d,e; Supplementary Fig. 2D,F). These results establish that while not universal, extreme clonotypic focusing is a common feature of the $V\delta 1$ and $V\delta 2^{neg}$ $\gamma\delta$ TCR repertoire. Applying a TCR δ D75 cut-off threshold of 6% (equivalent to the lowest quartile TCR δ D75 values), we defined this minority of individuals with higher D75 values as a ‘diverse adult’ subgroup (Fig. 2c). While the average TCR δ D75 values and Shannon-Weiner index for CDR3 $\delta 1$ diversity highlighted a trend towards decreased diversity (lower TCR δ D75) in CMV⁺ versus CMV^{neg} donors, the difference was not significant (Fig. 2f, left; Supplementary Fig. 4). Notably the diverse adult donors were mostly (5/7) CMV seronegative (Fig. 2c), and included the youngest members

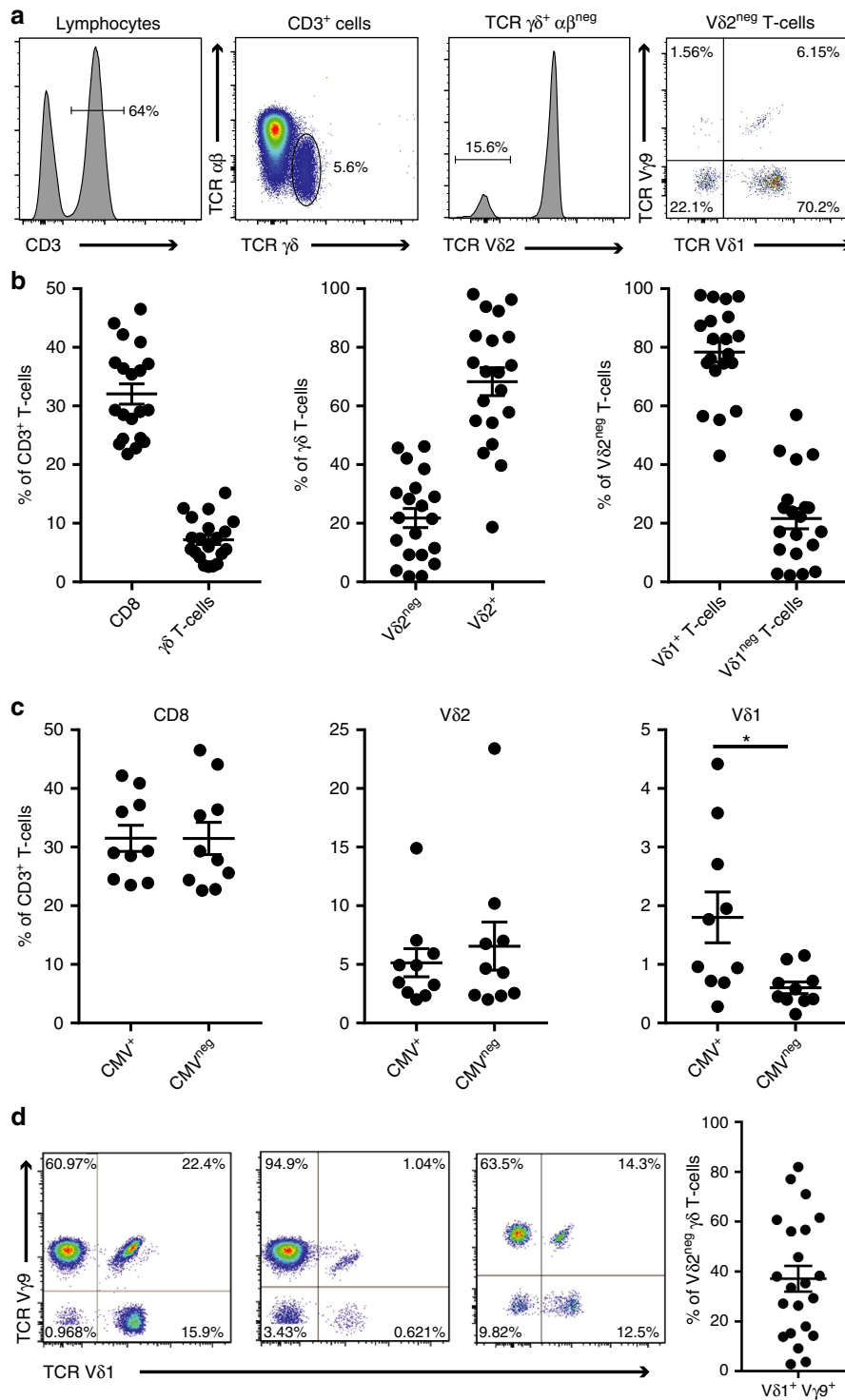


Figure 1 | Peripheral blood $\gamma\delta$ T-cell populations in donors analysed for $\gamma\delta$ TCR repertoires. (a) Major peripheral blood $\gamma\delta$ T-cell populations identified by $\gamma\delta$ TCR chain specific antibodies. Flow cytometry plots are representative of 20 donors. (b) Frequency of $\gamma\delta$ T cells in CD3⁺ lymphocytes (left graph), abundance of Vδ2⁺ and Vδ2^{neg} T cells in the $\gamma\delta$ T cell compartment (Middle), and proportion of Vδ1⁺ T cells in the Vδ2^{neg} $\gamma\delta$ T-cell sub-population (Right). Graphs show the mean \pm s.e.m. from 20 donors. (c) Effect of donor CMV-seropositivity on CD8⁺, Vδ2⁺ and Vδ1⁺ cell percentages in total T cells. Graphs show the mean \pm s.e.m. from 10 CMV-seropositive and 10 CMV-seronegative donors. (d) Prevalence of a Vγ9 chain pairing in Vδ1⁺ T cells. Graphs show the mean \pm s.e.m. and flow cytometry plots are representative of 20 donors. Data analysed by student's *t*-test, **P* = 0.0228.

of the cohort. The difference in mean TCRδ D75 values between adult focused and adult diverse donors was ~ 7 -fold (2.23 ± 0.53 versus 14.95 ± 2.74 respectively, *P* < 0.0002; Student's *t*-test) (Fig. 2f, right).

The cord blood Vδ1 TCR repertoire is unfocused. To investigate how the Vδ1 repertoire differed in early life, we carried out comparable TCR repertoire analyses on the Vδ1⁺ subpopulation of cord blood-purified $\gamma\delta$ T cells (Fig. 3a,b). Vδ1⁺ cells dominate

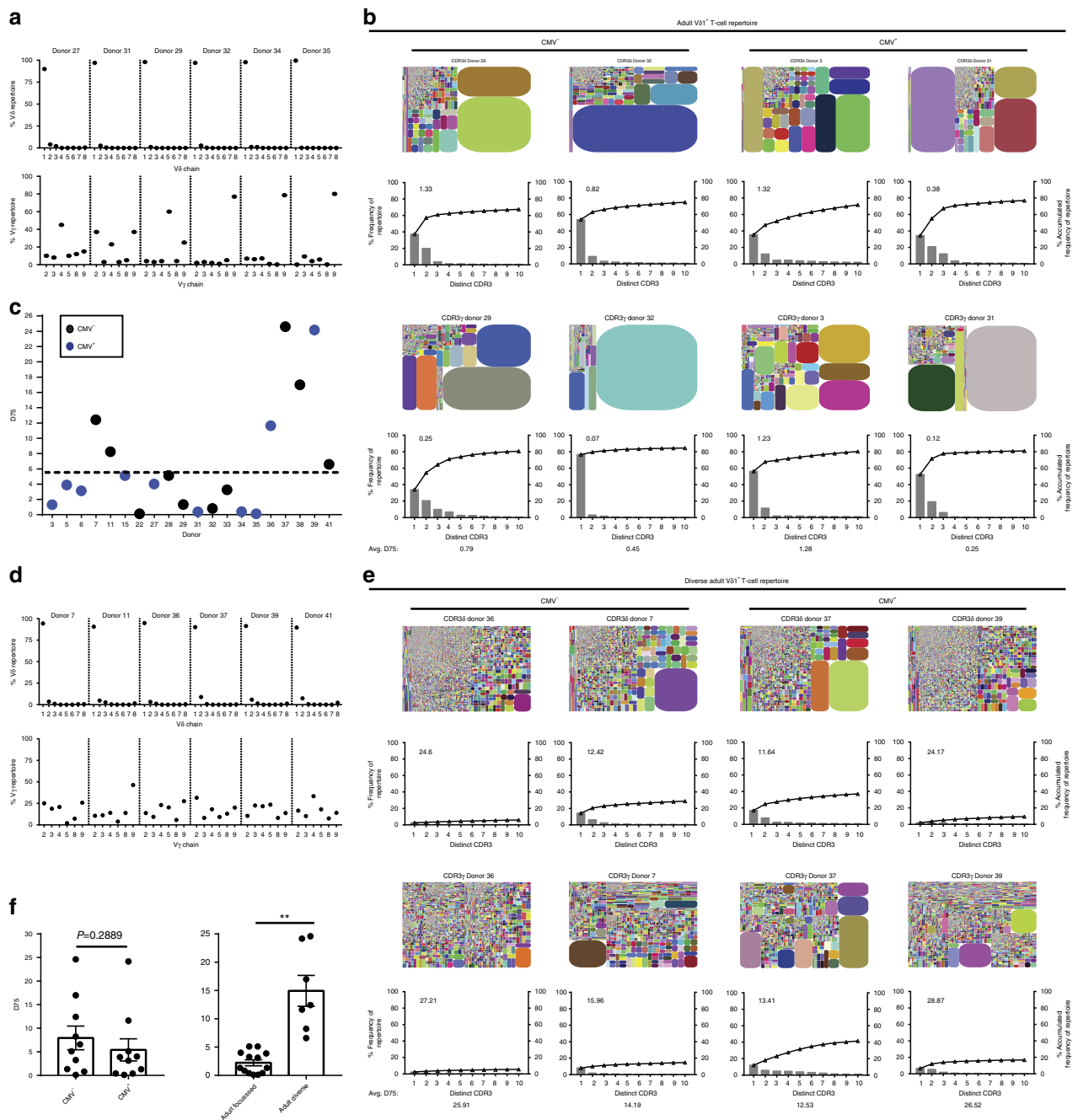


Figure 2 | The V δ 1⁺ TCR repertoire is focused on a few dominant clonotypes in healthy adults. (a) V γ and V δ chain usage by $\gamma\delta$ TCR sequences from sorted V δ 1⁺ T cells from peripheral blood. Graphs show six representative donors of 13. (b) Tree maps show CDR3 clonotype usage in relation to repertoire size (each CDR3 colour is chosen randomly and does not match between plots) and graphs show the individual clone frequency (left y axis) and the accumulated frequency for the first 10 most prevalent clonotypes (right y axis). (c) Analysis of inter-donor diversity by D75 (percentage of clonotypes required to occupy 75% of the total TCR repertoire) from TCR δ repertoire analyses from 20 donors with CMV-seropositive (blue dots), CMV-seronegative individuals (black dots) and lowest quartile range plotted (dashed line). (d) V γ and V δ chain usage and (e) Tree maps and accumulated frequency graphs, for $\gamma\delta$ TCR repertoires in donors with a D75 > 6. (f) Comparison of mean \pm s.e.m. of TCR δ D75 values for 10 CMV-seropositive and 10 CMV-seronegative donors (Left) and focused donors ($n=13$) against diverse donors ($n=7$) (Right). Data were analysed by student's t -test, ** $P=0.0002$.

the cord blood $\gamma\delta$ repertoire⁷, and expressed V δ 1 paired with diverse V γ regions (Fig. 3a). Cord blood TCR δ 1 and TCR γ CDR3 sequences were extremely unfocused (TCR δ D75 mean $14.06 \pm$ s.e.m. 2.76%), in contrast to focused adult V δ 1 repertoires (mean $2.23 \pm$ s.e.m. 0.53%), but similar to unfocused adult samples (mean $14.95 \pm$ s.e.m. 2.74%) (Fig. 3c), and comprised numerous low frequency clonotypes, the most prevalent of which represented <1.30% and <2.17% of the

total unique CDR3s detected, for TCR γ and TCR δ respectively (see cumulative frequency plots accounting for the 10 highest prevalence clonotypes, Fig. 3d).

The V δ 1 TCR repertoire is dominated by private clonotypes. Detailed comparisons of CDR3 length (presented as spectratype plots) within and between individuals indicated that in V δ 1⁺

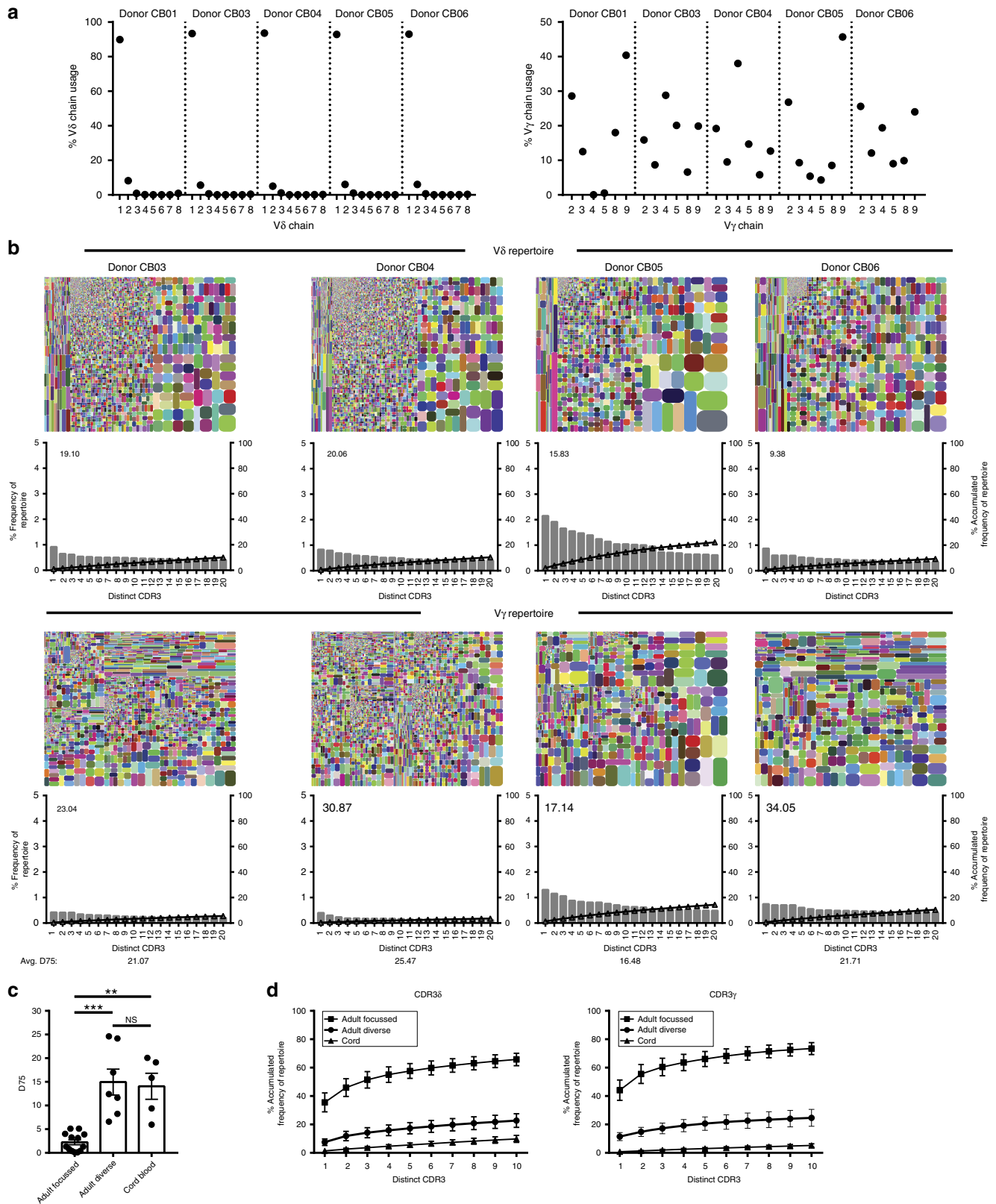
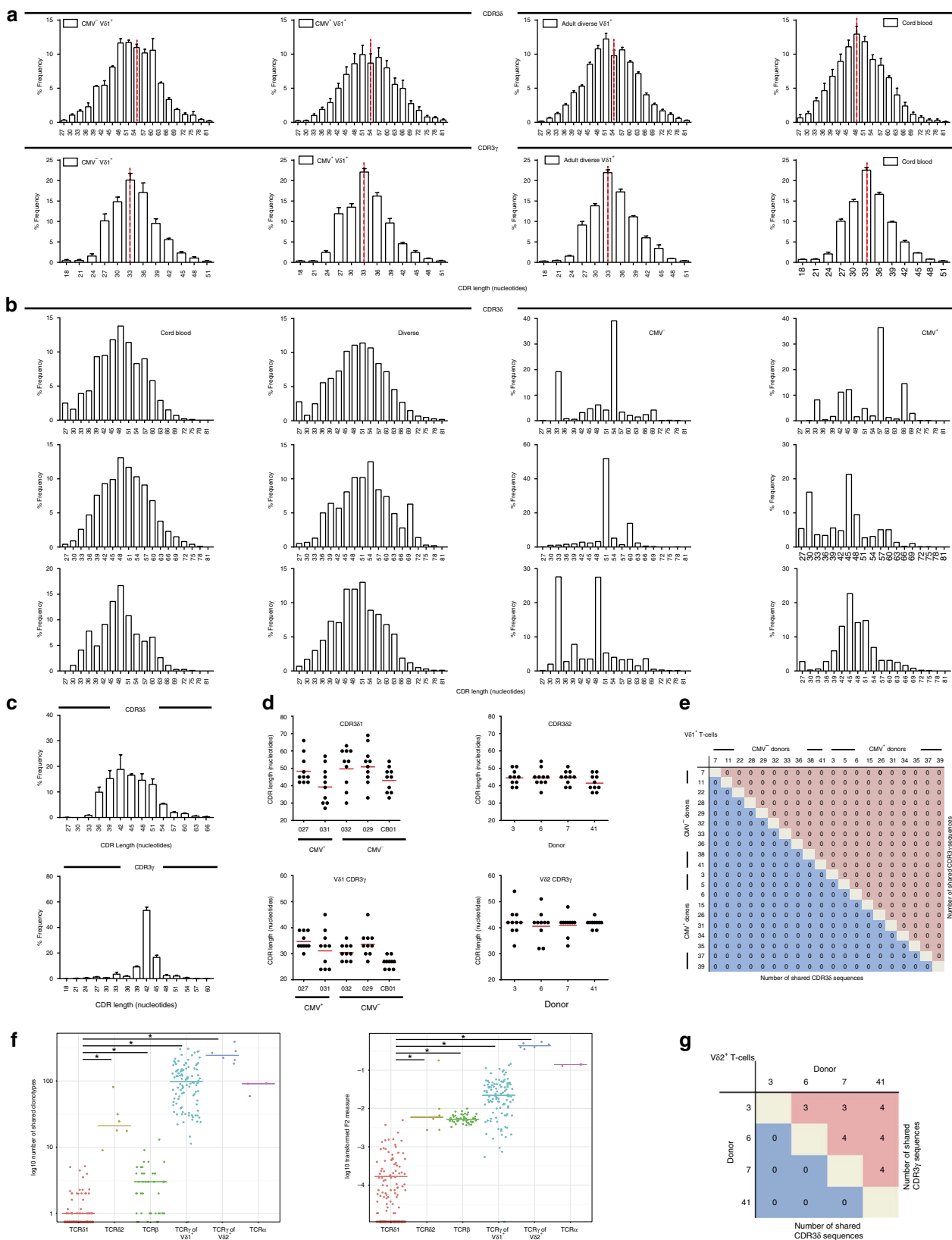


Figure 3 | The cord blood $V\delta 1^+$ TCR repertoire is composed of an unfocused set of $\gamma\delta$ TCRs. (a) $V\gamma$ and $V\delta$ chain usage by sorted $V\delta 1^+$ T cells from cord blood samples. (b) Tree maps for both $CDR3\gamma$ and $CDR3\delta$ clonotype usage in relation to repertoire size and accumulated frequency graphs for each of the top 20 most prevalent clonotypes. (c) Comparison of mean \pm s.e.m. of TCR δ D75 values from adult focused ($n=13$), adult unfocused ($n=7$) and cord blood ($n=5$) donors. (d) Accumulated frequencies means \pm s.e.m. occupied by the first 10 clonotypes for each donor and grouped into adult focused donors ($n=13$), adult diverse ($n=7$) and cord blood ($n=5$). Data were analysed by Kruskal-Wallis ANOVA with Dunn's post-test comparisons, $**P=0.0049$ and $***P=0.0007$.

T cells, the mean CDR3 δ 1 length was substantially greater than CDR3 γ (mean 54 versus 33 nucleotides (nt; Fig. 4a), as expected²²). In addition, we detected a minority of exceedingly long V δ 1 CDR3s of >87 nt, some having up to 52 nontemplated (N) nt added, which appear to be *bona fide* productive TCR

chains (Supplementary Fig. 5A,B). Frequency-normalized analyses of CDR3 lengths in focused adults, diverse adults and cord blood were essentially identical (Fig. 4a). However, non-normalized comparisons of CDR3 length distributions, taking into account the frequency of individual clonotypes, indicated



that only unfocused adults' repertoires had similar profiles to cord blood. In contrast, individuals with focused V δ 1 TCR repertoires displayed highly skewed profiles (Fig. 4b).

Comparable analyses of the human V δ 2⁺ repertoire in four adults highlighted that while V δ 1⁺ cells used various V γ and J γ gene segments, V δ 2⁺ cells almost exclusively used V γ 9 paired with J γ P (Supplementary Fig. 6A,B), with CDR3 γ 9 lengths of 11–18 amino acids (33–54 nt) (Fig. 4c), and >50% of CDR3s composed of 14 amino acids in all donors. Moreover, analysis of the ten most frequent TCR δ and TCR γ clonotypes in V δ 2⁺ cells from each donor revealed constrained lengths in both CDR3 γ 9 and CDR3 δ 2 (Fig. 4d). In contrast, in V δ 1⁺ cells the CDR3 γ and CDR3 δ lengths of the ten most frequent clonotypes, typically accounting for >50% of the repertoire, were extremely diverse both within and between individuals (Fig. 4d, Supplementary Fig. 6C). Consistent with this, multidimensional clustering analysis confirmed the TCR γ CDR3 length distributions of V δ 2⁺ T cells were similar across different donors, whereas those of the V δ 1 compartment were highly individual (Supplementary Fig. 6D).

Importantly, comparisons of the ten most prevalent TCR γ and TCR δ 1 clonotypes from each donor revealed they were private sequences, absent in any other individuals either at a nucleotide or amino acid level (Supplementary Tables 2–5; Fig. 4e). Consistent with this, they frequently involved extremely complex CDR3 regions, comprising numerous N/P nucleotide additions (1–11 nt for TCR γ ; 5–28 nt for TCR δ) in addition to D and J region nucleotides (Supplementary Tables 2–3), indicating rare recombination events. This was particularly pronounced for the predominant V δ 1 chains in each donor, which utilized 1–2 D δ regions and contained a mean of 16 N/P nucleotides. Indeed, after error correction, nearly all CDR3 δ and CDR3 γ sequences were found to be private. The very few TCR γ and TCR δ clonotypes observed in >1 individual generally resulted from relatively simple recombination events with little N nt addition, and were low in frequency. Comparison of V δ 1 repertoire data with age and sex matched TCR β repertoire data revealed that V δ 1 as a repertoire was even more private than TCR β (Fig. 4f). Therefore, the V δ 1 TCR repertoire was overwhelmingly private, with different TCR clonotypes present in each individual, and these observations also extended to non-V δ 1 sequences in our V δ 2^{neg} γ δ T cell analyses, suggesting it may be a generic property of the V δ 2^{neg} TCR repertoire.

In contrast, several V δ 2 subset-derived CDR3 γ protein sequences were shared between all four samples at a relatively high frequency (Fig. 4g; Supplementary Fig. 7A,B). These involved recombination of V γ 9 and J γ P segments with limited N/P nucleotide addition (generally <3 nt) indicating their origin from convergent recombination²³. V γ 9 sequences in V δ 2⁺ cells were constrained in length (Fig. 4c,d) and were more public than

TCR δ , TCR β chains and TCR γ in V δ 1⁺ cells (Fig. 4f), and often contained a typical 14 amino acid sequence motif (Supplementary Fig. 7C)^{6,7,24}. Although V δ 2 sequences were relatively private compared with TCR γ (Fig. 4f,g), more CDR3 δ 2 sequences were shared between donors than CDR3 δ 1 sequences (Fig. 4f). As previously noted, CDR3 δ 2 often contained a hydrophobic L or V residue at position 6 (Supplementary Fig. 7D)²⁴. Therefore, in stark contrast to V δ 1⁺ T cells, but analogous to iNKT²⁵ and MAIT²⁶ populations, the V δ 2V γ 9 population expresses a semi-invariant TCR.

V δ 1 clonal expansions are long-lived and differentiated. To confirm that the prevalent clonotypes we detected genuinely reflected differential lymphocyte expansion rather than disproportionate expression levels of specific TCR transcripts, we single cell sorted the V γ 9V δ 1 T cell population, which frequently featured highly dominant clonotypes (Fig. 2), from six healthy adult donors, and used RT-PCR to identify V γ 9V δ 1 TCR pairs (Fig. 5a). In each case, the dominant V γ 9 and V δ 1 TCR chain evident from NGS analyses was identified in >50% of sequences (Fig. 5b), confirming that the prevalent clonotypes detected in the NGS analyses truly reflected clonal dominance at the cellular level.

To assess whether the dominant V δ 1 expansions are stably maintained over time, we compared our ARM-based repertoire analyses with an analogous, RNA-based RACE TCR repertoire analysis, conducted previously on 5 individuals from our cohort (2 CMV-seronegative, 3 CMV-seropositive). In 5/5 donors analysed, the most frequent clonotypes from RACE analysis were detected in subsequent ARM analyses, conducted between 12–18 months later (Fig. 5c). Also, in most donors, the hierarchy of prevalent clonotypes was broadly conserved in both analyses (Fig. 5c). Therefore clonotypic expansions prevalent in the V δ 1 T-cell repertoire can be highly stable over time.

Next, we assessed how V δ 1⁺ T-cell differentiation status correlated with the extent of clonotypic focusing. We sorted sub-populations of V δ 1⁺ cells based on expression of CD27 and CD45RA, markers that have been used to identify naive and memory subsets in CD8 cells²⁷ and γ δ T cells¹⁶. Strikingly we observed the vast majority of clonal populations resided in CD27^{lo/neg} CD45RA⁺ populations (gates C and D), whereas clonotypes found in CD27^{hi} populations (gates A and B) were strikingly diverse (Fig. 5d). Notably, when applying a CD27^{hi} and CD27^{lo/neg} gating strategy to individuals with focused V δ 1 TCR repertoires, they displayed a dominant CD27^{lo/neg} CD45RA⁺ phenotype but also retained a minor CD27^{hi} population, whereas V δ 1 T cells of both cord blood, and V δ 1 diverse adults, were predominantly CD27^{hi} (Fig. 5e). Furthermore, focused donors had elevated percentages of

Figure 4 | CDR3 length and diversity within the V δ 1 and V δ 2 TCR. (a) Comparison of the mean \pm s.e.m. from frequency-normalized CDR3 δ and CDR3 γ length spectratyping for V δ 1⁺ T cells in CMV^{neg} ($n=5$), CMV⁺ ($n=8$), adult diverse ($n=7$) and cord blood ($n=5$) donors. (b) Comparison of non-normalized CDR3 δ length spectratyping for V δ 1⁺ T cells from 3 representative individuals from CMV-seronegative (representative of $n=5$), CMV-seropositive (representative of $n=8$), adult diverse (representative of $n=7$) and cord blood (representative of $n=5$) donor groupings. (c) Non-normalized length spectratyping for CDR3 δ and CDR3 γ in adult V δ 2⁺ T cells ($n=4$). (d) Length distribution and mean (red line) within the top 10 most prevalent clonotypes in CDR3 δ (left two panels) and CDR3 γ (right two panels) of V δ 1⁺ T cells (5 donors shown, representative of 20) and V δ 2⁺ T cells (from 4 donors). (e) Publicity in the 10 most prevalent clonotypes for each donor's V δ 1⁺ TCR repertoire compared against all other donors (both aa and nt sequences compared). (f) Comparison of relative publicity in TCR repertoires. Overlap of individual TCR repertoires in TCR δ 1 ($n=15$), TCR δ 2 ($n=4$), TCR β ($n=15$, ref PMID: 27183615), TCR γ of V δ 1⁺ cells, TCR γ of V δ 2⁺ cells and TCR α ($n=3$). Each dot shows relative similarity of repertoires for a pair of unrelated donors in terms of the shared TCR variants with identical amino acid CDR3 sequence, and V and J segments used. Overlap was estimated either as a number of clonotypes shared between the sets of top-1,000 largest clonotypes of each repertoire (left), or as a sum of clonotype frequencies shared between the total repertoires (F2 metrics of VDJTools software, right). (g) Publicity in the 10 most prevalent clonotypes for each donor's V δ 2⁺ TCR repertoire compared against all other donors (both aa and nt sequences compared). Mean overlap of sequences between each group was analysed by Kruskal-Wallis ANOVA with Dunn's post-test comparisons * $P<0.003$.

V δ 1⁺/CD27^{lo/neg} cells compared with diverse and cord blood donors (Fig. 5f, left). Moreover, the percentage of CD27^{lo/neg} cells each donor displayed inversely correlated with the TCR δ D75 and Chao 1 indices of V δ 1 diversity (Fig. 5f, right panels). These correlations suggested that V δ 1 TCR repertoire focusing was accompanied by transition of V δ 1⁺ T cells from a CD27^{hi} CD45RA⁺ to a CD27^{lo/neg} CD45RA⁺ phenotype. To test this directly, we sorted V δ 1⁺ CD27^{hi} versus CD27^{lo/neg} populations from two focused adult donors and performed NGS TCR repertoire analysis. This unequivocally confirmed that the V δ 1⁺/CD27^{hi} population displayed a diverse TCR $\gamma\delta$ repertoire, generating TCR δ repertoires and TCR δ D75 values similar to cord blood and diverse adult donors, whereas the V δ 1⁺/CD27^{lo/neg} population was comprised of even more pronounced dominant TCR clonotypes (Fig. 5g), compared with each donor's original TCR δ repertoire profile (Fig. 2b). Inter-individual comparisons revealed the majority of V δ 1⁺ CD27^{hi} T cells expressed other markers typical of naïve CD8 T cell populations including IL-7R α , CD28, and CCR7 and CD62L, while V δ 1⁺/CD27^{lo/neg} cells had downregulated surface expression of these markers similarly to memory CD8 compartments (Fig. 5h) (reviewed in Akbar and Fletcher, 2005)¹⁷. Although CD45RA and CD27 have been used before to assign $\gamma\delta$ memory compartments^{16,21}, our CD27^{hi} versus CD27^{lo/neg} gating strategy represents a new approach to immunophenotyping V δ 1 populations, which more closely aligns naïve/effector marker expression to V δ 1 TCR diversity/clonality.

V δ 1⁺ CD27^{lo/neg} clones respond to IL-15 and TCR stimulation.

Comparisons of the functional responsiveness of total V δ 1 T-cell subsets indicated robust CD3/CD28-dependent activation equivalent to CD8⁺ T cells and V δ 2⁺ $\gamma\delta$ T cells (Fig. 6a). However, V δ 1⁺ CD27^{lo/neg} T cells displayed a markedly enhanced responsiveness to both CD3/CD28 and IL-15 relative to CD27^{hi} V δ 1 T cells after short-term stimulation (Fig. 6b). Importantly, and unlike V δ 2⁺ T cells, V δ 1⁺ T cells were largely unresponsive to the innate T cell trophic IL-18 or IL-12 cytokines (Fig. 6a,b). In keeping with their high IL-7R α expression (Fig. 5g), CD27^{hi} V δ 1 subsets proliferated preferentially in response to IL-7 stimulation relative to CD27^{lo/neg} V δ 1 populations, whereas the latter displayed more pronounced IL-15-induced proliferation (Fig. 6c). Moreover, single cell PCR confirmed that cells that proliferated (that is, became CFSE^{lo}) in 7-day IL-7 cultures predominantly expressed diverse TCRs, irrespective of whether V δ 1 T cells were analysed on bulk or segregated into V δ 1 CD27^{hi} and V δ 1 CD27^{lo/neg} subsets, whereas expanded clonotypes proliferated preferentially in response to IL-15 (Fig. 6d). In addition, both CD27^{hi} and CD27^{lo/neg} populations responded to CD3/CD28 (Fig. 6c) and, separately, to anti- $\gamma\delta$ TCR antibody stimulation in 7-day cultures. CD27^{lo/neg} populations in general exhibited somewhat enhanced proliferative responses to anti- $\gamma\delta$ TCR antibody (Fig. 6c; $P=0.0458$) relative to CD27^{hi} cells. This suggests that although expanded V δ 1 clones have a CD45RA⁺/CD27^{lo/neg} phenotype normally associated with CD8 T_{EMRA} cells, they are capable of proliferating in response to signals through the TCR and IL-15.

V δ 1⁺ CD27^{lo/neg} clones express cytotoxic markers and CX₃CR1.

A hallmark of effector T cell subsets is the acquisition of intracellular cytotoxic granules, therefore we assessed intracellular cytotoxic marker expression in both CD27^{hi} and CD27^{lo/neg} V δ 1 T-cell subsets (Fig. 7a). CD27^{hi} V δ 1 T cells largely lacked Granzyme A or B and perforin expression, whereas these markers were markedly upregulated in CD27^{lo/neg} V δ 1 T cells, again

matching levels in naïve and effector memory CD8⁺ T-cell subsets, respectively. Next, we assessed the proportion of V δ 1 T cells that expressed Granzyme A/B and found this significantly correlated with the extent of focusing (TCR δ D75, $P=0.0071$). CX₃CR1 (fractalkine receptor) was preferentially expressed in CD27^{lo/neg} versus CD27^{hi} naïve-like V δ 1⁺ T cells (Fig. 7b) and CX₃CR1 expression in V δ 1⁺ T cells exclusively marked out Granzyme B⁺ cells whereas CX₃CR1^{neg} V δ 1⁺ T cells predominantly expressed IL-7R α (Fig. 7b). We then assessed TCR usage on the single cell level and in each donor, CX₃CR1⁺ cells within the V δ 1⁺ T-cell population were composed exclusively of clonotypically expanded sequences, with each sequence identity matching those detected in deep sequencing analysis, whereas CX₃CR1^{neg} cells were predominantly composed of multiple diverse TCRs (Fig. 7c). Together, these data indicate that clonal expansion is inextricably linked to changes in homing receptor, CD27 and cytolytic effector expression.

Discussion

$\gamma\delta$ T cells have been highlighted as a key cellular exemplar of lymphoid stress surveillance, which invokes unconventional lymphocytes that can quickly initiate responses to stress challenges without the obligatory delay associated with clonal expansion and differentiation²⁸, a paradigm thought to apply to some murine $\gamma\delta$ TCR subsets²⁹. Although V δ 2⁺ cells increase in number upon microbial challenge³⁰, they arguably fit this paradigm⁷. However, how it applies to human V δ 2^{neg} T cells has to date remained unclear.

Our findings expose several features of V δ 1 T cells, which comprise the dominant proportion of V δ 2^{neg} T cells, that differ fundamentally from this paradigm. Instead of being pre-expanded, in most adults a small number of specific clonotypes emerge from an initially unfocused neonatal V δ 1 T-cell repertoire, undergo pronounced clonal expansion, and ultimately dominate the V δ 1 $\gamma\delta$ T-cell compartment. Notably, such clonotypic expansions were relatively stable over time, and their occurrence was not an inevitable consequence of a maturing $\gamma\delta$ T-cell compartment, as a sizeable minority of adults had largely unfocused repertoires. CDR3 sequences of dominant clonotypes were extremely complex, suggesting heavy selection of initially low frequency clonotypes resulting from single, unlikely recombination events. Consistent with this, V δ 1 TCR sequences observed were, overwhelmingly, unique to each individual, indicating the V δ 2^{neg} repertoire, including dominantly expanded clonotypes, is essentially private. Conversely, analyses highlighted V δ 1/V δ 2 cells shared sequences in TCR γ and (to a lesser extent) TCR δ , confirming this subset featured a semi-invariant TCR.

Importantly V δ 1 clonal expansion was accompanied by phenotypic differentiation and a distinct functional biology. Unfocused adult TCR repertoires were associated with apparently naïve V δ 1 populations characterized by a CD27^{hi}CCR7⁺CD28⁺IL-7R α ⁺CD62L⁺ phenotype evident in all individuals but predominant in the diverse adult subgroup; moreover, cord blood V δ 1 cells largely conformed to this phenotype. Conversely, clonally expanded populations were analogous to CD8 T effectors in displaying a CD27^{lo/neg}CCR7^{neg}CD62L^{lo}CD28^{neg}IL-7R α ^{neg} phenotype, and similarly were marked out by CX₃CR1 expression. Relative to CD27^{hi} V δ 1⁺ cells, CD27^{lo/neg} V δ 1 subsets displayed more rapid activation and proliferation in response to CD3/TCR stimulation, upregulation of multiple cytotoxic markers equivalent to CD8 EMRA subsets, differential cytokine responsiveness (enhanced to IL-15 and a lack of response to IL-7), and differential homing receptor expression, consistent with a functional effector status. In contrast, CD27^{hi} V δ 1⁺

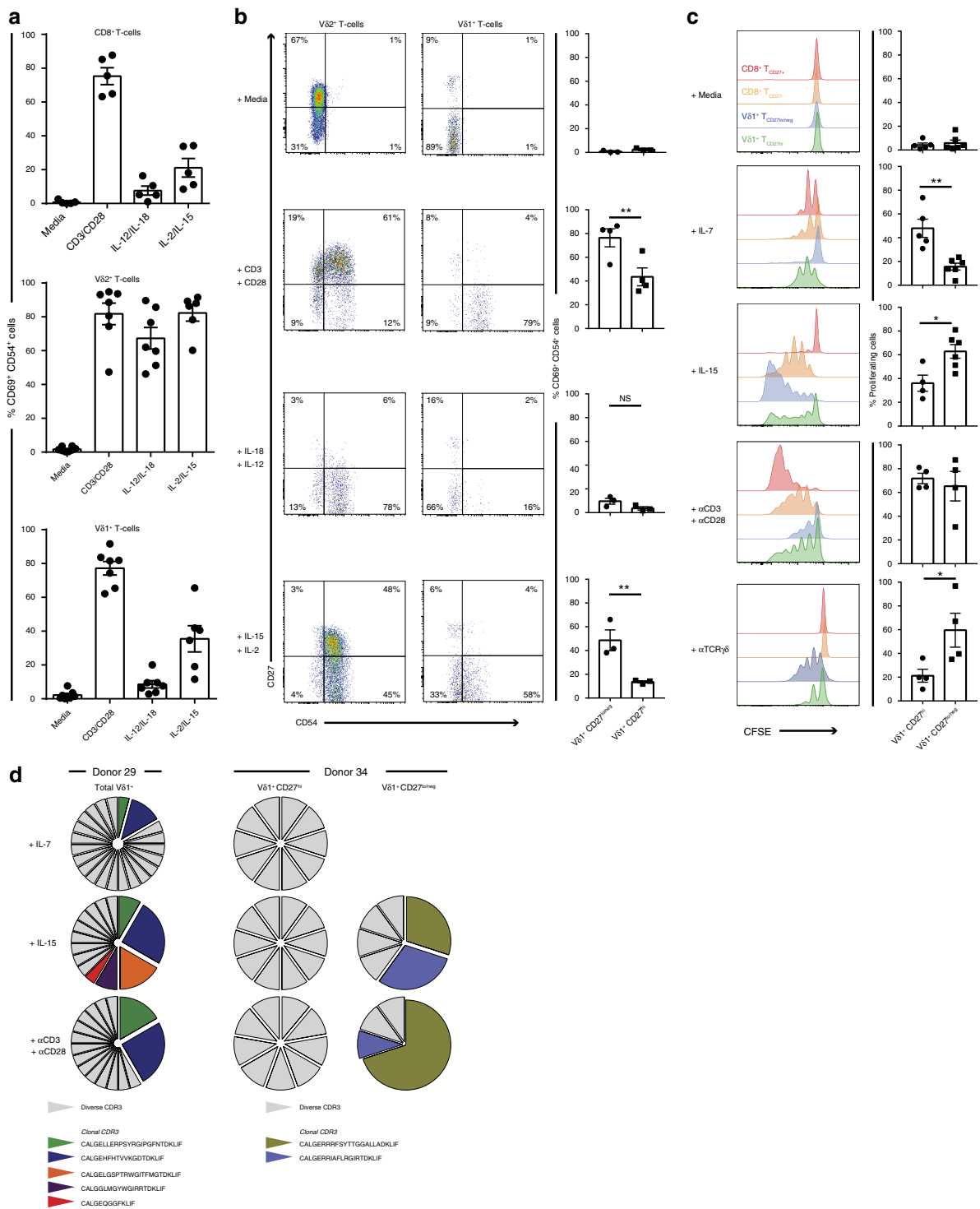


Figure 6 | Functional characteristics of clonally expanded CD27^{lo/neg} versus naive CD27^{hi} Vδ1⁺ T cells. (a) Sorted CD3⁺ T cells were incubated for 72 h with cytokines or anti-CD3/CD28 beads. CD8⁺, Vδ2⁺ and Vδ1⁺ T cells were then assessed for the upregulation of CD69 and CD54. Graphs show mean ± s.e.m. from medium controls (n = 5–7), CD3/CD28 (n = 5–7), IL-12/IL-18 (n = 5–7) and IL-2/IL-15 (n = 5–6) stimulation. (b) Flow cytometry analysis of Vδ2 and Vδ1 T cells from a, with cells analysed for CD27 and CD54 expression (left, representative flow cytometry plots) and graphs show mean ± s.e.m. of CD69⁺ CD54⁺ cells in Vδ1⁺ CD27^{hi} and Vδ1⁺ CD27^{lo/neg} populations, data from medium controls (n = 4), CD3/CD28 (n = 4), IL-12/IL-18 (n = 3) and IL-2/IL-15 (n = 3). (c) Proliferation of Vδ1 T cells, assessed by CFSE dilution, for 7 days in response to stimulation with IL-7, IL-15, anti-CD3/CD28 and anti-TCRγδ mAb. Histograms are from a representative focused adult donor’s Vδ1⁺ CD27^{hi} cells, Vδ1⁺ CD27^{lo/neg} cells, CD8⁺CD27⁺ or CD8⁺ CD27^{neg} T cells and graphs show mean ± s.e.m. of proliferating cells (n = 4–6). (d) Total proliferating Vδ1⁺ T cells (Left, donor 29) or CD27^{hi} and CD27^{lo/neg} Vδ1⁺ T cells were single cell sorted and CDR3δ sequenced by PCR, prevalent clonotypes detected by previous deep sequencing are coloured and diverse individual sequences are grey. Donor 29 had 24 single cells, and donor 34 had 10 single cells analysed from each condition. Data analysed by student’s t test, NS = P > 0.05, *P < 0.05 and **P < 0.01.

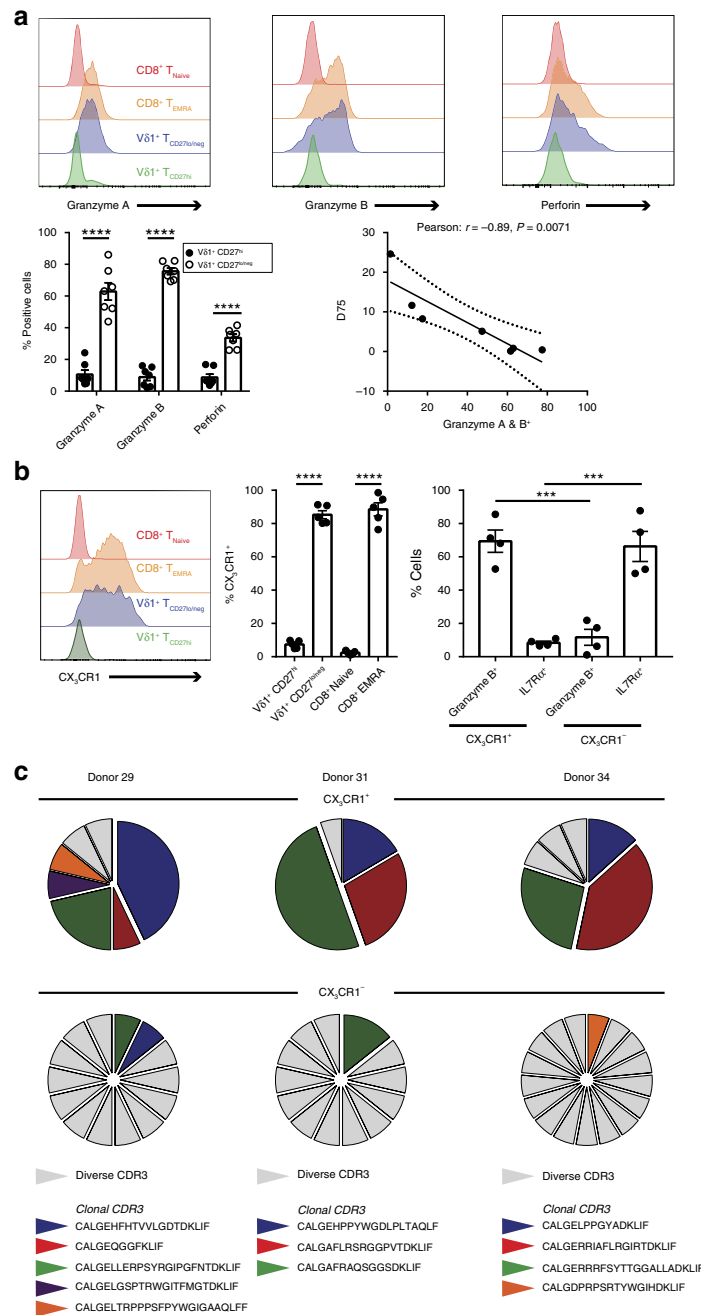


Figure 7 | Clonally expanded CD27^{lo/neg}Vδ1⁺ T cells express CX₃CR1 and cytotoxic effector molecules. (a) Expression of intracellular cytotoxic effector molecules, granzyme A, granzyme B and perforin by CD8⁺ T_{Naive}, CD8⁺ T_{EMRA}, Vδ1⁺ CD27^{lo/neg} and Vδ1⁺ CD27^{hi} cells. Correlation graph between all 7 donors and the corresponding TCR δ D75 calculated from TCR repertoire deep sequencing. Representative histograms, graph and dot plot are from 7 donors. (b) Expression of CX₃CR1 on the surface of CD8⁺ T_{Naive}, CD8⁺ T_{EMRA}, Vδ1⁺ CD27^{lo/neg} and Vδ1⁺ CD27^{hi} cells. Within CX₃CR1⁺ or CX₃CR1⁻Vδ1⁺ T cells the expression of granzyme B and IL7Rα. Representative histograms of 5 donors (left), with all 5 donors shown (middle) and 4 of these donors assessed for CX₃CR1/granzyme B/IL7Rα (right). (c) Single cell γδ TCR analysis from 3 donors, single cells were sorted from CX₃CR1⁺ or CX₃CR1⁻Vδ1⁺ T cells and CDR3 sequences analysed against dominant clonotypes identified by deep sequencing. Graphs show the mean ± s.e.m. and data were analysed by two-way ANOVA (a) and one-way ANOVA with Holm-Sidak's post-tests (b), ***P < 0.001 and ****P < 0.0001.

T cells were responsive to IL-7, expressed secondary lymphoid homing receptors, displayed relatively slow proliferation kinetics after TCR stimulation, and largely lacked expression of perforin/granzymes, consistent with a functionally naïve status. Collectively, these findings reveal a fundamentally adaptive biology for Vδ1 T cells, and suggest the γδ TCR has a central role in driving this biology. While they do not formally exclude the possibility that stochastic processes could explain the

expansions we observe, they strongly support a model involving clonal selection of naïve Vδ1 T cells that express functionally useful TCRs enabling responses to microbial/non-microbial stress challenges encountered, accompanied by differentiation to an effector phenotype. They argue against the idea that Vδ1 clonotypic focusing merely represents an immunological imprint of past stress challenges, and instead are more suggestive of long-lived, highly specific, functional γδ T-cell memory that

enables augmented responses to recurrent stress challenges, akin to classical immunological memory, although importantly, not MHC-restricted.

The model outlined above shares several key tenets with classical adaptive immunity, but differs critically in being MHC-unrestricted, and represents an unconventional mode of adaptive immune surveillance. Although one limitation of our study is that it focuses predominantly on V δ 1 T cells, our repertoire data highlight that V δ 3 and V δ 8 populations exhibited a degree of clonotypic focusing and were equivalently private to V δ 1 repertoires, suggesting the biology we observe for V δ 1 T cells could also apply to other human V δ 2^{neg} T cells. However, in several key respects this model does not apply to V γ 9/V δ 2 T cells. In contrast to V δ 1 populations our V γ 9/V δ 2 TCR repertoire data confirm highly restricted CDR3 lengths, including prevalent V γ 9 sequences of limited complexity that were common to multiple individuals. Consistent with these data, Dimova *et al.*⁷ detected prevalent V γ 9 sequences that were present at birth in multiple individuals, irrespective of pathogen exposure. These observations are consistent with a semi-invariant, innate-like biology for the V γ 9/V δ 2 subset that is in keeping with their polyclonal activation by pyrophosphate antigens. In contrast, a confluence of features we observe in V δ 1 T cells, which include profound clonotypic expansions of often highly complex TCRs from an initially completely unfocused, private repertoire, and concomitant phenotypic differentiation involving loss of secondary lymphoid homing markers and upregulation of effector molecules, point to a very different adaptive biology.

This model raises a number of questions, including regarding V δ 1-positive T-cell homing. The majority of naive CD27^{hi} V δ 1 subsets expressed both CCR7 and CD62L, suggesting they may access secondary or alternatively tertiary lymphoid organs, and may become primed there before differentiating to CD27^{lo/neg} effectors, which are CCR7^{neg} CD62L^{lo}, but also display CX3CR1 upregulation, which may affect peripheral or endothelial homing. How this transition occurs is unclear, however conceivably dendritic cells, which prime $\alpha\beta$ T-cell responses, may also prime MHC-independent V δ 1 responses. How our results relate to V δ 2^{neg} development in solid tissues, where they represent the dominant $\gamma\delta$ T-cell subset, is unclear, but could potentially involve central or local priming events. Also, the kinetics of V δ 2^{neg} T-cell responses merit further investigation, but might parallel those of conventional $\alpha\beta$ T-cell adaptive responses.

Although the stress challenges underlying V δ 2^{neg} clonotypic focusing are uncertain, one obvious possibility is infection. Although V δ 2^{neg} T-cell responses have been strongly linked with CMV infection^{11,15} they are not limited to this setting, since we found CMV-seronegative individuals also exhibited extreme clonotypic focusing. Further studies assessing in parallel V δ 2^{neg} TCR repertoire focusing and microbial exposure, including during stress stimuli such as acute CMV infection, will shed light on how V δ 2^{neg} adaptive immune surveillance operates during relevant infectious challenges. Our model would predict a small number of previously low frequency clonotypes may become heavily expanded during/after such challenges. Moreover, dissecting the reasons why some adults retain largely unfocused, naive V δ 1 repertoires is important. Although differential pathogen exposure may be one factor, 'holes' might conceivably exist in the V δ 1 TCR repertoires of certain individuals, resulting in an inability to respond to a specific pathogen. In addition, while we introduced a binary delineation of our cohort into 'focused' and 'diverse' individuals, both CD27^{hi} and CD27^{lo/neg} V δ 1 subpopulations were present in all individuals, highlighting both the universal nature of the adaptive biology we observe and also the fact that in reality there is likely to be a continuous spectrum of diversity. Understanding when clonotypic focusing

occurs in life is clearly important, including in neonates, when conventional adaptive immunity is less potent and $\gamma\delta$ T-cell responses may play an important role^{31,32}. Further studies are required to more comprehensively explore V δ 1 repertoire focusing throughout life, and how this links with pathogen exposure.

How V δ 2^{neg} adaptive immune surveillance relates to $\gamma\delta$ TCR ligand recognition merits consideration. As the focusing we observe is highly CDR3-specific, even within the same chain pairing combination, we hypothesize it results from TCR ligand-dependent selection. The identity of ligands for such specificities is largely unclear (see below), but might include self-encoded and/or foreign proteins^{33,33–37}. Furthermore, although the private TCR repertoires we observe may reflect reactivities restricted to each individual, they do not formally exclude the possibility of degenerate recognition of conserved ligands by diverse TCRs.

Studies on V δ 2^{neg} T cells have highlighted a diverse and somewhat confusing range of TCR ligands. While these ligands highlight the broad recognition capabilities of the V δ 2^{neg} $\gamma\delta$ TCR, their physiological importance is less clear. For future studies, our model strongly suggests that natural *in vivo* expansion and phenotypic differentiation may be important considerations in assessing the biological relevance of proposed $\gamma\delta$ TCR ligands to adaptive immune surveillance by V δ 2^{neg} T cells, and for prioritising clonotypes for ligand identification. From this perspective, while unequivocal binding and/or structural data have been determined for phycoerythrin (PE) - and CD1d-reactive V δ 2^{neg} TCRs^{33,35,37}, both PE and CD1d reagents published to date stain a small percentage (<0.1%) of V δ 1 T cells in peripheral blood in the absence of *in vitro* expansion, and the naive/effector phenotype of such cells is unclear. While such cells clearly do not represent dominantly expanded blood clonotypes, reactive populations could be preferentially localized to solid tissues or be lipid-specific. By analogy, notably CD1d-restricted iNKTs comprise a minor component of $\alpha\beta$ T cells in peripheral blood but are highly prevalent in liver³⁸. Furthermore, conceivably expanded clonotypes could recognize particular CD1d-presented lipids. Further studies are required to resolve these questions.

In this context, $\gamma\delta$ TCR specificities present on V δ 2^{neg} T cells naturally expanded during infection, which include the LES³⁶ and POS4 (ref. 39) TCRs, may be particularly relevant. The LES TCR, which directly binds Endothelial Protein C Receptor³⁶, conceivably represents a molecular exemplar of V δ 2^{neg} adaptive immune surveillance. Naturally expanded during acute CMV infection to ~20% of total T cells, the LES clone was CD28^{neg} CD45RO^{neg}, suggestive of an effector phenotype⁴⁰. Also, the LES TCR utilizes a highly complex TCR δ rearrangement (incorporating 14 N/P additions) and a simpler TCR γ chain, typical of many of the V δ 2^{neg} dominant clonotypes we observed in this study. However LES TCR δ exact sequences were not observed in any individual from our cohort, and at least the CDR3 region of the LES TCR γ chain has been highlighted as important for LES/EPCR ligand binding³⁶. These observations not only indicate the LES TCR was private to the individual in which it originated, but, raise the possibility that reactivity to EPCR might also be private, consistent with failure of previous attempts to identify reactivity to EPCR in other individuals³⁶.

The V γ 8V δ 1 POS4 TCR, also derived from a clonotype expanded in acute foetal CMV infection³⁹, would superficially appear to conflict with this study, as it was observed in multiple individuals. Tellingly, POS4 is exceptional in comprising CDR3 γ and CDR3 δ both resulting from recombination of germline-encoded segments without any N/P nt addition (Supplementary Tables 2 and 3). We suggest this TCR is preferentially generated in gestation before

TdT is expressed at 20 weeks⁴¹, and that its expansion during acute infection may reflect recognition of an important CMV-associated (although not necessarily CMV-encoded) ligand. Therefore, while our data stress the overwhelmingly private nature of the V δ 2^{neg} TCR repertoire, the POS4 TCR clonotype, because of its generation and expansion *in utero*, may be the 'exception that proves the rule', relative to most adult peripheral TCR sequences.

Pre-expanded, semi-invariant T cells such as MAIT, iNKT and some $\gamma\delta$ T-cell subsets, as well as NK cells, may permit rapid responses to stress challenges such as pathogen infection, before conventional adaptive immunity has time to develop²⁸. What advantage would a parallel V δ 2^{neg} adaptive immune surveillance system provide, involving clonal selection of private TCR clonotypes from a diverse repertoire? Possibilities include the potential for amplification of the stress response, and immunological memory to recurrent stress stimuli, both justifying further investigation. Secondly, the system may permit diverse routes to recognition of 'altered self'. One potential paradigm was suggested by LES reactivity to EPCR, which enabled functional reactivity to CMV-infected endothelial cells (a key target for CMV infection *in vivo*) via a TCR-extrinsic, CMV-induced 'multimolecular stress signature'³⁶. However additional paradigms will no doubt emerge from identification of further ligands for clonotypes naturally expanded *in vivo*. Finally, another important consideration is the protection from pathogen immune escape mechanisms provided by V δ 2^{neg} adaptive immune surveillance versus stress sensing by alternative routes such as innate immune subsets, NK cells, and semi-invariant T cells. Generally, these alternative cell types rely on conserved germline-encoded receptors/ligands such as PRRs that sense PAMPs/DAMPs, NKG2D that recognizes MHC-like stress antigens, and MHC-like molecules such as MR1/CD1. Notably, there is strong evidence for pathogen escape from both PRRs⁴² and NKG2D⁴³. Moreover, CD1 molecules recognized by NKT cells, like class I MHC molecules themselves, are targeted by various viral proteins⁴⁴, and MAIT cells are decreased in HIV⁴⁵. In contrast, the evolution of a parallel adaptive immune surveillance system, involving a radically different biology centred on clonal amplification from within a diverse, private V δ 2^{neg} antigen receptor repertoire, and potentially exploiting diverse ligands private to each individual, may provide a much greater challenge for pathogens to evade.

V δ 2^{neg} T cells are strongly implicated in pathogen-specific¹¹ and anti-tumour immunity⁴⁶, and are the subject of increasing immunotherapeutic interest. Three aspects of the adaptive biology we outline here have translational relevance. Firstly, major differences in the ability of specific, private V δ 2^{neg} $\gamma\delta$ TCRs to mediate physiologically relevant antigen recognition events would open the possibility of identifying and exploiting optimal V δ 2^{neg} TCR clonotypes (for example, *via* T-cell engineering), to enhance pathogen/cancer-specific immunity. Secondly, the longevity of dominant clonotypes suggests interaction of vaccination approaches with V δ 2^{neg} immune surveillance merits further investigation, and might be manipulable to enhance vaccine protection. Finally, a greater understanding of the relationship between different V δ 2^{neg} TCR ligands, their mode of recognition, tissue expression and regulation/dysregulation, will undoubtedly provide novel therapeutic avenues and insights.

Note added in proof: Consistent with the suggestion that viral infection may be one stress challenge that drives clonal expansions in the V δ 2-negative compartment, a recent study from Ravens *et al.* and published in Nature Immunology (doi: 10.1038/ni.3686) has highlighted clonotypic $\gamma\delta$ T cell expansions following CMV reactivation after allogeneic stem cell transplantation.

Methods

T cell isolation and culture and activation. Human peripheral blood mononuclear cells (PBMC) were isolated from heparinized venous blood from consenting healthy donors (protocol approved by the NRES Committee West Midlands ethical board; REC reference 14/WM/1254). Briefly, blood was layered over lymphoprep (Stem Cell Technologies) with resulting PBMC used for subsequent experiments. Plasma was also harvested for CMV IgG (ELISA kit) measurement. For repertoire analysis, all T-cell populations were sorted directly into RNeasy (Sigma) or RLT buffer (Qiagen) supplemented with β -mercaptoethanol (Sigma) on a MoFlo Astrios Cell Sorter (Beckman Coulter). For activation and proliferation of T cells, either PBMC or isolated CD3⁺ T cells, obtained by positive magnetic bead isolation (Miltenyi), were labelled or not with 0.3 μ M CFSE (eBioscience) and cultured with cytokines, 25 ng ml⁻¹ IL-7 (Peprotech), 100 IU ml⁻¹ IL-2, 25 ng ml⁻¹ IL-15, 5 ng ml⁻¹ IL-12, 5 ng ml⁻¹ IL-18 (all Miltenyi), and/or antibodies directed against CD3 (OKT3; eBioscience), CD28 (28.2), mlgG1k (MOPC-21), TCR $\gamma\delta$ (B1; all Biologend) or CD3/CD28 T activator beads (Invitrogen), where indicated and for up to 7 days in RPMI-1640 medium (Invitrogen) supplemented with 2 mM L-glutamine, 1% sodium pyruvate, 50 μ g ml⁻¹ penicillin/streptomycin (Invitrogen) and 10% fetal calf serum (Sigma).

Antibodies and flow cytometry. For cell sorting, V δ 1⁺ and V δ 2⁺ populations were labelled with anti-CD3 (UCHT1; 1:100), TCR $\alpha\beta$ (IP26; 1:50), TCR V δ 1 (TS8.2 or REA173; 1:100) or TCR V δ 2 (B6; 1:100) and where indicated CD27 (M-T271; 1:200) and CD45RA (HI100; 1:200). Alternatively, V δ 2^{neg} T cell populations were sorted by labelling with anti-CD3 (UCHT1; 1:100), TCR $\alpha\beta$ (IP26; 1:50), TCR $\gamma\delta$ (IMMU510; 1:200), TCR V δ 2 (B6; 1:100), although this sorting strategy was subject to antibody interference leading to V δ 2⁺ sequences contaminating TCR repertoire analyses. For phenotypic analysis, freshly isolated, frozen PBMC or cultured cells were labelled with Zombie Aqua viability dye (Biolegend), and the cells were then subsequently stained for cell surface antigens with antibodies directed against CD3 (UCHT1 or HIT3a; 1:100), CD8 (SK1; 1:200), CD45RA (HI100; 1:200), CD27 (M-T271; 1:200), CCR7 (G043H7; 1:100), CD62L (DREG-56; 1:100), CD28 (28.2; 1:80), CD161 (HP-3G10; 1:100), CD16 (3G8; 1:100), CD69 (FN50; 1:100), CD25 (2A3; 1:100), CD54 (HA58; 1:100), TCR V δ 2 (B6; 1:100), TCR $\gamma\delta$ (B1; 1:100), TCR $\alpha\beta$ (IP26; 1:50); all Biologend. CD127 (IM1980U; 1:20), TCR $\gamma\delta$ (IMMU510; 1:200) and TCR $\gamma\gamma$ 9 (IMMU360; 1:400); Beckman Coulter. TCR V δ 1 (TS8.2; 1:100); Fisher Scientific. TCR V δ 1 (REA173; 1:100) and TCR V δ 2 (123R3; 1:200); Miltenyi. For intracellular staining, after surface antibody staining cells were fixed in IC Fixation buffer (eBioscience) and finally stained in Permeabilisation Buffer (eBioscience) with antibodies directed against Granzyme A (CBO9; 1:100), Granzyme B (GB11; 1:100) and Perforin (B-D48; 1:80); all Biologend. Cells were acquired on an LSR II (Beckton Dickinson) and data analysed with FlowJo V10.1 (TreeStar).

RNA-based TCR repertoire analysis. RNA was purified from sorted cells (cell numbers detailed in Supplementary Table 1 and FACS sorting strategy identified in Supplementary Fig. 8) using an RNAmicro kit (Qiagen) according to the manufacturer's instructions. For high throughput deep sequencing of TCRs, we used amplicon rescued multiplex (ARM)-PCR and NGS methods⁴⁷ to analyse all sorted $\gamma\delta$ T cell populations. Following initial first-round RT-PCR using high concentrations of gene-specific primers universal primers were used for the exponential phase of amplification⁴⁸ (Patent: WO2009137255A2), allowing deep, quantitative and non-biased amplification of TCR γ and TCR δ sequences. All cDNA synthesis, amplification, NGS library preparation and sequencing were performed by iRepertoire, Inc. (Huntsville, USA). We analysed positively sorted V δ 1⁺ $\gamma\delta$ T cells from CMV-seronegative ($n = 10$), CMV-seropositive individuals ($n = 10$), Umbilical Cord blood ($n = 5$); Anthony Nolan Trust, Nottingham), TCR $\gamma\delta$ ⁺ V δ 2^{neg} T cells ($n = 4$) and V δ 2⁺ T cells ($n = 4$). For low throughput TCR repertoire sequencing, V δ 1⁺ T cells were sorted into RNeasy using an ARIA II (BD) flow sorter. cDNA was synthesized using SMARTer RACE cDNA Amplification Kit (Clontech) and TCR γ or TCR δ sequences were amplified using a template-switch anchored RT-PCR with a 3' C γ or C δ specific primer. Amplicons were cloned into a TOPO-TA vector (Life Technologies), transformed into *Escherichia coli*, and 96 colonies sequenced.

TCR sequence analyses. The CDR3 length was defined as the number of amino acids between the second Cys of the V region and the Phe of the J region, according to IMGT. N and P nucleotides were identified using the IMGT Junction Analysis tool^{49,50}. V γ 9 and V δ 2 sequence logos were generated on the Seq2Logo server⁵¹ in Shannon format without the use of pseudocounts, and give a visual representation of amino acids enriched at different positions in the observed CDR3 sequences. The different amino acids are coloured according to physicochemical properties (acidic (DE), red; basic (RKH), blue; hydrophobic (ACFILMPVW), black; and neutral (NGSGTY), green). For TCR γ sequences from V δ 2⁺ cells, the 20 most prevalent CDR3 γ of 14aa from each of the four adult donors were included (80 sequences in total). For TCR δ sequences, the ten most abundant clonotypes of 13-15 amino acids using V δ 2-J δ 1 from each donor were aligned using Clustal Omega⁵² with default parameters, before logo generation. Narrower bars in the sequence logo correspond to gaps in the sequences.

Single cell PCR analysis of $V\delta 1^+$ T cells. PBMC were labelled as above and $V\delta 1^+$ T cells were single cell sorted directly into individual wells in a 96-well plate containing 2 μ l of Superscript VILO cDNA synthesis kit reaction mix (ThermoFisher) containing 0.1% Triton X-100, and incubated according to manufacturer's instructions. TCR γ and TCR δ cDNAs were amplified by two rounds of nested PCR using GoTaq mastermix (Promega) and following primers: for $V\delta 1$, CAAGCCAGTCATCC (external) and CAACTCCGACGA AAGAGATG (internal); for $C\delta$ GCAGGATCAAACCTCTGTATCTTC (external) and TCCTTCACCAGACAAGCGAC (internal); for $V\gamma 1-8$ ctgtctaccacaggagg ggaagg (external) and TGTGTTGGAATCAGGAVTCAG (internal); for $V\gamma 9$ AGAGAGACCTGGTGAAGTCATACA (external) and GGTGGATAGGATAC CTGAAACG (internal) and for $C\gamma$ CTGACGATACATCTGTGTTCTTTG (external) and AATCGTGTGTCTTCTTTCTT (internal). PCR products were separated on 1.2% agarose gels, and products of successful reactions were incubated with ExoSAP-IT PCR cleanup enzyme (Affymetrix) before sequencing with BigDye Terminator v3.1 (Applied Biosystems) following manufacturer's instructions and cleanup and running on an ABI 3730 capillary sequencer (Functional Genomics Facility, University of Birmingham).

TCR repertoire data analysis. V, D and J gene usage and CDR3 sequences were identified and assigned and tree maps generated using iRweb tools (iRepertoire, Inc, Huntsville, AL, USA)⁵³. Tree maps show each unique CDR3 as a coloured rectangle, the size of each rectangle corresponds to each CDR3s abundance within the repertoire and the positioning is determined by the V region usage. For more detailed analysis and error correction data sets were then processed using the MiXCR software package⁵⁴. Diversity metrics, clonotype overlap and gene usage were plotted in R, by VDJTools⁵⁵. Data are either presented as normalized (each unique CDR3 is assigned a count of one, regardless of frequency), or as non-normalized (which takes into account the frequency of each unique CDR3).

Statistical analysis. Tabulated data were analysed in Graphpad PRISM 7 (Graphpad Software Inc) and sequencing data by VDJTools⁵⁵. Each data set was assessed for normality using Shapiro-Wilko normality tests. Two-tailed Student's *t*-tests were used for normally distributed data and Mann-Whitney for non-parametric data. Differences between groups were analysed using one-way ANOVA with Holm-sidak's post-tests for normally distributed data or with Kruskal-Wallis ANOVA and Dunn's post-tests for non-parametric data; two-way ANOVA was used when comparing groups with independent variables. **P* < 0.05, ***P* < 0.01, ****P* < 0.001 and *****P* < 0.0001. Correlation was assessed for normally distributed data with Pearson's correlation coefficient or Spearman correlation for non-parametric data.

Data availability. The sequence data that support the findings of this study have been deposited in the NIH NCBI sequence read archive (SRA) database with the primary accession code SRP096009.

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Author contributions

M.S.D. and C.R.W. designed and performed molecular and cellular experiments, analysed data and wrote the manuscript. S.P.J. prepared samples and analysed data. K.L., J.E.M. and D.A.P., performed RACE-PCR TCR sequencing, analysed data and provided advice. S.A.K. and D.M.C. designed and performed bioinformatics analysis of the TCR repertoire data. F.M. wrote the manuscript. S.H. carried out cell sorting and data analysis. M.S. carried out single cell PCR development. B.E.W. supervised the study, designed experiments and wrote the manuscript.

Additional information

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