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Shared and distinct transcriptional programs underlie the hybrid nature of α NKT cells

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Abstract

Invariant natural killer T (α NKT) cells are innate-like T lymphocytes that act as critical regulators of the immune response. To better characterize this population, we profiled α NKT cell gene expression during ontogeny and in peripheral subsets as part of the Immunological Genome Project (ImmGen). High-resolution comparative transcriptional analyses defined developmental and subset-specific α NKT cell gene expression programs. In addition, α NKT cells were found to share an extensive transcriptional program with natural killer (NK) cells, similar in magnitude to that shared with major histocompatibility complex (MHC)-restricted T cells. Strikingly, the NK- α NKT program also operated constitutively in $\gamma\delta$ T cells and in adaptive T cells following activation. Together, our findings highlight a core effector program regulated distinctly in innate and adaptive lymphocytes.

Introduction

The Immunological Genome Project (ImmGen) is a consortium of immunologists and computational biologists who aim, using rigorously standardized experimental and analysis pipelines, to generate a high-resolution, comprehensive definition of gene expression and regulatory networks in the mouse immune system¹. In this context, we determined global gene expression profiles for thymic and peripheral invariant natural killer T (α NKT) cell subsets to gain insight into the α NKT cell transcriptional landscape, its unique features, and the relationships of α NKT cells to other innate and adaptive cell lineages.

α NKT cells are a subset of $\alpha\beta$ T cells with an semi-invariant T cell antigen receptor (TCR) recognizing lipid antigens presented by CD1d². By rapidly producing cytokines, these cells modulate both the innate and adaptive arms of the immune system, critically affecting biological processes in anti-microbial immunity, tumor rejection, and inflammation³. Like MHC-restricted T cells, α NKT cells undergo thymic differentiation with somatic

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recombination⁴, recognize self and foreign antigens^{2,3}, secrete T_H1, T_H 2, and T_H17 cytokines⁵, and provide help to B cells⁶.

The term “NK T” was coined to reflect the expression of the natural killer (NK) cell marker NK1.1⁷. While a number of other NK receptors (NKR) can also be expressed by λ NKT cells⁸, the validity of the term “NKT” has been called into question⁹ because λ NKT cells are developmentally more closely related to the T than the NK cell lineage, and because NKRs are neither specific to λ NKT cells nor expressed on all λ NKT cells.

While a central role for TCR-mediated activation in λ NKT cell biology is clear, striking parallels in the behavior of both NK and λ NKT cells have nevertheless emerged. The homeostatic distribution and survival requirements of λ NKT cells are similar to those of NK cells^{10,11,12,13}. Also comparable are their trafficking and activation kinetics. Both cell types constitutively express inflammatory chemokine receptors, accumulate at sites of infection within 24–72 h, and exert their effector functions without a priming requirement^{14,15}. In addition, evidence suggests that λ NKT cells, like NK cells, can use activating NKRs to sense stress-induced ligands^{15–19}. λ NKT cells also detect cellular stress via their TCRs, which are reactive to inflammation-induced alterations in CD1d-presented self-lipid antigens^{20–22}. Finally, NK and λ NKT cells engage in comparable bidirectional interactions with antigen presenting cells (APCs) during which APC-derived inflammatory cytokines potentiate NK and λ NKT responses to surface ligands, and NK or λ NKT cells, in return, promote APC maturation^{23–28}.

In this report, we shed light on the transcriptional programs operating over the course of λ NKT cell development and in peripheral CD4⁺ and CD4⁻ λ NKT cell subsets. Utilizing the ImmGen compendium, which allows direct comparison of gene expression in developing and mature λ NKT, NK, and T cell subsets, we assess the transcriptional basis for NK- λ NKT similarities. Our data demonstrate that shared NK- λ NKT transcriptional programs are more extensive than currently appreciated and comparable in breadth to those shared by λ NKT and MHC-restricted T cells. Finally, we show that the transcriptional patterns expressed constitutively by both NK and λ NKT cells represent a core effector program also operational in other innate lymphocytes and induced in adaptive lymphocyte populations following activation.

Results

λ NKT cell-specific developmental programs

λ NKT cells, like other T lymphocytes, mature in the thymus, where they diverge from MHC-restricted $\alpha\beta$ T cells at the CD4⁺ CD8⁺ double-positive (DP) stage. λ NKT cells subsequently undergo sequential stages of differentiation characterized by differential expression of CD44 and NK1.1⁴ (Supplementary Fig. 1). To characterize the developmental transcriptional programs in λ NKT cells in relation to those operating in maturing adaptive $\alpha\beta$ T cells, we profiled CD44⁻ NK1.1⁻ (stage 1), CD44⁺ NK1.1⁻ (stage 2) and CD44⁺ NK1.1⁺ (stage 3) thymic λ NKT cells in the context of the ImmGen Project (Fig. 1a). 1850, 155 and 697 genes were differentially expressed from DP to stage 1, stage 1 to stage 2, and stage 2 to stage 3, respectively, using an arbitrary fold change (FC) threshold of FC > 2 (Fig. 1b, c). Transcripts modulated between thymic λ NKT cell populations included a number of genes involved in λ NKT cell maturation⁴ as well as several genes of unknown function (Supplementary Tables 1–6). At the DP branch point, we identified a subset of genes modulated selectively by stage 1 λ NKT cells but not by early stage CD4⁺ adaptive T cells (CD4⁺8^{int}) (Fig. 1d). Although some of these genes such as *Zbtb16* (PLZF) and *Vdr* (vitamin D receptor) are known to play important functions in λ NKT cell lineage specification^{29–31}, many have not yet been linked to λ NKT cell development

(Supplementary Tables 7, 8). At the last λ NKT cell maturation stage, many of the most strongly upregulated genes belonged to the killer lectin receptor family, which encodes activating and inhibitory NK receptors (NKR) (Fig. 1c, bottom panel). By the final stage of ontogeny, λ NKT cells expressed several NKR mRNAs at levels comparable to those of splenic NK cells (Supplementary Fig. 2a). In addition, NKR upregulation occurs selectively in developing λ NKT cells but not in maturing MHC-restricted T cells or at any stage in early T cell development, with a few exceptions (Fig. 1e). Flow cytometric analysis of thymic λ NKT cells confirmed the acquisition of surface NKRs over the course of maturation (Fig. 1f and Supplementary Fig. 2b). K-means clustering analysis determined that a large number of genes follow the same expression kinetics as NKRs over the course of the DP to stage 3 transition (Fig. 1g) suggesting that the progressive upregulation of NKRs may be part of a broader gene program. Together, these data comprehensively characterize shared and distinct gene expression changes occurring in maturing λ NKT cells in the broader context of $\alpha\beta$ T cell development.

Peripheral λ NKT cell transcriptional signatures

In both mouse and human, differential cytokine production has been reported between $CD4^+$ and $CD4^-$ λ NKT cells^{5,32,33}. In addition, λ NKT cell subsets from the liver have also been suggested to be functionally distinct³⁴. To characterize the transcriptional basis that may underlie subset-specific functional differences, we assessed the gene expression profiles of $CD4^+$ and $CD4^-$ λ NKT cells sorted from the spleen, liver and lungs of mice. 159 and 261 genes were differentially expressed between $CD4^+$ and $CD4^-$ λ NKT cells from the spleen or lung, respectively, while only 17 transcripts were differentially expressed between the liver subsets (Fig. 2a, Supplementary Fig. 3 and Supplementary Tables 9–14), suggesting that splenic and pulmonary λ NKT cell subsets may be more functionally distinct from each other than are liver λ NKT cell subsets. In all three tissues, we found that a number of NKRs were among the most differentially expressed genes, with elevated levels in $CD4^-$ compared to $CD4^+$ subsets (Fig. 2a and Supplementary Fig. 3). In liver and spleen, this reflected a larger percentage of NKR-positive cells in $CD4^-$ compared to $CD4^+$ λ NKT cells, as determined by flow cytometry (Fig. 2b). NKR mRNA expression in peripheral λ NKT cells, although reduced compared to stage 3 thymic λ NKT cells, was maintained at higher levels than most MHC-restricted $\alpha\beta$ T cell subsets (Fig. 2c and data not shown). In addition, comparison of liver λ NKT cell subsets to their splenic counterparts revealed that $CD4^-$ populations are more transcriptionally similar to one another than are $CD4^+$ λ NKT cells across tissues. A small number of genes were expressed differentially between tissues regardless of $CD4$ expression (Supplementary Fig. 4), supporting the idea that λ NKT cells subsets may perform organ-specific functions.

An extensive NK- λ NKT shared transcriptional program

Because λ NKT cells share broad functional features with NK cells, we hypothesized that NKR expression by λ NKT cells might reflect a much larger NK-NKT shared transcriptional program than currently appreciated. To assess the extent of transcriptional relatedness between λ NKT cells and NK cells at a global level, and to compare the NK- λ NKT relationship and with that of λ NKT to T cells, we calculated Euclidian distances between subsets of steady-state NK, T and λ NKT cells. Euclidian distance, a measure of the similarity between the gene expression patterns of pairwise compared subsets, was determined using the 15% of gene probes with the highest variability among the subsets analyzed, and is displayed as a matrix (Fig. 3). This revealed a strong degree of similarity between mature λ NKT and NK cell gene expression (Fig. 3, top panel, area i), contrasting greater distances observed between all MHC-restricted T cells and NK cells (Fig. 3, top panel, area ii). Compared to the λ NKT-NK cell distance, λ NKT cells exhibited a somewhat closer relationship to memory $CD8^+$ T cells and certain memory $CD4^+$ T cell, however, the latter

were sorted using markers expressed at similar levels by iNKT cells (CD44^+ and $\text{CD62L}^{\text{low}}$) and likely thus themselves contain a significant percentage of iNKT cells. The average Euclidian distance between iNKT and NK cells was only slightly larger than that separating iNKT cells from naive CD4^+ and CD8^+ T cells (Fig. 3, top panel, area iii). These relative relationships were maintained when the analysis was performed using all genes and not just the 15% most variable (data not shown). To determine whether the NK- iNKT relationship is dependent on the shared expression of NKR, we recalculated the distance matrix after removing NKR and related molecules from the data (see on-line methods). The outcome of the analysis remained essentially unchanged (Supplementary Fig. 5). Thus, the transcriptional relationship between NK and iNKT cells is not limited to the shared expression of NKR. Together, these data support an unexpectedly substantial transcriptional relationship between iNKT and NK cells that is close in magnitude to that occurring between iNKT and naive T cells.

Shared and distinct iNKT cells programs

We next sought to identify the specific concordantly-regulated genes among iNKT , NK and T cells. For this purpose, we performed one-way analysis of variance (ANOVA) comparing the transcriptomes of peripheral steady-state iNKT cells, NK cells and naive and memory CD4^+ and CD8^+ T cells. Genes with low variability over the entire ImmGen dataset were excluded from the analysis. 20.2% (1192 genes) of the remaining genes were differentially expressed (Bonferroni corrected P value < 0.05) between the three groups. The modulated genes were further classified into 6 categories (see on-line methods): genes expressed similarly in NK and iNKT cells compared to T cells (A_1 or A_2 , higher or lower than in T cells, respectively), genes expressed similarly in iNKT and T cells compared to NK cells (B_1 or B_2 , higher or lower than in NK cells, respectively), and genes expressed differentially in iNKT cells (C_1 or C_2 , higher or lower than T and NK cells, respectively) (Fig. 4a). A number of transcription factors, TCR signaling components, and cytokine or chemokine-related molecules that are known to be expressed differentially by NK, iNKT , and T cells partitioned as expected in the ANOVA categories (Fig. 4b–d). For example, the transcription factor *PLZF* (*Zbtb16*, Fig. 4b), the chemokine receptor *Cxcr6* (Fig. 4c), and a component of the high-affinity IL-12 receptor (*Il12rb1*) (Fig. 4d), all known to be expressed at higher levels in iNKT cells than in resting T or NK cells^{29,30,35,36}, partitioned to category C_1 (higher in iNKT cells relative to NK and T cells). The transcription factor T-bet (*Tbx21*, Fig. 4b) as well as *Il12rb2* (Fig. 4d), known to be upregulated in NK and iNKT cells³⁷, partitioned to category A_1 (higher in iNKT and NK cells relative to T cells). TCR signaling components such as *Cd3e*, *Itk*, *Plcg1*, and *Zap70* (Fig. 4c) segregated as anticipated to category B_1 (higher in iNKT and T compared to NK, Fig. 4c, d). Functional biological process enrichment analysis using DAVID software³⁸ of category A_1 genes showed a statistically significant enrichment for effector functions including NK cell-mediated immunity, chemokine or cytokine responses, signal transduction, and cell motility (Table 1). Distinct biological processes were also enriched in the group of genes upregulated in iNKT cells as compared to NK and MHC-restricted T cells (category C_1), and indicated a role for these genes in proliferation and survival, likely reflecting the uniquely activated phenotype of steady state iNKT cells (Table 2).

We found that a comparable number of genes were expressed similarly in iNKT and NK lineages (36.91%, 440 genes, categories A_1 and A_2) as in iNKT and T cells (43.88%, 523 genes, categories A_2 and B_2). In addition, about one-fifth of the differentially expressed genes were regulated uniquely in iNKT cells (19.21%, 229 genes, categories C_1 and C_2) (Fig. 4a, Supplementary Table 15). Thus, in addition to expressing a distinctive genetic program, iNKT cells share a transcriptional program transcriptional with steady-state NK

cells that is extensive and similar in magnitude to that shared between $\alpha\beta$ T cells and other $\alpha\beta$ T cells, consistent with the Euclidian distance analysis.

Thymic induction of NK- $\alpha\beta$ T shared programs

To determine at what point during thymic development the transcriptional program shared by mature $\alpha\beta$ T and NK cells is induced, we analyzed the expression patterns of ANOVA category A₁ genes over the course of MHC-restricted T and $\alpha\beta$ T cell differentiation by hierarchical clustering. Although approximately 75% of the shared, upregulated NK- $\alpha\beta$ T gene program is expressed in early thymic precursors (ETP), these genes are then largely shut-down or downregulated by the DP thymocyte stage, and are not reactivated in differentiating CD4⁺ or CD8⁺ T cells. In contrast, differentiating $\alpha\beta$ T cells upregulated these same genes, such that stage 3 thymic $\alpha\beta$ T cells expressed more than 90% of the program (Fig. 5a). Consistent with this observation, the FC distribution of category A₁ genes calculated by comparing the expression of each gene in developing $\alpha\beta$ T cells and their DP progenitor showed an increasing shift towards higher FC values with $\alpha\beta$ T maturation. All three distributions were significantly different from the baseline FC distribution for all expressed genes as determined by a Kolmogorov-Smirnov (K-S) test, with *P* values for enrichment of 3.97×10^{-15} , 1.28×10^{-19} and 9.14×10^{-48} for stage 1, 2 and 3 $\alpha\beta$ T cells respectively (Fig. 5b). In contrast, the FC distribution calculated by comparing naïve splenic CD4⁺ or CD8⁺ T cells to DP was not significantly different between the category A₁ geneset and all expressed genes (*P* = 0.79 and *P* = 0.65, respectively). Conversely to category A₁ genes, the genes that were significantly downregulated in mature NK and $\alpha\beta$ T cells compared to T cells (ANOVA category A₂) were not as strongly elicited in differentiating thymic $\alpha\beta$ T cells as in CD4⁺ and CD8⁺ T cells (Supplementary Fig. 6). These data extend our earlier observation that $\alpha\beta$ T cells acquire NKR expression at the end of development, and indicate that a large part of the transcriptional program $\alpha\beta$ T cells share with NK cells is acquired late in thymic maturation.

$\alpha\beta$ T cell programs expressed in $\gamma\delta$ T cells

We next asked if other lymphocytes with innate features might also express this transcriptional program. $\gamma\delta$ T cells can be categorized on the basis of their TCR V γ and V δ chain usage. The subset bearing the V γ 2 chain tends to be IL-17 polarized, whereas the V γ 2⁻ subsets (including V γ 1.1⁺V δ 6.3⁺ and V γ 1.1⁺V δ 6.3⁻ subsets) predominantly secrete T_H1 or T_H2 cytokines³⁹. Distinct intraepithelial lymphocyte (IEL) CD8 $\alpha\alpha$ ⁺ $\gamma\delta$ T cell populations possess an effector phenotype similar to that of $\alpha\beta$ T cells^{40,41}.

In splenic $\gamma\delta$ T cells negative for the activation marker CD44, NK- $\alpha\beta$ T shared genes (ANOVA category A₁) were expressed at relatively low levels, similar to those observed in resting T cells. A subset of these genes was upregulated in splenic CD44⁺ V γ 2⁺ and V γ 2⁻ cells. Strikingly, we found that all tissue-resident IEL $\gamma\delta$ T cells expressed a large cluster of category A₁ genes at levels surpassing those of the reference NK and $\alpha\beta$ T populations (Fig. 6a). FC distributions comparing the expression of category A₁ genes in splenic or IEL $\gamma\delta$ T cells and T cells revealed an enrichment of over-expressed genes (*P* value 4.67×10^{-41} and 3.90×10^{-34} , respectively) (Fig. 6b). IEL $\gamma\delta$ T cells expressed an even smaller proportion of ANOVA category A₂ genes (downregulated in NK and $\alpha\beta$ T compared to T) than did $\alpha\beta$ T cells, although most of these genes were expressed in splenic $\gamma\delta$ T cells (data not shown). Although less prominently than for the shared NK- $\alpha\beta$ T cell program (category A₁) a portion of the genes upregulated in $\alpha\beta$ T cells but not T or NK subsets (category C₁) were also relatively highly expressed in $\gamma\delta$ T cell subsets (Supplementary Fig. 7a). Together, these data suggest that most of the gene program shared by NK and $\alpha\beta$ T cells, as well as part of the program differentially upregulated in $\alpha\beta$ T cells, is also utilized by populations of $\gamma\delta$ T cells at steady state.

NK- iNKT shared program induction in CD8⁺ T cells

We next investigated the expression of the shared NK- iNKT transcriptional program in CD8⁺ effector T cells, a cell population that shares functional characteristics with NK and iNKT cells, including the expression of certain NKRs⁴². We examined the expression of ANOVA categories A₁ and A₂ in CD8⁺ T cells from the spleen of ovalbumin (OVA)-reactive $\alpha\beta$ TCR transgenic (OT-I) mice following infection with *Listeria monocytogenes* expressing OVA. Only a small fraction of ANOVA category A₁ genes became upregulated in effector CD8⁺ T cells at 12, 24, and 48 h following *Listeria* infection. By day 6, however, the NK- iNKT shared program was dramatically upregulated, with a FC distribution significantly enriched for higher expression, and this genetic program was maintained in CD8⁺ memory T cells as late as day 100 following infection (Fig. 7a, b). In contrast, only a limited portion of category C₁ genes (differentially expressed by iNKT cells) followed a similar pattern in effector CD8⁺ T cell populations (Supplementary Fig. 7b). The genes downregulated in NK and iNKT cells compared to T cells (ANOVA category A₂, which by definition are widely expressed in naive OT-I transgenic CD8⁺ T cells), were partially repressed following infection (Supplementary Fig. 8). Similar results were obtained when the expression of the NK- iNKT shared transcriptional programs were examined in CD8⁺ T cells from OT-I transgenic mice infected with OVA-expressing vesicular stomatitis virus (VSV) (Supplementary Fig. 9). We found that the homologous human genes comprising the NK- iNKT shared program (ANOVA category A₁) were also expressed at significantly higher levels in human peripheral blood effector memory CD8⁺ T cell populations as compared to naive CD8⁺ T cells⁴³ (Fig. 7c, d). Thus, a large proportion of the genetic program shared by NK and iNKT cells is elicited in effector $\alpha\beta$ T cells, but only several days following their activation.

Discussion

iNKT cells do not fit the classical paradigm of adaptive T cell immunity. Indeed, innate features are at the core their physiological functions^{3,14}. The transcriptional basis for these features, however, remains incompletely defined.

The transcriptional programs and regulatory factors we found to be operating during iNKT cell maturation were consistent with previous reports, and included *Zbtb16* (PLZF), *Vdr*, *Tbx21* (Tbet), components of the NF- κ B and Ras-MapK pathways, and NKRs^{4,37,44,45}. By comparing developing iNKT cells to differentiating MHC-restricted T cells, we define transcriptional programs expressed specifically by stage 1 iNKT cells shortly after the DP branch point. We thus highlight a large number genes not previously known to affect iNKT cell biology but likely modulating iNKT cell thymic maturation specifically.

A number of genes reported to be involved in iNKT cell development were not expressed in an iNKT cell specific-manner. For instance, NF- κ B and Ras/MapK pathway members such as *NFkb1*, *RelB*, Ras/MapK and *Egr2* were upregulated in both iNKT and non- iNKT thymocyte populations⁴ (data not shown). Other genes known to affect iNKT cells ontogeny, *Bcl11b*⁴⁶ and the chromatin modifier *Med1*⁴⁷ for example, exhibited little or no transcriptional variation over the course of iNKT cell differentiation. The functional regulation of these and other genes not detected in our analyses may thus be controlled at post-transcriptional levels.

Mature iNKT cells share several innate functional features with NK cells, developmentally distant relatives. We hypothesized that NK and iNKT cells shared a broader transcriptional program than is currently appreciated. Our analyses revealed that the transcriptional patterns iNKT cells share with NK cells make up nearly as large a part of the iNKT transcriptome as those shared with MHC-restricted T cells. Further, we found that the NK- iNKT cell shared

program was also active in steady-state $\gamma\delta$ T cells subsets similarly poised for rapid, innate-like responsiveness. The NK- \mathcal{N} KT program can in addition be induced in adaptive $\alpha\beta$ T cells, but only days following antigen-specific stimulation. These data suggest that the NK- \mathcal{N} KT shared program represents a core effector program operational in lymphocytes of distinct lineages, consistent with the many functional capabilities \mathcal{N} KT, NK and activated MHC-restricted T cells have in common.

The factors that regulate expression of this shared effector program remain to be fully defined. Nevertheless, our data provides several leads. Acquired largely at the end of thymic \mathcal{N} KT cell maturation, the shared program mirrors the cells' acquisition of NKR. NKR expression is driven by the transcription factor T-bet both in NK and \mathcal{N} KT cells³⁷. Thus, it is likely that T-bet, which we found to be among the genes significantly upregulated in both NK and \mathcal{N} KT compared to resting T cells, plays an important role in eliciting and maintaining at least part of the shared effector lymphocyte program. T-bet-deficient \mathcal{N} KT cells express reduced mRNA and protein levels of IFN- γ , granzyme B, Fas ligand, CCR5, and CD38, all molecules that are part of the shared program⁴⁴. IL-15, recently reported to act upstream of T-bet in maturing \mathcal{N} KT cells⁴⁵, is also likely to be involved in \mathcal{N} KT cell acquisition of this program. Furthermore, IL-15 and T-bet are important for regulating CD8⁺ effector T cell responses⁴⁸ as well as for the homeostasis of IEL $\gamma\delta$ T cells⁴⁹. Thus, IL-15 and T-bet may play an important role in inducing the expression of the shared effector program in several cell types.

We also highlight a number of previously unappreciated transcriptional regulators exhibiting similar expression patterns in NK and \mathcal{N} KT cells, and that may help regulate the core effector program in innate lymphocytes. For example, the transcription factor Bhlhe40, a circadian rhythm regulator⁵⁰ possessing immune-modulatory functions in CD4⁺ T cells^{51,52}, as well as Smad3, a transcription factor important for tuning TGF- β -mediated lymphocyte activation, were upregulated in both NK and \mathcal{N} KT cells compared to resting T cells. Also, a number of factors were downregulated in NK and \mathcal{N} KT cells. Among these genes were *Lef1* and *Tcf7*, transcription factors downstream of the Wnt signaling pathway that are important for the establishment and maintenance of T cell identity⁵³. Wnt signaling, which is typically repressed upon T cell activation^{54,55}. The relatively low expression of *Tcf7* and *Lef1* in NK and \mathcal{N} KT cells during development is consistent with the acquisition their terminally differentiated effector phenotype at steady state.

Approximately 20% of the significantly differentially expressed genes between NK, \mathcal{N} KT, and T cells exhibited transcriptional patterns specific to \mathcal{N} KT cells. As expected, PLZF (*Zbtb16*) and Gata-3 were among these factors. The genes preferentially upregulated in \mathcal{N} KT cells (category C₁ genes) were enriched for cellular activation and survival programs. For instance, several AP-1 family members (*Jun*, *Junb*, *Jund*, *Fos*, *Fosb* and *Cebpb*) normally induced in cells only after activation, were expressed relatively highly in \mathcal{N} KT cells. Constitutive expression of AP-1 transcription factors by \mathcal{N} KT cells is consistent with their poised effector phenotype.

Together, these data offer a new view of \mathcal{N} KT cells and their relationships to other lymphocyte lineages. Using the Immunological Genome consortium database, we have uncovered gene expression programs that both link to and differentiate \mathcal{N} KT cells from other innate and adaptive lymphocytes. Our data highlight extensive genetic modules that are shared with NK cells and other innate-like T cells, and that are also elicited several days following activation in adaptive T cells. By defining both distinct and shared transcriptional programs in \mathcal{N} KT cells, our data opens avenues for future research and brings into clearer focus how lymphocyte populations that differ markedly in their ontogeny can ultimately

carry out similar effector functions through modular expression of similar transcriptional programs.

Online Methods

Mice

6 week old C57BL/6 male mice shipped from Jackson Laboratories one week prior to organ harvest were used. Mice were maintained under specific pathogen free conditions. All studies were approved by the Animal Care and Use Committee of the Dana-Farber Cancer Institute.

Antibodies

Anti-CD19 (MB19-1), anti-B220 (RA3-6B2), anti-Ter119 (TER119), anti-CD11b (M1/70), anti-CD11c (N418), anti-Ly6G/Gr1 (A18), anti-CD8 α (53/6.7), anti-TCR β (H58-597), anti-NK1.1 (PK136), anti-CD44 (IM7), anti-CD4 (GK1.5), anti-CD45 (102), anti-CD3e (145-2C11), anti-Ly49e,f (CM4), anti-NKG2D (CX5), anti-NKG2A (16a11), anti-2B4 (ebio244F4), and anti-CD16,32 (2.4G2) were from eBioscience. Anti-Ly49a (A1) and anti-Ly49c,1 (5F6) were from BD biosciences. CD1d-tetramers loaded with PBS-57 (an α -galactosylceramide analog) were provided by the NIH tetramer facility.

Cell isolation, microarray analysis and subset nomenclature

All immune cells purification were performed in strict adherence to the ImmGen standard Operating Procedure guidelines (available at www.immgen.org). Further details on thymic, NK cell, $\gamma\delta$ T cell, and CD8 $^+$ T cell populations used for comparison to λ NKT cells can be found at the ImmGen website. For λ NKT cells, thymocytes, splenocytes, liver and lung mononuclear cells were isolated from 5–10 mice per sample. Thymocytes were disaggregated, blocked with anti-CD16 and CD32 (clone 2.4G2), then stained with fluorophore-labeled antibodies for depletion of non- λ NKT cell populations, and separated with anti-fluorophore magnetic beads (Miltenyi). Spleens were disaggregated, treated with ACK lysis buffer (Lonza) to remove red blood cells, and then depleted of non- λ NKT cells as above. Lungs and livers were harvested after perfusion with cold PBS and mechanically homogenized. Lungs were digested for 15 minutes at 37 $^{\circ}$ C in 7 U/ml of Liberase III enzyme (Roche) in DMEM, then filtered and washed. Livers were homogenized and liver mononuclear cells (LMNC) were isolated by Ficoll density gradient centrifugation. λ NKT cell-enriched thymocytes, splenocytes, LMNCs and lung cells were stained for cell surface markers (see www.immgen.org for complete staining procedure including gating strategy) and double sorted directly into Trizol (Invitrogen) at a purity of >99%. By staining thymocytes from CD1d-deficient mice that lack λ NKT cells, a false positive rate of $2.7 \pm 0.9\%$ was estimated in the case of CD44 $^-$ NK1.1 $^-$ (Stage 1) λ NKT cells, the rarest thymic subset. Contamination was negligible for other λ NKT cell populations. Two to four replicates were obtained for each sample using a FACSAria, with the exception of the CD4 $^-$ λ NKT subset from the lung, for which only a single replicate passed quality control (see below). RNA extraction, microarray hybridization (Affymetrix MoGene 1.0 ST array) and data processing were performed at the ImmGen processing center. For further details, please see Supplementary Table 16 (subset nomenclature key), the Data Generation and Quality Control pipeline documentation, the ImmGen Quality Control Statistics or the ImmGen website (www.immgen.org). Non-ImmGen human and mouse datasets were downloaded from NCBI Geo datasets^{43,56}. Human homologs of mouse genes were determined using NCBI HomoloGene.

Data analysis and visualization

Data from the March 2011 ImmGen release (802 arrays with 22,268 probesets) were used. Probesets associated with the same gene symbol were consolidated by selecting the probeset with the highest mean expression overall. For heatmaps, data were log₂-transformed and a relative color scale with row centering (subtraction of the mean) and normalization was used. Heatmaps were produced by using the HeatmapViewer module of GenePattern (www.broadinstitute.org/cancer/software/genepattern/). When indicated, Pearson correlation with pair-wise complete linkage was applied to rows for clustering analysis. Volcano plots were produced by using the Multiplot module of GenePattern.

For K-means clustering analysis, genes were pre-filtered for mean expression value ≥ 120 (cut-off above which genes have a 95% chance of expression) and for FC > 2 between any two subsets analyzed. Clustering was performed using the ExpressCluster application (Scott Davis, Harvard Medical School, Boston MA – application and documentation available at <http://cbdm.hms.harvard.edu>) with K=10.

For Euclidian distance matrices, the 15% most variable genes were identified using the PopulationDistances PCA application (Scott Davis), which filters probes based on a variation of ANOVA analysis using the geometric standard deviation of populations to weight genes that vary in multiple populations. The selected genes were log₂-transformed, filtered for probes with a mean expression value ≥ 120 , and mean centered prior to visualization. Activating and inhibitory NKR, adaptors and signaling partners (*Klra1*, *Klra2*, *Klra3*, *Klra5*, *Klra6*, *Klra8*, *Klra9*, *Klra10*, *Klra17*, *Klr1a*, *Klr1b*, *Klr1c*, *Klr1f*, *Klrc1*, *Klrc2*, *Klrc3*, *Klrd1*, *Klre1*, *Klri1*, *Klri2*, *Klrk1*, *Klrg2*, *Ncr1*, *Cd244*, *Fcer1g*, *Tyrbp* and *Hcst*) were present in the initial gene list used in the first analysis (Fig. 3, top panel) and were manually removed as indicated for the second analysis (Fig. 3, bottom panel). *Klra1*, *Klra3*, *Klra5*, *Klra6*, *Klra8*, *Klra9*, *Klra10*, *Klr1a*, *Klr1b*, *Klr1c*, *Klr1f*, *Klrc1*, *Klrc2*, *Klrc3*, *Klrd1*, *Klre1*, *Klri1*, *Klri2*, *Klrk1*, *Ncr1*, *Cd244*, *Fcer1g*, *Tyrbp* (but not *Klra2*, *Klra17*, *Klrg2* or *Hcst*) were present after filtering for 15% most variable gene list and were contributed to the first, but not the second Euclidian distance analysis.

For ANOVA, data were log₂-transformed, low-variability genes with a standard deviation of ≤ 0.5 across all ImmGen samples were removed and only genes with expression values ≥ 120 in 2 or more arrays were considered, leaving 5,900 genes. The ANOVA was performed using the Matlab (MathWorks) function “anova1” to compare *n*NKT, NK and T cell populations. Bonferroni correction was applied to the resulting list of *P* values, and 1192 genes passed the ANOVA ($p < 0.05$ out of 5,900). A secondary test was used to determine which of the three populations significantly differed from the other two, as indicated by the “multcompare” function of Matlab. Based on the results of this analysis, the 1,192 genes were then separated into 14 gene categories. By comparing the average expression levels in NK, *n*NKT, and T cells for each gene, these categories were then sorted into 6 groups of genes: genes expressed most similarly by NK and *n*NKT cells (either A₁, up- or A₂, downregulated compared to T), genes expressed most similarly in T and *n*NKT (either B₁, up- or B₂, downregulated compared to NK) and genes expressed uniquely in *n*NKT (either C₁, up- or C₂, downregulated compared to NK and T). Functional geneset enrichment analysis was performed using DAVID software (Version 6.7, National Institutes of Health, National Institute for Allergy and Infectious Diseases)⁵⁷. Panther biological processes³⁸ are shown in Tables 1 and 2. *P* values calculated by DAVID represent a modified Fisher Exact test. Biological processes with *P* values less than 0.01 are shown.

For estimation of the significance of enrichment for the FC distributions associated with the heatmaps in Figs. 5–7, Kolmogorov-Smirnov *P* values were calculated with JMP (SAS

Institute) comparing the selected geneset to all genes meeting the criteria for expression (>120) in the samples tested.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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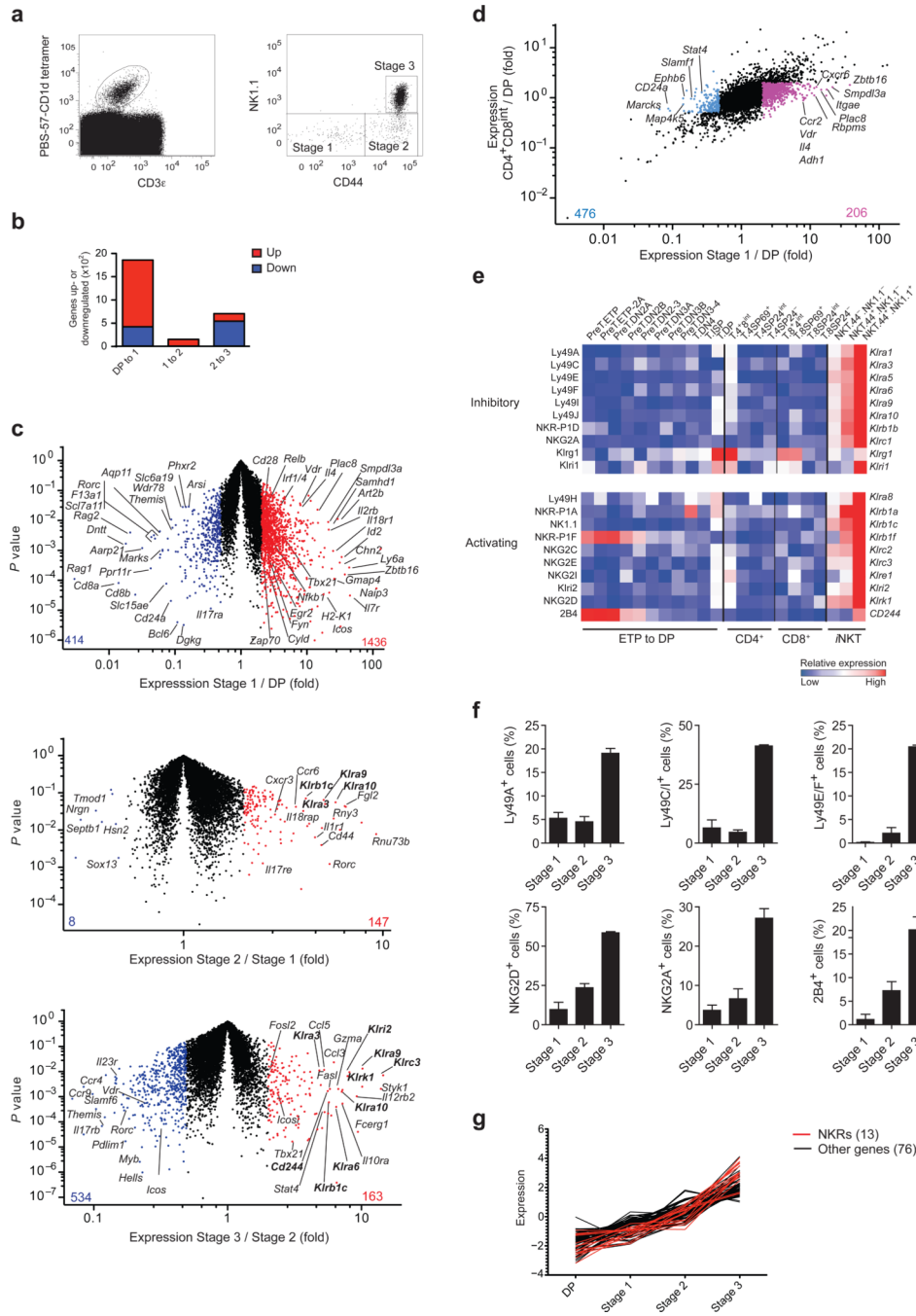
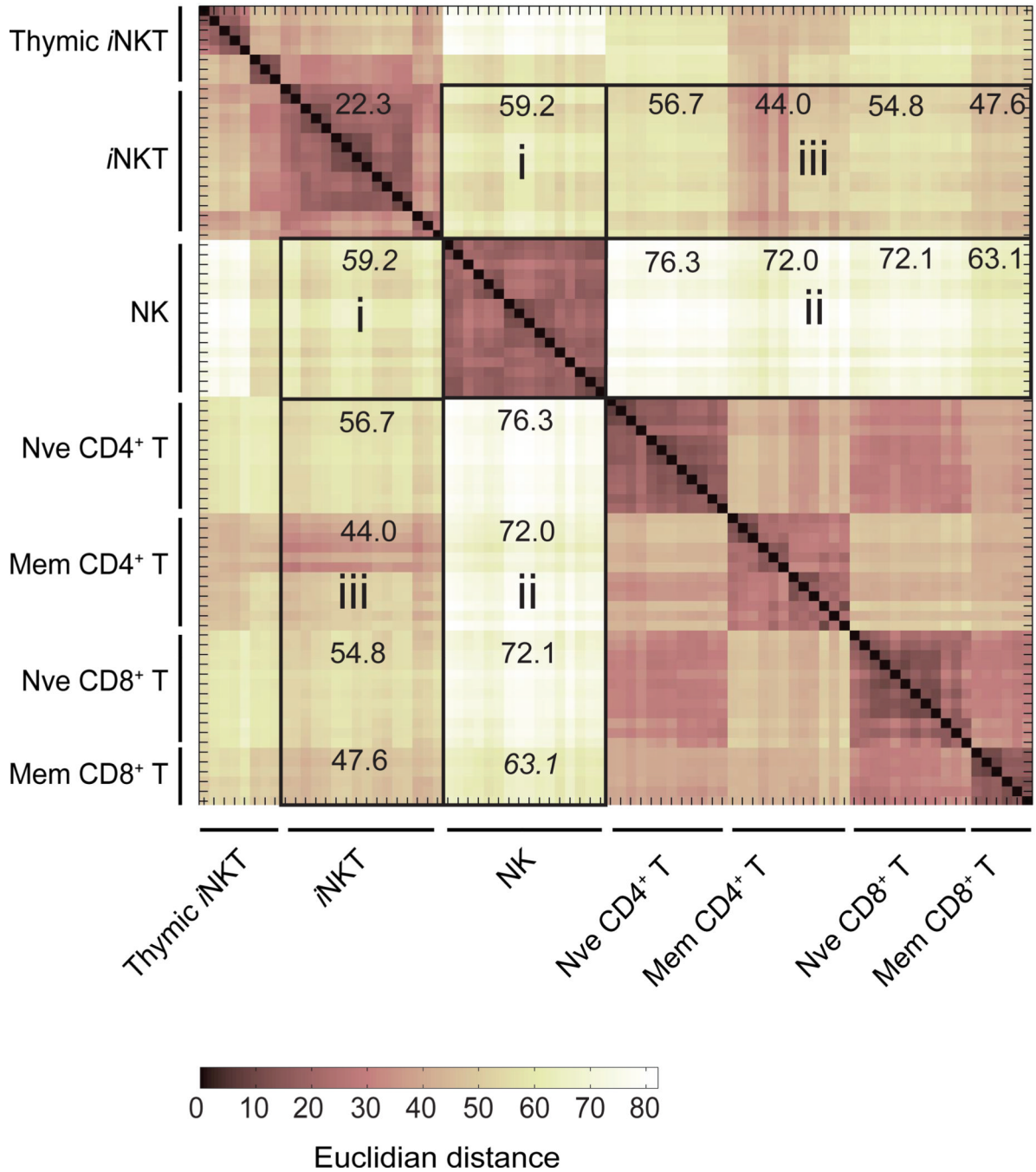


Fig. 1. *NKT* cells upregulate NKRs at the end of thymic differentiation. **(a)** Flow cytometric identification of thymic *NKT* cells. **(b)** Number of genes differentially expressed during *NKT* cell developmental transitions. **(c)** Genes differentially expressed between DP thymocytes and stage 1 (top), stage 1 and stage 2 (middle), and stage 2 and stage 3 *NKT* cells (bottom). Genes upregulated are highlighted in red or blue, respectively. See Supplementary Tables 1–6 for complete lists. **(d)** Genes differentially expressed in stage 1 *NKT* cells versus DP thymocytes. Colored highlights indicate genes differentially regulated in *NKT* but not in CD4⁺CD8^{int} compared to DP thymocytes. See Supplementary Tables 7 and

8 for complete lists. For **b-d**, only genes with expression above the detection level one or more subsets and a coefficient of variation (CV) < 0.5 in all subsets were considered. The differential expression threshold used was FC > 2. **(e)** Expression of NKRs in differentiating thymocytes (see Supplementary Table 16 for key to subset nomenclature). Values were log₂-transformed, row centered and locally color scaled. **(f)** NKR surface expression as determined by flow cytometry. Bars, mean percentage-positive ± s.e.m., n=3 mice. Data is representative of at least two independent experiments. **(g)** Expression of an NKR-containing gene cluster derived from a Euclidian distance-based K-means clustering analysis (mean correlation, 0.958). Genes were pre-filtered for expression and for FC > 2 between any 2 subsets, and data was log₂-transformed. *Klra3*, 5, 6, 9, 10, *Klr1b*, c, f, *Klrc1*, 2, 3, *Klrd1*, *Klri2* and *Klrk1* are labeled in red.

experiments. (c) NKR expression in peripheral MHC-restricted T and λ NKT cell subsets. Values were log₂-transformed, gene row centered and local color scaling was used. See Supplementary Table 16 for key to subset nomenclature.

**Fig. 3.**

The global transcriptional relationship between NK and *i*NKT cells is similar in magnitude to the relationship between T and *i*NKT cells. Euclidian distance matrix calculated using the 15% most variable probes. Only genes with mean expression values above 120 were included in these analyses, and data was log₂ transformed and mean centered. Numbers represent average Euclidian distances between intersecting subsets. Note that the matrix is symmetrical along the indicated diagonal. Areas of interest are marked with lowercase Roman numerals.

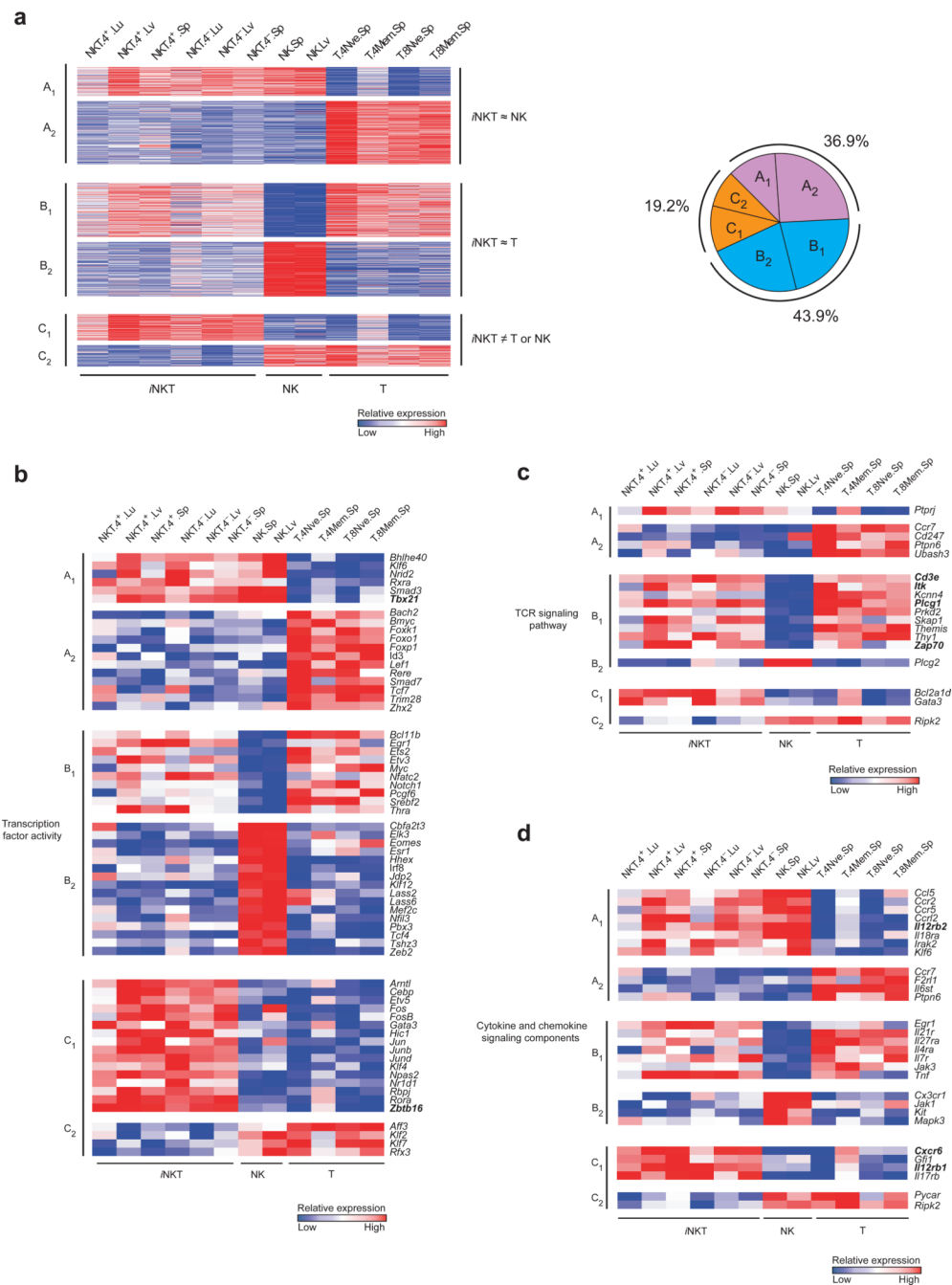


Fig. 4. Characterization of shared and differential gene expression among *n*NKT, NK, and T cells. One-way ANOVA was performed to compare gene expression in *n*NKT, NK, and T cell populations. Differentially expressed genes were separated into six categories depending on common patterns in 2 of the 3 subsets. Genes up- (*A*₁) or down- (*A*₂) regulated in NK and *n*NKT compared to T cells; genes up- (*B*₁) or down- (*B*₂) regulated in *n*NKT and T compared to NK cells; genes up- (*C*₁) or down- (*C*₂) regulated in *n*NKT compared to T or NK cells. (a) *Left*, heatmap of genes expressed differentially in *n*NKT, NK, and T cells for the indicated cell subsets, separated according to category; *right*, proportion of differentially expressed

genes in each category. **(b-d)** Expression of ANOVA category genes in relevant manually selected functional gene groups (see methods). Genes reported in the literature to be highly expressed in each category shown in underlined bold. In all heatmaps, rows are mean-centered and normalized, and local scaling is used. See Supplementary Table 16 for key to subset nomenclature.

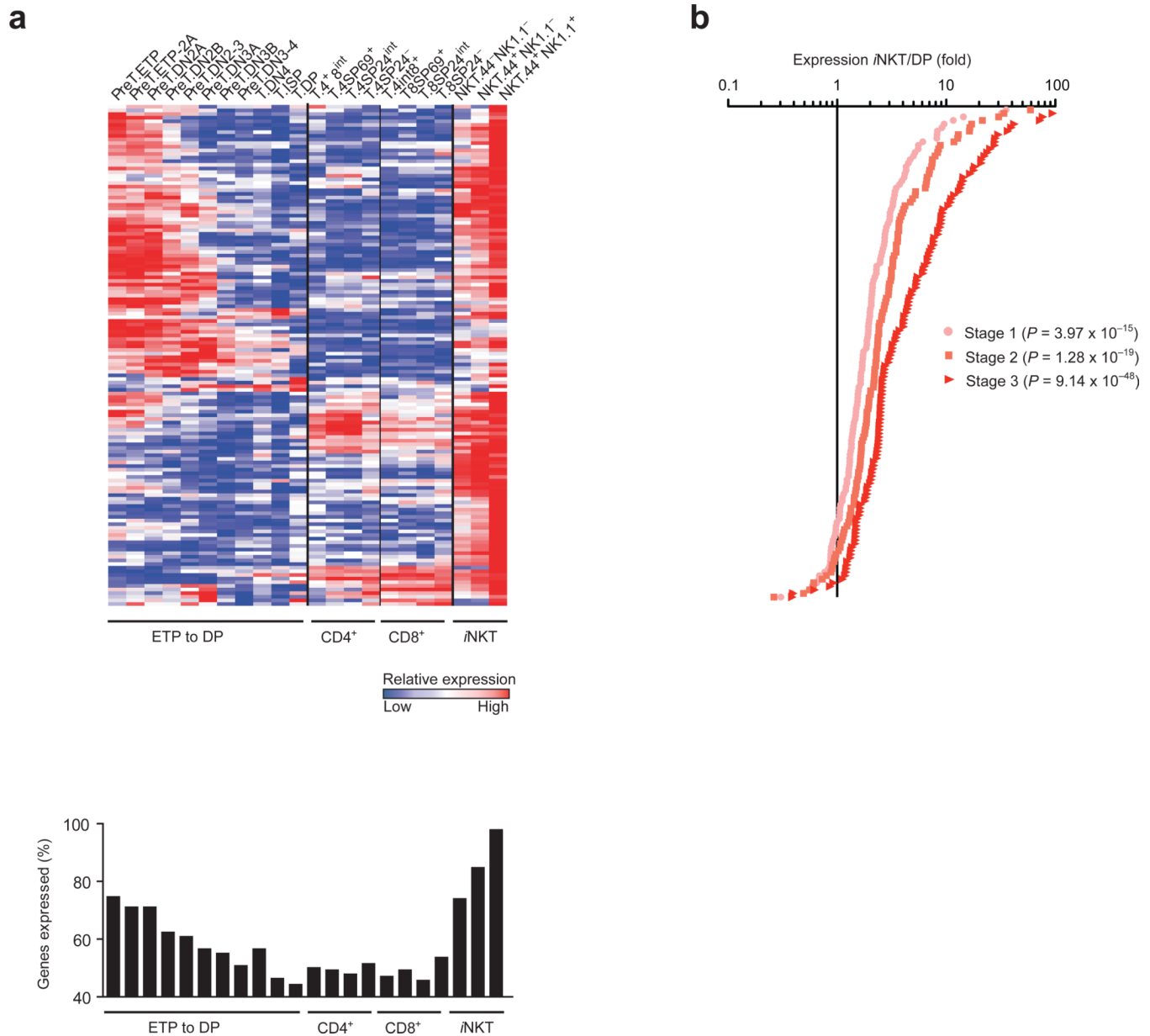


Fig. 5. Transcriptional programs shared between NK and nNKT cells are acquired during thymic nNKT cell maturation. **(a)** Top, relative expression of genes significantly upregulated in peripheral NK and nNKT cells (ANOVA category A₁) over the course of thymic T and nNKT cell maturation. Genes were ordered by hierarchical clustering using Pearson correlation. Rows are mean-centered and normalized, and local scaling is used. Bottom, percentages of genes exceeding the threshold for expression over the course of thymic maturation. T cell populations are represented in the same order as in the heatmaps. **(b)** FC distribution of category A₁ genes in stage 1, 2 and 3 nNKT cells compared to DP thymocytes with individual genes displayed in rank-order along the y-axis. *P* values represent significance of K-S test comparing the FC distribution of the ANOVA category A₁ geneset to that of all expressed genes. See Supplementary Table 16 for key to subset nomenclature.

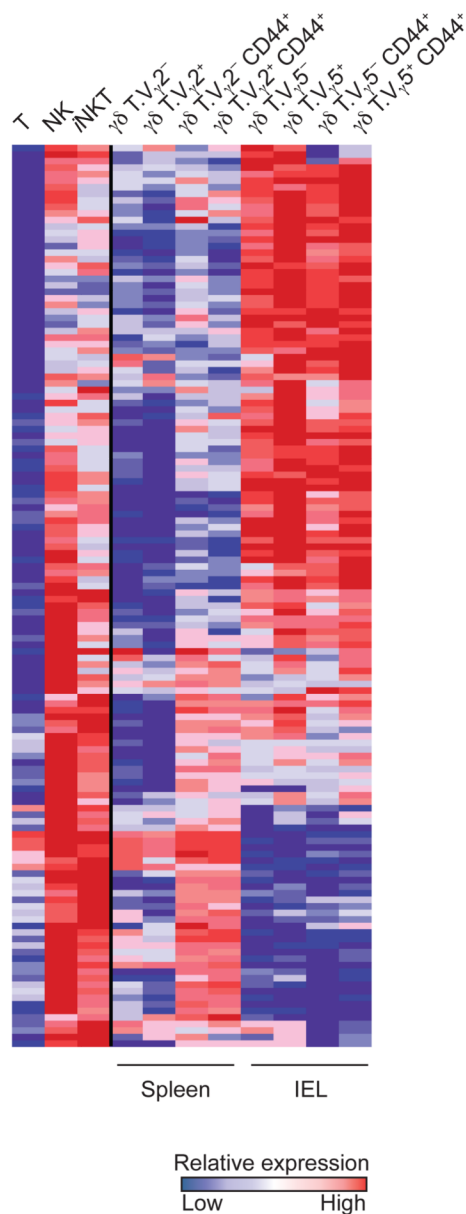
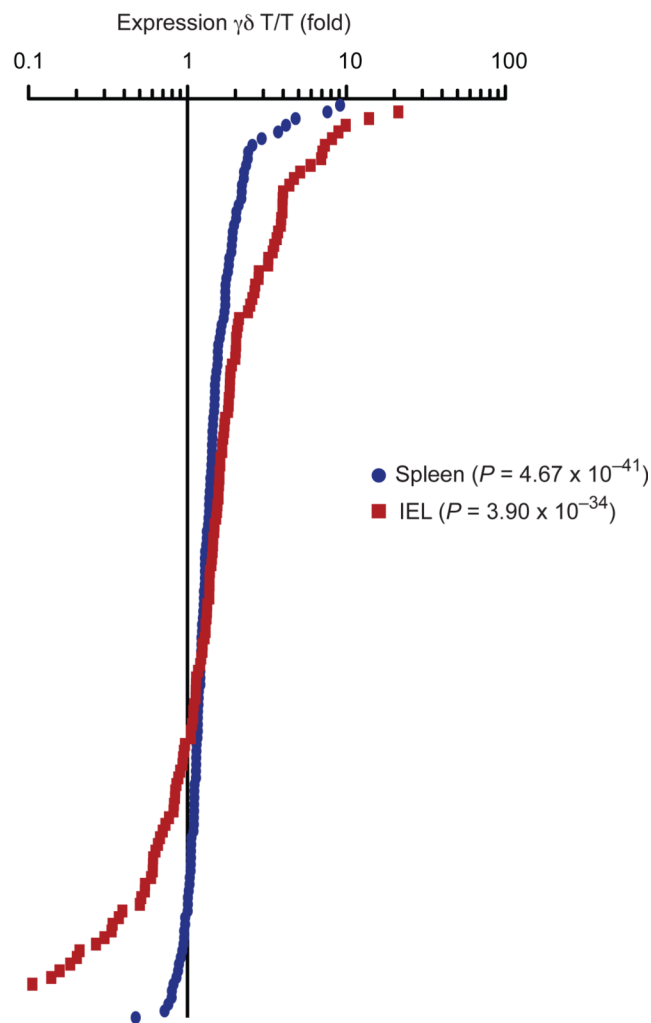
a**b**

Fig. 6. Activated splenic $\gamma\delta$ T cells and IEL $\gamma\delta$ T cells express NK- δ NKT shared gene programs. **(a)** Relative expression of genes significantly upregulated in peripheral NK and δ NKT compared to T cells (ANOVA category A_1) in the splenic and IEL $\gamma\delta$ T cell subsets indicated. Averaged values for the ANOVA subsets (δ NKT, NKT and T) are displayed for comparison. Genes are ordered by hierarchical clustering using Pearson correlation. Rows are mean-centered, normalized and local color scaling is used. **(b)** ANOVA category A_1 gene FC distributions for averaged splenic and IEL $\gamma\delta$ T cell subsets compared to the averaged T cell subset displayed with individual genes displayed in rank-order along the y-

axis. *P* values represent significance of K-S test comparing the distribution of the ANOVA category A_1 geneset to that of all expressed genes. See Supplementary Table 16 for key to subset nomenclature.

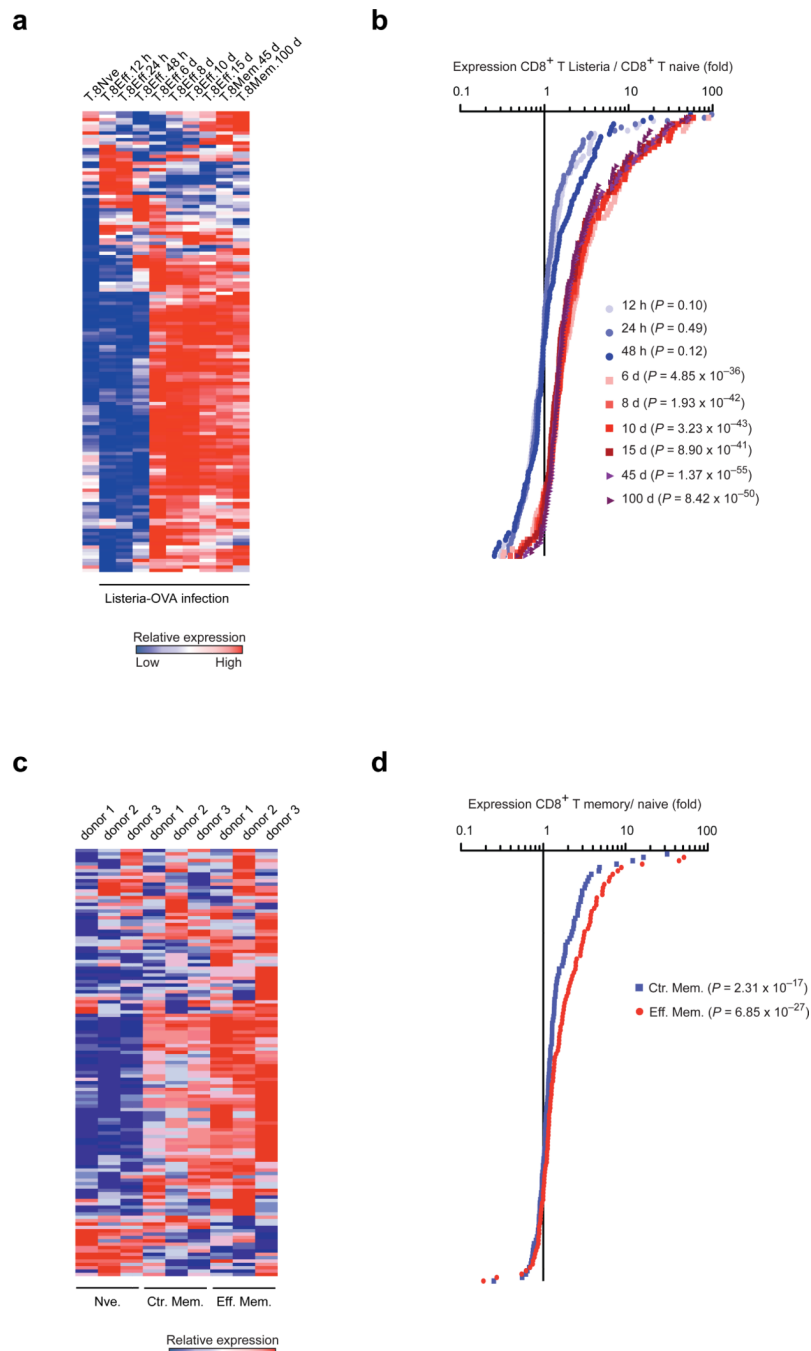


Fig. 7. NK- \mathcal{N} KT shared gene programs are induced in activated CD8⁺ T cells. **(a)** Relative expression of genes significantly upregulated in peripheral NK and \mathcal{N} KT cells (ANOVA category A₁) in antigen-specific CD8⁺ T cells over the course of *Listeria*-OVA infection. See Supplementary Table 16 for key to subset nomenclature. **(b)** ANOVA category A₁ gene FC distributions for activated CD8⁺ T cells compared to the naive control with individual genes displayed in rank-order along the y-axis. **(c)** Relative expression of the human gene homologs from ANOVA category A₁ in human peripheral blood CD8⁺ T cell subsets from different donors⁴³. **(d)** FC distributions for human memory CD8⁺ T cells compared to the

naïve control, using human homologs of the ANOVA category A₁ geneset. For all heatmaps, genes were ordered by hierarchical clustering using Pearson correlation. Rows are mean-centered and normalized, and relative scaling is used. For FC distribution plots, *P* values represent significance of K-S test comparing the distribution of the ANOVA category A₁ geneset to that of all expressed genes. Nve., naïve; Ctr. Mem., central memory; Eff. Mem., effector memory.

Table 1Functional pathway enrichment for ANOVA category A₁ genes

Biological process	Genes present	Fold-enrichment	P value
BP00157: Natural killer cell mediated immunity	<i>Klrc2, Klrc3, Ifng, Klrk1f, Klrk1, Klrk1c, Klrc1</i>	13.70	1.11×10^{-5}
BP00255: Cytokine/chemokine mediated immunity	<i>Ccr12, Ccr5, Ifng, Ccr2, Xcl1, Ccl5</i>	7.31	1.33×10^{-3}
BP00107: Cytokine and chemokine mediated signaling pathway	<i>Ccr12, Il12rb2, Ccr5, Ifng, Ccr2, Inpp5d, Xcl1, Ccl5</i>	4.31	2.49×10^{-3}
BP00287: Cell motility	<i>Ccr12, Coro2a, Dok2, Ccr5, Ccr2, Anxa1, Abi2, Dock5, Diap1</i>	3.68	2.98×10^{-3}
BP00148: Immunity and defense	<i>F2rl2, Klrc2, Klrc3, Fgr, Cysltr2, Adora2a, Tbx21, Klrk1, Ccl5, Ccr12, Cd97, Il12rb2, Ifng, Irak2, Klf6, Il18rap, Lgals3, Gzmb, Sh2d2a, Ccr5, Ccr2, Klrk1f, Xcl1, Klrk1c, Klrc1, Sema4a</i>	2.11	3.57×10^{-4}
BP00102: Signal transduction	<i>F2rl2, Klrc2, S100a6, Gna15, Klrc3, Fgr, Adora2a, Cysltr2, Gpr65, Klrk1, Abi2, Itgb2, Ccl5, Prkx, Il12rb2, Cd97, Ccr12, Coro2a, Zfp3612, Plcb3, Ifng, Rhob, Fgl2, Rhoc, Fas1, Inpp5d, Ptpnj, Irak2, Abr, Rxra, Anxa1, Ntng2, Smad3, Gem, Dock5, Arhgap26, Dusp5, Dok2, Dusp2, Ccr5, Rgs2, Rgs3, Ccr2, Chn2, Xcl1, Sema4a, Klrc1</i>	1.55	6.50×10^{-4}

Table 2Functional pathway enrichment for ANOVA category C₁ genes

Biological process	Genes present	Fold-enrichment	P value
BP00116: JNK cascade	<i>Vav3, Dusp1, Jun, Jund, Junb, Cxcl10</i>	14.49	5.45×10^{-5}
BP00265: Oncogene	<i>Fos, Vav3, Lmo4, Jun, Jund, Etv5, Junb</i>	10.35	5.53×10^{-5}
BP00263: Inhibition of apoptosis	<i>Il4, bcl2a1d, bcl2a1c, cebpb, socs2, bcl2a1b, bcl2a1a</i>	8.11	2.13×10^{-4}
BP00179: Apoptosis	<i>Il4, bcl2a1d, bcl2a1c, cebpb, socs2, bcl2a1b, bcl2a1a, tnfrsf14, nfkb1a, gadd45b, emp1</i>	3.25	1.88×10^{-3}
BP00281: Oncogenesis	<i>Fos, vav3, lmo4, jun, jund, fam129a, etv5, junb, emp1</i>	3.13	7.59×10^{-3}
BP00111: Intracellular signaling cascade	<i>Il4, cap2, vav3, socs2, rab4a, nfkb1a, junb, cxcl10, plk3, dusp1, jun, jund, gadd45b, tbkbp1, dusp6, rab27a</i>	2.78	5.12×10^{-4}
BP00040: mRNA transcription	<i>Dtx4, cebpb, lmo4, nfkb1a, fosb, arntl, zbtb16, rora, junb, hic1, fos, npas2, nr1d1, gata3, jun, jund, dennd4c, thoc4, gfi1, rbpi, etv5, klf4</i>	1.76	9.97×10^{-3}