Transcriptome and Chromatin Landscape of iNKT cells are Shaped by Subset Differentiation and Antigen Exposure

(21/130)

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Abstract

Invariant natural killer T cells (iNKT cells) differentiate into thymic and peripheral NKT1,

NKT2 and NKT17 subsets. We determined if the gene programs associated with these

thymic subsets were maintained in peripheral sites, the influence of tissue location, and

if there were large-scale changes after antigen exposure. RNA-seq and ATAC-seq

analyses showed that iNKT cells in any subset were similar, regardless of tissue

location. Lung iNKT cell subsets possessed the most distinct location-specific features,

shared with other innate lymphocytes in the lung, possibly consistent with increased

activation. After antigenic stimulation, iNKT cells underwent chromatin and transcription

changes leading to two populations: one similar to follicular helper T cells and the other

like NK or effector cells. Phenotypic analysis indicated these changes were observed

long-term, suggesting that iNKT cells gene programs are not fixed, but they are capable

of chromatin remodeling after antigen to give rise to several new subsets.

Introduction

Invariant Natural Killer T (iNKT) cells are considered to be an innate-like T lymphocyte population that can initiate or inhibit immune responses, depending on the context. Following activation, iNKT cells rapidly produce copious amounts of cytokines, similar to other innate-like lymphocytes[1]. iNKT cells express an invariant TCRα chain comprised of a Vα14-Jα18 (*Trav11-Traj18*) rearrangement in mice, with a conserved rearrangement in humans and many other mammals. These cells are activated by either self or microbial glycolipid antigens, presented by CD1d, a non-classical MHC class I molecule[2].

In the thymus, iNKT cells differentiate into three effector cell subsets, NKT1, NKT2, and NKT17, without exposure to exogenous antigen. Their effector functions and cytokine profiles resemble T_H1, T_H2, and T_{H17} CD4$^+$ T cells and subsets of other lymphocytes, including ILC, mucosal associated invariant T (MAIT) cells and γδ T cells[3, 4, 5]. Within the thymus, these iNKT cell subsets have highly divergent epigenetic landscapes and transcriptional programs[6, 7, 8]. Remarkably, several hundred genes are differentially expressed between thymic iNKT cell subsets, despite their similar specificity and despite sharing a distinct positive selection pathway[9]. Evidence suggests that some iNKT cells are long-term thymic residents, and these resident cells may contribute to thymic homeostasis[6]. Following egress from the thymus, iNKT cells localize to tissues throughout the body and the majority of peripheral iNKT cells do not recirculate[10, 11].

Although divergent thymic iNKT cell subsets have been identified, their relationship to

the corresponding peripheral iNKT cell subsets has not been assessed. Also, the

impact of tissue localization on gene expression programs remains incompletely

understood. To address these issues, we compared transcriptomic and epigenomic

data of iNKT cells from the thymus to several peripheral sites. Similar methods were

used to track changes in these cells after antigen exposure. Our genome-wide analysis

of the transcriptome and epigenome of iNKT cell subsets provides insights into the

stability and plasticity of the chromatin landscapes that are potentially initiated in the

thymus.

Results

Divergent chromatin landscape of thymic iNKT cell subsets

Previously, we showed that thymic iNKT cell subsets possess highly divergent

transcriptomes[8]. Similar results were obtained by others[7, 11, 12]. Further, we

demonstrated by genome-wide analysis of H3K27 acetylation modification that there

were significant differences in enhancer marks between the thymic iNKT cell subsets[8].

Because the epigenetic landscape of a cell population is more stable than the

transcriptome, we analyzed the epigenetic landscape of thymic iNKT cell subsets more

broadly with the assay for transposase-accessible chromatin using sequencing (ATAC-

seq)[13]. The thymic iNKT cell subsets were sorted based on expression of surface

proteins and validated by transcription factor staining (Supplementary Fig. 1a, 1b).

Based on our previous RNA-seq analysis of thymic iNKT cell subsets, we excluded a

population of CD1d-tetramer$^+$ cells with an intermediate phenotype, ICOS^{high} or IL17RB$^+$

cells that express CXCR3 or CD122, to obtain more purified subsets (Supplementary

Fig. 1c). Expression of *Rorc* and *Tbx21* transcripts by each iNKT cell subset in multiple

tissue tissues further demonstrates sorting efficiency; *Rorc* transcripts are only

expressed in NKT17 cells, whereas *Tbx21* transcripts are predominately expressed in

NKT1 cells (Supplementary Fig. 1d).

Consistent with previous results, we found that the profiles of accessible chromatin in

iNKT cell thymic subsets were strikingly divergent, with between approximately 5,000-

7,500 differentially accessible regions of chromatin (Fig. 1a). For comparison, naïve

versus memory CD8^{+} T cells have approximately 5,700 differentially accessible regions

of chromatin[14, 15]. Fig. 1b highlights the results from some key cytokine and

transcription factor gene loci. For example, there was a higher ATAC-seq signal at the

Ifng locus in thymic in NKT1 cells (Fig. 1b). Although some signal at several peaks also

was apparent in NKT2 cells, no accessibility was detected at a proximal enhancer 5 kb

upstream of the TSS (vertical grey bar) required for *Ifng* transcription (Fig. 1b)[16]. As

expected, we found the *Il17a* locus was most accessible in NKT17 cells. The *Il4* and

Il13 loci were open in both NKT2 and NKT1 cells, likely reflecting the ability of NKT1

cells to produce some Th2 cytokines after strong activation (Fig. 1b). Similarly, for

transcription factors that drive the expression of key cytokines, the *Tbx21* locus

encoding T-bet was more accessible in NKT1 cells and accessibility of *Rorc* was

increased in NKT17 cells (Fig. 1b, right). *Zbtb16* encoding PLZF, a transcription factor

required for the generation of all iNKT cells[9], was accessible in all subsets, although

mRNA and protein expression (Supplementary Fig. 1b) were higher in NKT2

thymocytes.

We partitioned all differentially accessible regions between thymic subsets (Fig. 1a) into

eight groups with *k*-means clustering to identify potential regulatory elements with

similar changes in ATAC-seq signal. We then examined the degree to which the

regions in each group were accessible in the different thymocyte iNKT cell subsets (Fig.

1c). Regions in clusters 1-3 had the highest signal in NKT1 cells, while clusters 4-5 and

6-8 had the highest signal in NKT2 and NKT17 cells, respectively. To associate the

changes in regulatory element accessibility with transcription factors, we determined the

enrichment of known motifs associated with DNA binding proteins. Within clusters 1-3,

typical of NKT1 cells, accessible regions frequently contained Tbox motifs, and to a

lesser extent Runt and Et1 motifs. HMG box protein motifs, associated with Tcf1 and

Lef1, were enriched in NKT2 thymocytes along with some enrichment for zinc finger and

RHD domain motifs, which include Egr1 and Nfat motifs, respectively. Expression of

Tcf1 (encoded by *Tcf7*) is enriched in NKT2 cells and required for iNKT cell

development[17]. Additionally, Lef1 is required for iNKT cell expansion and NKT

differentiation, independent of Tcf1[18]. Regions accessible in NKT17 cells were enriched

for consensus motifs of nuclear receptors, which can include Rorc and Reverb (Fig. 1d).

iNKT cell subsets in different sites are similar

To understand the degree to which the gene programs associated with thymic subsets

were also present in the periphery, and to assess the impact of tissue localization on

chromatin accessibility and the transcriptome, we compared sorted iNKT cell subsets

from thymus to those in spleen, liver and lung by both RNA-seq and ATAC-seq

analysis. Previous work showed that NKT1 cells were the predominant iNKT cell

population in C57BL/6J mice, comprising the majority in all the tissue sites analyzed[6].

NKT17 cells preferentially localized to the lung, lymph nodes and skin, and NKT2 cells

were more abundant in the spleen and mesenteric lymph nodes[6]. Because of the very

low cell numbers, NKT2 and NKT17 cells from liver were not analyzed. Although we

used a different RNA-seq technology allowing for greater sequencing depth[19], we found

exceedingly similar gene expression profiles in thymic NKT1, NKT2 and NKT17

thymocytes compared to the previous study[8] (Supplementary Fig. 2). Based on bulk

RNA-seq analysis, we observed that, as in the thymus, iNKT cell subsets within a given

tissue were distinct from one another (Supplementary Fig. 2). Similarly, the chromatin

accessibility profiles of iNKT subsets from spleen showed a divergent pattern of

accessible regions (Fig. 2a). Although splenic NKT2 and NKT17 cells were more

similar to one another than their thymic counterparts, there remained more than 3,500

differentially accessible loci (Fig. 2a).

In comparing thymic iNKT cell subsets with their peripheral counterparts, we found

smaller differences related to the tissue location compared to differences that were

associated with the subset identity. For example, comparing peripheral NKT1 to thymic

NKT1 cells, we found less than 1,000 differentially accessible chromatin regions (data

not shown). Similarly, we observed relatively few differences in accessible chromatin

regions comparing NKT1 cells between different peripheral tissues (Fig. 2b). Similar

results were obtained from analyzing chromatin accessibility in NKT2 and NKT17 cells

from different tissues. Principal component analyses (PCA) of the ATAC-seq data

revealed the strong influence of subset identity (Fig. 2c). A similar conclusion was

obtained for the RNA-seq data, although we did find some separation based on tissue

(Fig. 2d). These data are consistent with a model in which the chromatin accessibility

patterns set up for iNKT cells in the thymus largely carry over into the periphery, where

iNKT cell subset transcriptomes exhibit a high degree of similarity to thymic

counterparts.

Despite the overall similarity between the thymus and peripheral tissues, there are

transcripts that were enriched specifically in a given thymic subset compared to the

same subset in each peripheral site, including *Egr2* and *Tox* (Fig. 2e). These

transcription factors are required for the early stages of iNKT cell differentiation[20, 21], so-

called NKT0 cells, and therefore this may reflect residual expression of these genes in

mature thymic iNKT cell subsets, long-lived in the thymus. Some transcripts were the

converse, enriched in all or several peripheral tissues compared to thymus, without

subset restriction. These include *Art2* and *P2rx7*, previously reported to be increased in

total populations of peripheral iNKT cells[22], which make cells sensitive to NAD-induced

cell death, and *Osgin1*, identified as a growth inhibitory protein in other contexts[23]. The

expression of these genes might reflect the need for brakes on the expansion and

function of potentially autoreactive iNKT cells[24]. Also enriched in all sites in peripheral

iNKT cells were *Tspan13*, and *Klf3*, whose expression was increased in memory CD8^{+}

T cells[25].

Identification of a gene expression signature in lung

Although the iNKT cell subset is a predominant factor driving genomic differences, lung

iNKT cells shared common features that distinguished them from their counterparts in

the other locations. This was revealed by PC2 of the RNA-seq data (Fig. 2d), or PC3

analysis of the ATAC-seq data (Fig. 3a). Transcripts encoding AP-1 and other bZIP

family members, as well as some members of the NF-κB family were enriched in all

lung iNKT cell subsets, as were transcripts encoding CTLA-4, CD69 and *Nr4a1*

encoding Nur77 (Fig. 3b and Supplementary Fig. 3). Furthermore, regions more

accessible in lung iNKT cells were enriched for bZIP motifs, which are associated with

the transcription factors Ap1 and Atf, as well as RHD motifs, which can include NFκB-

p65 binding sites (Fig. 3c). Together these data are consistent with tissue-residency or

increased activation of lung iNKT cells, and indeed, we found a subpopulation of lung

iNKT cells that expressed CTLA-4 by flow cytometry (Fig. 3d). To ascertain that the

signature in lung iNKT cells could not be attributed to infection or inflammation in a

single mouse, we sorted iNKT cell subsets from individual mice obtained only one week

earlier from a commercial supplier and performed RNA-seq. We found a similar lung

gene expression signature in each individual (Supplementary Fig. 3).

Cells within the lung are exposed to a diverse environment of environmental and

microbial antigens, as well as differences in oxygen. We next asked if iNKT cells from

another antigen-rich site, the small intestine, displayed a similar increase in CTLA-4

expression. We found that total iNKT cells from the small intestinal lamina propria (SI-

LPL) express CTLA-4 similarly to lung iNKT cells, whereas splenic iNKT cells do not

(Fig. 3e). These data suggest antigen-rich environments may imprint the lung activation

signature.

Other innate or innate-like lymphocyte populations are found in lung, including $\gamma\delta$ T

cells, MAIT cells, ILC and NK cells, as well as mainstream resident lymphocytes and

some circulating cells. We tested if the lung activation signature of iNKT cells extended

to several other lung populations. Therefore, we performed ATAC-seq and RNA-seq

analyses on sorted $\gamma\delta$ T cells, NK cells, as well as naïve CD4$^+$ T cells from the lung and

spleen. Lung γδ T cells and NK cells displayed the lung signature based on increased

chromatin accessibility in regions enriched for bZIP and RHD motifs (Fig. 4a), with γδ T

cells having accessibility in regions enriched for nuclear receptor motifs, which can

include RORγt binding sites, while NK cells were enriched for T-box motifs. Lung CD4$^+$

T cells had a different pattern from the other cell types, but with some increased signal

at regions containing bZIP (ATF) and RHD (NF-κB-p65) motifs (Fig. 4a). PCA analysis

of the RNA-seq data, which included total iNKT cells from spleen or lung, showed

separation of each lung cell type, including CD4$^+$ T cells, from the corresponding cell

type in spleen (Fig. 4b). Further, we found increased expression of the iNKT cell lung

signature genes, listed in Supplementary Fig. 3, in lung γδ T cells, and NK cells

compared to the corresponding splenic populations (Fig. 4c). The transcriptome of lung

CD4$^+$ T cells was more divergent, but still had some features in common with the lung-

resident innate or innate-like lymphocyte populations (Fig. 4c). This is illustrated in Fig.

4d, which shows that expression of *Fosl2, Bhlhe40* and *Tnfaip3* was higher in all cell

types from the lung. Gene set enrichment analysis (GSEA) pre-ranked analysis

comparing each cell type from the lung versus spleen using the iNKT cell lung signature

further demonstrated the strong enrichment of the lung signature in each cell type (Fig.

4e).

Epigenomic and transcriptomic changes following antigen challenge

A unifying hypothesis based on these data is that iNKT cell subsets are formed in the

thymus and seed peripheral tissues with fixed functions and relatively minor impacts to

their chromatin landscape and transcriptomic profiles, with the partial exception of those

in the lung. To test this, we determined if these profiles remained after a strong

antigenic challenge in total splenic iNKT cells, which are mostly NKT1 cells. To

examine how the chromatin landscape and transcriptome of iNKT cells was altered in

response to antigen, we injected mice with αGalCer and harvested the spleen 6 days

later. It has been reported that following exposure to the potent glycolipid antigen α-

galactosyl ceramide (αGalCer), some iNKT cells display a T follicular helper cell (T_{FH})-

like phenotype, with increased expression of CXCR5, PD-1, and BCL6 (Supplementary

Fig. 4a, 4b). These so-called NKT_{FH} cells produce IL-21, and localize to germinal

centers[26], and may play a role in early germinal center formation[27], but their gene

expression programs had not been elucidated. Putative NKT_{FH} (αGalCer loaded CD1d

tetramer$^+$CXCR5$^+$PD-1$^+$) and the remaining population of iNKT cells from antigen-

injected mice (CXCR5$^-$PD-1$^-$ or NKT non-FH) cells were sorted and analyzed by ATAC-

seq and RNA-seq. Of note, NKT1, NKT2 and NKT17 cells as described above are not

identifiable 6 days following αGalCer challenge and therefore were not analyzed. As

shown in Fig. 5a, accessible regions of chromatin were exceptionally different

comparing NKT_{FH} and the antigen-exposed non-FH cells, which we refer to as iNKT cell

effectors (NKT_{eff}). Chromatin accessibility regions in NKT_{FH} were also very different

from the NKT1, NKT2 and NKT17 subsets in the spleen from uninjected mice, most

different from NKT17 cells (Fig. 5a, left). There was increased chromatin accessibility in

NKT_{FH} in the *Il21* locus and the *Pdcd1* locus encoding PD-1 in NKT_{FH} cells (Fig. 5b),

reflecting a T_{FH} state. The accessible regions of chromatin within NKT_{eff} also greatly

varied when compared to the iNKT cell subsets from unchallenged mice but were most

similar to NKT1 cells (Fig. 5a, right). These data suggest that most of the splenic iNKT

cells were exposed to antigen, including those that did not become NKT$_{FH}$.

We partitioned all differentially accessible regions between NKT$_{FH}$ and NKT$_{eff}$ cells and

splenic iNKT cell subsets from unimmunized mice into ten groups with *k*-means

clustering to identify regions with similar changes in ATAC-seq signal. As above, we

examined the degree to which the regions in each group were differentially accessible in

iNKT cell populations (Fig. 5c) and their association with DNA binding protein motifs

(Fig. 5c). Notably, the two populations from αGalCer immunized mice had increased

accessibility for cluster 7, with motifs for T-box proteins and to a lesser extent NFκB

(RHD motifs) and IRF proteins. There also was decreased accessibility in regions

containing motifs associated with the lineage driving transcription factors RORγt

(nuclear receptor motifs) and GATA3 (zinc finger motifs) enriched in clusters 1 and 2.

Accessible regions specific to NKT$_{FH}$ cells within clusters 8 and 9 were increased for

motifs for RHD domain transcription factors, which include NFAT and NFκB, and bZIP

motifs, characteristic of Ap-1 family transcription factors, suggesting a more activated

state. Clusters 4 and 5 were more accessible in NKT$_{eff}$ and also in NKT1 cells from

unimmunized mice. These accessible regions were enriched for T-bet, Ets and Runt

domain-associated motifs. NKT$_{eff}$ cells also had increased accessibility in regions

containing more Zinc finger transcription factor and Ets motifs (cluster 6). Although they

are reported to be self-reactive, these data suggest that iNKT cells greatly remodel their

chromatin landscape following encounter with a potent exogenous glycolipid antigen.

We also performed RNA-seq on the two populations of iNKT cells from αGalCer-treated

mice, as well as total splenic iNKT cells from unimmunized mice. Gene expression by

NKT_{FH} was greatly different from total splenic iNKT cells (Fig. 5d) or from each of the

iNKT cell subsets from unchallenged mice (Fig. 5e, Supplementary Fig. 4c).

Comparison of differentially expressed genes distinguishing $CD4^+$ T_{FH} and T_H1 cells[28]

demonstrated that NKT_{FH} shared a more similar expression profile to T_{FH}, whereas, not

surprisingly, NKT1 cells were similar to T_H1 (Supplementary Fig. 4d). Similarities

between NKT_{FH} and T_{FH} also were revealed by GSEA analysis (Fig. 5f, top panel).

GSEA of NKT_{FH} compared to NKT_{eff} revealed an enrichment for $CD8^+$ T cell effector-

related genes in NKT_{eff} (Fig. 5f, bottom, left and right panels). Neither antigen-

experienced subset was significantly enriched for memory cell-related signatures.

Because of the great prevalence of NKT1 cells in the spleens of unimmunized

C57BL/6J mice[6], it was not feasible to assess directly the separate contributions of the

NKT1, NKT2 and NKT17 subsets to the antigen-activated iNKT cell populations. To

address their origin, we utilized mice in which T-bet expression could be fate-mapped[29].

Whereas close to 90% of spleen NKT1 cells from unimmunized mice expressed the T-

bet fate map marker, only 74% or less of NKT_{FH} did (Fig. 5g). Notably, the T-bet fate

map marker was not expressed in NKT2 cells. Therefore, some NKT_{FH} may have

originated from the prevalent NKT1 cell pool, and despite their separation from NKT1

cells, we found expression of some NKT1 signature genes by NKT_{FH} (Supplementary

Fig. 4d). However, because prior T-bet expression was selected against in NKT_{FH} cells,

these data suggest that NKT2 and/or NKT17 cells also may have contributed.

Furthermore, the fate-mapping may underestimate how efficiently NKT2 and/or NKT17

converted to NKT$_{FH}$; T-bet expression could have been induced in some iNKT cells after

antigen activation.

Enhanced effector function after antigen challenge

As shown in Fig. 5a (right column), iNKT cells from αGalCer-immunized mice that did

not become NKT$_{FH}$ also had a chromatin landscape different from all of the subsets in

unimmunized mice, with the biggest divergence again from NKT17 cells. PCA analysis

of the RNA-seq data showed that the transcriptome of these iNKT cells was highly

different from total iNKT cells from unimmunized mice (Fig. 5d). Previous analyses

have shown that after i.v. exposure to DCs loaded with αGalCer, a KLRG1^{+} population

of iNKT cells develops, especially in the lung, in a process dependent on expression of

the transcription factor Eomes[30, 31]. Cells with this phenotype persisted for weeks and

they exhibited enhanced effector function. Pathway analysis of genes enriched in

NKT$_{eff}$ in spleen following αGalCer alone, using the ConsensusPath Database,

identified NK cell-mediated cytotoxicity as the most enriched pathway (Supplementary

Fig. 4e). This is in line with the gene expression profile in these lymphocytes indicative

of an enhanced effector phenotype found by GSEA (Fig. 5f). Intriguingly, there was

similarity in chromatin accessibility in some key loci between NKT$_{eff}$ and splenic NK

cells, with increased ATAC-seq peaks within the loci for genes encoding Granzyme A

and B, KLRG1 and CX3CR1, as well as Spry2, which is also highly expressed by NK

cells (Fig. 6a). There also were some regions of increased chromatin accessibility in

genes associated with NK cell function in NKT1 cells, but these regions had higher

signals in NKT$_{eff}$ and NK cells.

To validate the existence of the NKT$_{eff}$ population, we assessed the expression of

KLRG1 and CX3CR1, NK cell markers with increased chromatin accessibility in NKT$_{eff}$

(Fig. 6a). We detected increased expression of each of these markers on NKT$_{eff}$

compared to NKT$_{FH}$ and iNKT cells from uninjected mice (Fig. 6b). T-bet fate-mapping

analysis revealed that virtually all KLRG1^{+} NKT$_{eff}$ had expressed T-bet, suggesting

either these cells differentiated from NKT1 cells or acquired expression T-bet when

activated (Fig. 5g). To determine if the phenotypic changes we observed were

maintained, we also analyzed splenic iNKT cell populations at day 30 or later after

antigen exposure. iNKT cells with the NKT$_{eff}$ phenotype were still a sizeable fraction of

the iNKT cells (Fig. 6c). Similarly, NKT$_{FH}$ cells also persisted in the spleen beyond day

30 (Supplementary Fig. 4f), consistent with a report showing elevation of NKT$_{FH}$ 60 days

post-treatment with αGalCer and ovalbumin-loaded liposomes[32]. These data suggest

that antigen challenge induces dynamic and prolonged changes in the phenotype of

iNKT cells reflecting changes in the transcriptome and chromatin landscape.

Discussion

There are functional subsets of iNKT cells, analogous to CD4 T_{H1}, T_{H2} and T_{H17} cells, as well as several other lymphocyte populations[7], and it has been established that the chromatin landscape and transcriptomes of the thymic iNKT cell subsets are distinct[7, 12]. Here, we addressed three questions. First, to what extent are the gene programs driving the thymic iNKT cell subsets present in peripheral iNKT cells? Second, considering that iNKT cells are mostly non-recirculating lymphocytes[11], what is the imprint of localization in different tissues on these gene programs? Third, to what extent are the iNKT cell gene programs subject to dynamic and long-term changes following antigenic stimulation, as such changes might be suggestive of trained immunity or an effector-memory response?

Our data indicated that the status of chromatin accessibility and the transcriptome in any one subset are relatively similar to one another, regardless of location. Although this suggests that iNKT cells become fully mature and committed to a subset in the thymus and maintain their status in the periphery, there is evidence based on the expression of diagnostic surface proteins that iNKT cell recent thymic emigrants are not fully mature[33, 34, 35]. Perhaps the epigenome of the iNKT cell subsets is set up in the thymus prior to emigration, but with the mature, subset-specific transcriptome only initiated after thymus emigration. ATAC-seq analysis of stage 0, stage 1 and mature NKT1 cells identified regions accessible in mature NKT1 cells were already accessible in stage 0 cells, providing further evidence to support this hypothesis[36]. Alternatively, it is possible that the recent thymic emigrants are not fully differentiated but receive

tissue-specific cues allowing the cells to mature into an effector subset resembling their

thymic counterparts.

Although the imprint of tissue localization was comparatively limited, in the lung iNKT

cells exhibited motif enrichment in regions of accessible chromatin for bZIP domain

transcription factors, which can include AP-1 and ATF, and RHD (NF-κB) transcription

factors, regardless of the functional subset. This may be related to an activation

signature, consistent with the increased CTLA-4 expression by lung iNKT cells. These

data are consistent with a recent report describing a similar gene expression signature

in lung MAIT and iNKT cells, although it was also consistent with a tissue-residency

pattern[11]. Regardless, the lung signature was present not only in iNKT cell subsets, but

also in NK cells and γδ T cells, and to a lesser extent even in CD4$^+$ T cells compared to

the corresponding cell type in the spleen. A recent study comparing the epigenome of

alveolar CD8$^+$ resident memory T cells (Trm) found that Trm cells within the lung

interstitial space were enriched for AP-1, FOS and CREM motifs compared to splenic

Trm[37]. In other studies, this lung signature was not just specific to lymphocytes, with

some similarities to the lung epigenome of alveolar macrophages[38]. Based on these

findings and the present study, the lung microenvironment may dictate epigenetic

remodeling and subsequent transcriptional changes. One potentially important factor is

increased oxygen concentration[39, 40], and also, the lung may face more environmental

exposure to external substances and microbes[40]. Perhaps immune cells in the lung

need to be poised to rapidly respond to challenges. If this were correct, then we would

predict that iNKT cells in sites such as skin or intestine might also have gene programs

distinct from cells in thymus, spleen and liver. Consistent with this hypothesis, we found

increased CTLA-4 expression on iNKT cells from the SI-LPL. Additionally, iNKT cells

from the the draining lymph nodes of the lung and the small intestine, the inguinal lymph

node and mesenteric lymph node, express a large number of lung signature genes

including *Fos*, *Fosb*, and *Nr4a1* compared to the thymus and spleen[35]. A more detailed

exploration of the lung activation signature in iNKT cells and other innate populations

within antigen exposed tissues is needed.

Six days after antigenic exposure, we detected two different iNKT cell populations, one

is NKT_{FH} that is similar to T_{FH}. Previously, NKT_{FH} were reported, based on expression

of BCL-6, a few key surface proteins, and functional assays for T cell help[26]. Here, we

demonstrated that this NKT_{FH} population has a dramatically different chromatin

landscape and transcriptome that resembles T_{FH}. These cells likely originated in part

from NKT1, the major splenic subset population, but probably also from other activated

subsets considering reduced prior T-bet expression, and they persisted for at least 30

days after antigenic challenge. At later time points, NKT_{FH} maintain the capacity to

produce IL-21, but downregulate BCL-6 expression and increase expression of CD62L

and CCR7, consistent with memory T_{FH}[32]. As detected by immune assays, the half-life

of αGalCer complexes with CD1d on the surface of DCs *in vivo* was less than 24h[41, 42].

Given this half-life, it is unlikely that these cells experience any recent exposure to

αGalCer. Therefore, chromatin remodeling in iNKT cells after antigen exposure led to

the generation of a persisting population of iNKT cells that is expected to have

enhanced helper function for B cells.

The second population called NKT_{eff} more closely resembled NK cells. iNKT cells with

this phenotype also were present for at least 30 days. Previously a similar population

was present in lung after injection of antigen-loaded DCs[31], but here we show that

NKT_{eff} can be generated systemically following the same antigenic challenge that also

induces the NKT_{FH} population. In other experiments, it was reported that iNKT cells

exposed to αGalCer were anergic for many weeks[43, 44]. In previous work, we did not

find evidence for anergy in the total iNKT cell population, because at 30 days following

αGalCer, re-challenged iNKT cells remained cytotoxic, effectively signaled through their

TCR, and had increased proliferation compared to iNKT cells responding to αGalCer for

the first time[45]. However, we did find reduced pro-inflammatory cytokine production,

which could reflect the distinct functions of NKT_{FH} cells that were likely generated, and a

minority of the iNKT cells that acquired the ability to produce IL-10[45]. Therefore, it is

likely that iNKT cells from mice injected with antigen that did not become NKT_{FH} are

heterogenous, including not only NKT_{eff} but IL-10 producers and perhaps some anergic

cells. Further, in studies of KLRG1^{+} iNKT cell induction by antigen-loaded DCs, these

cells maintain long-term anti-tumor function[31]. The size of the NKT_{eff} population is

difficult to quantify because KLRG1^{+} cells accounted for only a portion, with other cells

expressing high amounts of CX3CR1 and granzymes (Fig. 6b, d). The contributions of

TCR signal strength, co-stimulation, cytokines and other aspects to the generation of

disparate iNKT cell populations remain to be determined, but apparently pulsing DC

with αGalCer is a more effective method for generating NKT_{eff} almost exclusively in the

lung[31].

iNKT cells have been classified as innate-like T lymphocytes that bridge the innate and

adaptive immune systems, sharing components of cells within each major branch of the

immune response[5]. The capacity for innate-like cells to exhibit long-term changes in

their functional programs in response to antigen exposure has been referred to as

trained immunity[46]. Do iNKT cells exhibit an effector memory response or a form of

trained immunity? At steady-state, iNKT cells have some properties of tissue-resident

memory cells. Many of them express molecules characteristic of canonical resident

memory T cells, such as CD103 and CD69, and like effector memory cells, they

produce cytokines in a TCR-dependent or cytokine-dependent manner within a few

hours[9, 11]. In response to αGalCer, however, dynamic, long-term changes occur in iNKT

cells, generating NKT_{FH}, NKT_{eff} populations, and likely others, indicating a degree of

plasticity and heterogeneity that allow these cells to adapt to their history of prior

antigenic stimulation and respond in a variety of contexts.

Materials and Methods

Mice

C57BL/6J female mice aged 6-8 weeks old were purchased from Jackson Laboratories

or bred in-house at La Jolla Institute for Immunology. B6;CBA-Tg(Tbx21-cre)1Dlc/J

(Tbet-cre) were purchased from Jackson Laboratories and then bred with

B6.Cg-Gt(ROSA)26Sor[tm14(CAG-tdTomato)Hze/J] (Td-tomato) mice (also obtained from

Jackson Laboratories) to generate the T-bet fate mapping line. All studies were

approved by the Institutional Animal Care and Use Committee at the La Jolla Institute

for Immunology.

Tissue Preparation

Following euthanasia, thymus tissue and spleens were removed, lungs and livers were

perfused with 3-10 mL of liver perfusion medium (Gibco) until tissues cleared. Livers

were mashed through a 70 μM nylon filter (Fisher). Liver lymphocytes were isolated by

centrifugation at 850x*g* in 37.5% Percoll for 20 minutes. Lungs were placed in

GentleMacs C tubes (Miltenyi Biotec) with 2 mL Spleen Dissociation Medium

(STEMCELL Technologies) and homogenized using the Miltenyi GentleMacs

dissociator. Following homogenization, suspensions were filtered with a 70 μM filter

and washed twice with RPMI + 10% FBS. Thymus and spleens were homogenized

through a 70 μM nylon filter and washed with RPMI + 10% FBS. For lamina propria

lymphocyte isolation, small intestines were collected from mice and Peyer's patches

removed. The tissue was washed and cut into pieces that were then incubated in 25 ml

of HBSS (5% FBS, 25mM HEPES and 1mM DTT) in a shaker at 225 r.p.m., 37°C, for

20 min. Samples were filtered and the tissue debris was incubated in 20 ml of HBSS

(25mM HEPES and 20mM EDTA) in a shaker at 225 r.p.m., 37°C, 2 times for 15 min to

further remove epithelial cells. Then, tissues were incubated at 37°C for 25 min with

rotation in media containing collagenase type VIII (Sigma). The filtered cell suspension

was re-suspended in 40% Percoll solution and overlaid above 80% Percoll solution. LPL

were collected from the interface.

Antigen challenge

α-galactosyl ceramide (αGalCer or KRN7000) was supplied as a lyophilizate in vehicle

and provided by Kyowa Kirin Pharmaceutical Research. It was resuspended at 200

μg/mL in water and then diluted to 10 μg/mL in PBS. 0.2 mL of 10 μg/mL αGalCer was

administered via retro-orbital injection, and 6- or ≥30-days later mice were euthanized

and organs harvested.

Cell Sorting

For RNA-seq and ATAC-seq experiments, unless otherwise noted iNKT cell subsets

were sorted in parallel from tissues pooled from 15-20 female C57BL/6J mice,

approximately 6 weeks of age. Cell suspensions from thymus, spleen and lung were

enriched for iNKT cells by negative selection using biotinylated antibodies against CD8α

(53–6.7, BD Biosciences), CD19 (1D3, Tonbo Biosciences), CD24 (M1/69, BD

Biosciences), CD62L (MEL-14, Invitrogen), CD11b (M1/70, Tonbo Biosciences), CD11c

(N418, Tonbo Biosciences), F4/80 (BM5.1, Tonbo Biosciences), EpCam(G8.8,

BioLegend), and TER-119 (TER-119, Tonbo Biosciences) together with Rapidspheres

(StemCell technologies) and either the Big Easy or Easy eight magnets (StemCell

technologies) using protocols from the manufacturer. The remaining cells were then

suspended at 10^8 cells/mL, incubated with 1 μg/mL of Streptavidin A (Sigma-Aldrich).

Liver lymphocytes were not enriched for iNKT cells. iNKT cells were stained using a 12-

parameter panel of reagents including tetramers of CD1d loaded with αGalCer (BV421,

in house preparation), live/dead yellow (ThermoFisher Scientific), anti-TCRβ-APC-

eF780 (H57-597, ThermoFisher Scientific), anti-CD8α-PE CF594 (53-6.7, BD

Biosciences) and anti-CD19-PE CF594 (1D3, BD Biosciences), anti-CD4-AF700

(GK1.5, BioLegend), anti-IL-17RB-AF488 (FAB10402G, R&D Systems), anti-ICOS-

PerCP Cy5.5 (C398.4A, BioLegend), anti-CD122-BV650 (5H4, BD Biosciences), anti-

CXCR3-APC (CXCR3-173, BioLegend), anti-SDC1-PE (281-2, BioLegend), and anti-

FR4-PE Cy7 (ebio12A5, ThermoFisher Scientific). Cells were sorted using a FACSAria

III or FACSAria Fusion (BD Biosciences) for live lymphocytes, singlets, $CD8^-CD19^-$,

$Tetramer^+TCR\beta^+$ iNKT cells and separated into NKT1, NKT2, and NKT17 cell subsets

based on the following expression profiles: NKT1: $CXCR3^+ICOS^-CD122^+SDC1^-IL-17RB^-$

; NKT2: $CXCR3^-ICOS^+CD122^-SDC1^-IL-17RB^+CD4^+$; NKT17: $CXCR3^-ICOS^+CD122^-$

$SDC1^+IL-17RB^+FR4^-$.

For NKT_{FH} sorts, spleens were harvested 6 days following antigen challenge. Single

cell suspensions were enriched for iNKT cells as described above. iNKT cells were

stained with CD1d tetramers loaded with αGalCer, live/dead yellow, anti-CD8α-PE

CF594 and anti-CD19-PE CF594, anti-TCRβ-APC-eF780. NKT_{FH} cells were identified

based on expression of CXCR5 (anti-CXCR5-PE, clone L138D7, BioLegend), and PD-1

(anti-PD-1-APC, clone RMP1-30, BioLegend). $CXCR5^-PD-1^-$ iNKT cells from antigen

challenged mice were also sorted for comparison (NKT_{eff}).

For sorting of $\gamma\delta$ T cells, $CD4^+$ T cells, NK cells, and iNKT cells from lung and spleen,

tissues were prepared and enriched as described above. Populations were sorted

based on the following gating strategy: live lymphocytes, singlets, $CD8^-CD19^-$; iNKT

cells, $Tetramer^+TCR\beta^+$; $\gamma\delta$ T cells, $TCR\beta^-TCR\gamma\delta^+$ (anti-TCR$\gamma\delta$-FITC , clone GL3, BD

Biosciences); NK cells, TCRβ$^-$, NK1.1$^+$ (anti-NK1.1-PE Cy7, clone PK136, BD

Biosciences); CD4$^+$ T cells, TCRβ$^+$CD4$^+$.

Flow Cytometry

Cells isolated from the lung or spleen were stained for iNKT cell subsets, NKT$_{FH}$ and

NKT$_{eff}$, as described above. In addition to the antibodies and other reagents used

for iNKT isolation described above, we also used anti-PLZF-AF647 (clone R17–809),

anti-T-bet-AF488 (clone O4–46), anti-RORγt-PE-CF594 (clone Q31-378), anti-BCL-6-

AF488 (clone K112-91), all from BD Biosciences, anti-KLRG1- PECy7 (clone 2F1), and

anti-CTLA-4-PE (clone UC10-4B9), all from Thermo-Fisher Scientific, and anti-

CX3CR1-BV711 (clone SA011F11, BioLegend). Staining for total CTLA-4 expression

was performed according to a using Cytofix (BD Biosciences) and eBioscience

permeabilization buffer (Thermo-Fisher Scientific). Stained samples were analyzed

using a Fortessa flow cytometer (BD Biosciences) and FlowJo software (Treestar).

RNA-seq

Cells representing specific iNKT subsets were sorted by pools of cells ranging between

200 to 400 directly into 0.2 ml PCR tubes containing 8 µl of low-input lysis buffer (0.2%

Triton-X-100 and RNase inhibitor) and stored at -80°C until processed further. For

thymic subsets, n = 5 (NKT1), n = 4 (NKT2), n = 6 (NKT17). For peripheral subsets,

NKT1: lung n = 5, liver n = 5, spleen n = 7; NKT2: lung n = 6, spleen n = 7; NKT17: lung

n = 7, spleen n = 6. For NKT$_{FH}$, n = 6, NKT$_{eff}$, n = 3. For lung cell types, NK: lung n = 3,

spleen n = 4; γδ T cells: lung n = 3, spleen n = 3; CD4$^+$ T cells: lung n = 3, spleen n = 5.

For bulk library preparation for sequencing we used the Smart-Seq2 protocol[47], adapted

for samples with small cell numbers. We followed the protocol as described previously[19,]

[47] with following modifications: (i) the pre-amplification PCR cycle was set between 17

to 23 cycles; (ii) to eliminate any traces of primer-dimers, the PCR pre-amplified cDNA

product was purified using 0.8x Ampure-XP beads (Beckman Coulter) before using the

DNA for sequencing library preparation. One ng of pre-amplified cDNA was used to

generate barcoded Illumina sequencing libraries (Nextera XT library preparation kit -

Illumina) in 8 µl reaction volume. Samples failing any quality control step (DNA quality

assessed by capillary electrophoresis (Fragment analyzer, Advance analytical) and

quantity (Picogreen quantification assay, Thermofisher) were eliminated from further

downstream steps[19]. Libraries were then pooled at equal molar concentration and

quantified (KAPA SYBR® FAST qPCR Kit - Roche)[19]. Samples from the experiment

comparing splenic NKT_{FH} and NKT_{eff} cells from αGalCer-challenged mice with

unchallenged splenic iNKT cells were sequenced via a 100 x 100 bp paired-end read

strategy using the NovaSeq6000 sequencing platform (NovaSeq 6000 S4 P200 kits -

Illumina). Sequencing for all other samples was performed according to a 50 bp single-

end strategy using the HiSeq2500 sequencer (HiSeq SBS Kit v4; Illumina). Post-

sequencing, stringent quality controls were applied and samples that failed quality

control standards were eliminated from further analysis[19]. Samples we sequenced to

obtain at least 8 million uniquely mapped reads.

The single-end reads that passed Illumina filters were filtered for reads aligning to tRNA,

rRNA, adapter sequences, and spike-in controls. The reads were then aligned to mm10

reference genome using TopHat (v 1.4.1)[48]. DUST scores were calculated with

PRINSEQ Lite (v 0.20.3)[49] and low-complexity reads (DUST > 4) were removed from

the BAM files. The alignment results were parsed via the SAMtools[50] to generate SAM

files. Read counts to each gene were obtained with the htseq-count program (v 0.7.1)[51]

using the "union" option. After removing absent features (zero counts in all samples),

the raw counts were then imported in most cases to the R/Bioconductor package

DESeq2 (v 1.6.3)[52] to identify differentially expressed genes among samples, with P-

values for differential expression calculated using the Wald test for differences between

the base means of two conditions. For the analysis of iNKT samples collected after in

vivo stimulation, the R/Bioconductor package EdgeR was used, and P values were

determined using the quasi-likelihood F test. For determination of signature genes of

specific iNKT subsets, we included genes that exhibited a 2-fold or greater expression

difference with a P value of ≤0.1 in all pairwise comparisons between the given subset

and the other two subsets in each of the organs from which all three subsets were

collected (thymus, spleen and lung). Similarly, the signature genes of spleen, lung and

thymus were defined as those genes exhibiting a fold change of ≥2 with a P value of

≤0.1 in all possible comparisons between the same iNKT subset from different organs.

Signature genes of splenic iNKT populations that either expressed or lacked the FH

markers PD-1 and CXCR5 after αGalCer stimulation were determined in a similar

fashion, except that P-values were adjusted for multiple test correction using Benjamini

Hochberg algorithm[50], and both stimulated populations were also compared to

unchallenged total splenic iNKT. Principal Component Analysis (PCA) was performed

using the 'prcomp' function in R. The sequences used in this article will be submitted to

the Gene Expression Omnibus and the accession number will be reported prior to

publication (http://www.ncbi.nlm.nih.gov/geo/). Data were also analyzed using the Pre-

ranked Gene Set Enrichment Analysis algorithm (Broad Institute and University of

California), as well as the Consensus Path Database platform (Max Planck Institute).

ATAC-seq

ATAC-seq was performed as previously described with some modifications[13]. For

thymic subsets, n = 4 (NKT1), n = 4 (NKT2), n = 3 (NKT17). For peripheral subsets,

NKT1: lung n = 3, liver n = 2, spleen n = 2; NKT2: lung n = 1, spleen n = 2; NKT17: lung

n = 2, spleen n = 2. For NKT_{FH}, n = 6, NKT_{eff}, n = 3. For lung cell types, NK: lung n = 1,

spleen n = 2; $\gamma\delta$ T cells: lung n = 2, spleen n = 3; $CD4^+$ T cells: lung n = 2, spleen n = 3.

iNKT cells or lung lymphocytes (10,000) were sorted into 1.5 mL Eppendorf tubes

containing PBS with 5% FCS. Cells were centrifuged at 600g for 10 minutes at 4°C,

washed with 50 μL PBS, then resuspended in 50 μL ATAC lysis buffer (10 mM Tris pH

7.5, 10 mM NaCl, 3 mM $MgCl_2$, 0.1% NP-40). Cells were centrifuged in lysis buffer for

10 minutes at 600g, 4°C. Following lysis, the pellet was resuspended in 50 μL ATAC

reaction mix (25uL 2X TD buffer, 2.5 μL Nextera Enzyme, 22.5 μL water, Illumina). The

transposase reaction was carried out at 37°C for 30 minutes. Libraries were amplified

using a KAPA HiFi real-time library amplification kit with barcoded primers for 11-12

cycles followed by 2x50 cycle paired-end sequencing. Reads were mapped to mouse

genome (mm9) using bowtie. Unmapped reads were processed with trim galore, re-

mapped with bowtie and merged with previous mapping output. Duplicate reads

identified by picard MarkDuplicates and reads mapping to chrM were excluded. Wiggle

files of coverage for individual replicates were computed with MEDIPS[51] using full

fragments captured by ATAC-seq on 10 bp windows and used to generate average

coverage with the Java Genomics Toolkit (available

at: https://github.com/timpalpant/java-genomics-toolkit) for each group. Accessible

regions were identified using MACS2[52] from individual replicate bam files downsampled

to a maximum of 5 million reads and limited to a q value of less than 0.001. Peaks that

intersected ENCODE blacklisted regions and those on chromosome Y were excluded.

We refined the groups of accessible regions to non-overlapping peaks with a uniform

width of 500 nucleotides with the readNarrowpeaks function from chromVAR[53]. The

number of reads within each region was computed using all reads from each replicate

with the getCounts function from chromVAR. Differentially accessible regions were

identified with limma/voom, using quantile normalized counts, and selected based on an

fdr adjusted p value of less than 0.1 and an estimated fold change of at least 4. We

associated transcription factors binding motifs from the HOMER database by

determining the enrichment of motifs in groups of peaks with HOMER and comparing

the variability in ATAC-seq signal with chromVAR.

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Author Contributions

M.P.M., I.E. and G.S. designed and performed experiments and analyzed data. S.H.M.,

S.L.R. and G-Y.S. performed experiments. A.S., A.L.R.P. and J.G. analyzed the RNA-

seq data. P.V. designed the study. J.S.B. analyzed the ATAC-seq data. M.P.M and

M.K. wrote the manuscript. J.S.B and M.K. supervised the project, designed the study,

and analyzed data.

Competing interests

The authors declare no competing interests.

References

1.   Mori, L., Lepore, M. & De Libero, G. The Immunology of CD1- and MR1-Restricted T
660   Cells. *Annu Rev Immunol* **34**, 479-510 (2016).
661
662   2.   Godfrey, D.I. & Kronenberg, M. Going both ways: Immune regulation via CD1d-
663   dependent NKT cells. *Journal of Clinical Investigation* **114**, 1379-1388 (2004).
664
665   3.   Verykokakis, M., Zook, E.C. & Kee, B.L. ID'ing innate and innate-like lymphoid cells.
666   *Immunol Rev* **261**, 177-197 (2014).
667

668　4.　Godfrey, D.I., Koay, H.F., McCluskey, J. & Gherardin, N.A. The biology and functional
669　　　importance of MAIT cells. *Nat Immunol* **20**, 1110-1128 (2019).
670

671　5.　Godfrey, D.I., Uldrich, A.P., McCluskey, J., Rossjohn, J. & Moody, D.B. The burgeoning
672　　　family of unconventional T cells. *Nat Immunol* **16**, 1114-1123 (2015).
673

674　6.　Lee, Y. *et al.* Tissue-Specific Distribution of iNKT Cells Impacts Their Cytokine
675　　　Response. *Immunity* **43**, 566-578 (2015).
676

677　7.　Lee, Y. *et al.* Lineage-Specific Effector Signatures of Invariant NKT Cells Are Shared
678　　　amongst γδ T, Innate Lymphoid, and Th Cells. *The Journal of Immunology* **197**, 1460-
679　　　1470 (2016).
680

681　8.　Engel, I. *et al.* Innate-like functions of natural killer T cell subsets result from highly
682　　　divergent gene programs. *Nature Immunology* **17**, 728-739 (2016).
683

684　9.　Crosby, C.M. & Kronenberg, M. Tissue-specific functions of invariant natural killer T
685　　　cells. *Nat Rev Immunol* **18**, 559-574 (2018).
686

687　10.　Lynch, L. *et al.* Regulatory iNKT cells lack expression of the transcription factor PLZF
688　　　and control the homeostasis of Treg cells and macrophages in adipose tissue. *Nature
689　　　Immunology* **16**, 85-95 (2015).
690

691　11.　Salou, M. *et al.* A common transcriptomic program acquired in the thymus defines tissue
692　　　residency of MAIT and NKT subsets. *J Exp Med* **216**, 133-151 (2019).
693

694　12.　Georgiev, H., Ravens, I., Benarafa, C., Forster, R. & Bernhardt, G. Distinct gene
695　　　expression patterns correlate with developmental and functional traits of iNKT subsets.
696　　　*Nat Commun* **7**, 13116 (2016).
697

698　13.　Buenrostro, J.D., Giresi, P.G., Zaba, L.C., Chang, H.Y. & Greenleaf, W.J. Transposition
699　　　of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-
700　　　binding proteins and nucleosome position. *Nature Methods* **10**, 1213-1218 (2013).
701

702　14.　Scott-Browne, J.P. *et al.* Dynamic Changes in Chromatin Accessibility Occur in CD8+ T
703　　　Cells Responding to Viral Infection. *Immunity* **45**, 1327-1340 (2016).
704

705　15.　Scharer, C.D., Bally, A.P., Gandham, B. & Boss, J.M. Cutting Edge: Chromatin
706　　　Accessibility Programs CD8 T Cell Memory. *J Immunol* **198**, 2238-2243 (2017).
707

708　16.　Lee, D.U., Avni, O., Chen, L. & Rao, A. A Distal Enhancer in the Interferon-γ (IFN-γ)
709　　　Locus Revealed by Genome Sequence Comparison. *Journal of Biological Chemistry* **279**,
710　　　4802-4810 (2004).
711

712　17.　Berga-Bolanos, R., Zhu, W.S., Steinke, F.C., Xue, H.H. & Sen, J.M. Cell-autonomous
713　　　requirement for TCF1 and LEF1 in the development of Natural Killer T cells. *Mol*
714　　　*Immunol* **68**, 484-489 (2015).
715

716　18.　Carr, T. *et al.* The transcription factor lymphoid enhancer factor 1 controls invariant
717　　　natural killer T cell expansion and Th2-type effector differentiation. *J Exp Med* **212**, 793-
718　　　807 (2015).
719

720　19.　Rosales, S.L. *et al.* A Sensitive and Integrated Approach to Profile Messenger RNA from
721　　　Samples with Low Cell Numbers. *Methods Mol Biol* **1799**, 275-302 (2018).
722

723　20.　Lazarevic, V. *et al.* The gene encoding early growth response 2, a target of the
724　　　transcription factor NFAT, is required for the development and maturation of natural
725　　　killer T cells. *Nat Immunol* **10**, 306-313 (2009).
726

727　21.　Aliahmad, P. & Kaye, J. Development of all CD4 T lineages requires nuclear factor
728　　　TOX. *J Exp Med* **205**, 245-256 (2008).
729

730　22.　Chen, Y.G. *et al.* CD38 is required for the peripheral survival of immunotolerogenic
731　　　CD4+ invariant NK T cells in nonobese diabetic mice. *J Immunol* **177**, 2939-2947
732　　　(2006).
733

734　23.　Huynh, H., Ng, C.Y., Ong, C.K., Lim, K.B. & Chan, T.W. Cloning and characterization
735　　　of a novel pregnancy-induced growth inhibitor in mammary gland. *Endocrinology* **142**,
736　　　3607-3615 (2001).
737

738　24.　Tsagaratou, A. *et al.* TET proteins regulate the lineage specification and TCR-mediated
739　　　expansion of iNKT cells. *Nat Immunol* **18**, 45-53 (2017).
740

741　25.　Best, J.A. *et al.* Transcriptional insights into the CD8(+) T cell response to infection and
742　　　memory T cell formation. *Nat Immunol* **14**, 404-412 (2013).
743

744　26.　Chang, P.-P. *et al.* Identification of Bcl-6-dependent follicular helper NKT cells that
745　　　provide cognate help for B cell responses. *Nature Immunology* **13**, 35-43 (2011).
746

747　27.　Gaya, M. *et al.* Initiation of Antiviral B Cell Immunity Relies on Innate Signals from
748　　　Spatially Positioned NKT Cells. *Cell* **172**, 517-1082130432 (2018).
749

750　28.　Choi, Y.S. *et al.* LEF-1 and TCF-1 orchestrate T(FH) differentiation by regulating
751　　　differentiation circuits upstream of the transcriptional repressor Bcl6. *Nat Immunol* **16**,
752　　　980-990 (2015).
753

754　29.　Yu, F., Sharma, S., Edwards, J., Feigenbaum, L. & Zhu, J. Dynamic expression of
755　　　transcription factors T-bet and GATA-3 by regulatory T cells maintains
756　　　immunotolerance. *Nat Immunol* **16**, 197-206 (2015).
757

758 30. Shimizu, K. *et al.* Eomes transcription factor is required for the development and
759   differentiation of invariant NKT cells. *Commun Biol* **2**, 150 (2019).
760
761 31. Shimizu, K. *et al.* KLRG+ invariant natural killer T cells are long-lived effectors. *Proc
762   Natl Acad Sci U S A* **111**, 12474-12479 (2014).
763
764 32. Chen, Z. *et al.* Memory Follicular Helper Invariant NKT Cells Recognize Lipid Antigens
765   on Memory B Cells and Elicit Antibody Recall Responses. *J Immunol* **200**, 3117-3127
766   (2018).
767
768 33. Wang, H. & Hogquist, K.A. CCR7 defines a precursor for murine iNKT cells in thymus
769   and periphery. *Elife* **7** (2018).
770
771 34. Pellicci, D.G. *et al.* A Natural Killer T (NKT) Cell Developmental Pathway Involving a
772   Thymus-dependent NK1.1−CD4+ CD1d-dependent Precursor Stage. *The Journal of
773   Experimental Medicine* **195**, 835-844 (2002).
774
775 35. Jimeno, R. *et al.* Tissue-specific shaping of the TCR repertoire and antigen specificity of
776   iNKT cells. *Elife* **8** (2019).
777
778 36. Gioulbasani, M. *et al.* The transcription factor BCL-6 controls early development of
779   innate-like T cells. *Nat Immunol* **21**, 1058-1069 (2020).
780
781 37. Hayward, S.L. *et al.* Environmental cues regulate epigenetic reprogramming of airway-
782   resident memory CD8(+) T cells. *Nat Immunol* **21**, 309-320 (2020).
783
784 38. Lavin, Y. *et al.* Tissue-resident macrophage enhancer landscapes are shaped by the local
785   microenvironment. *Cell* **159**, 1312-1326 (2014).
786
787 39. Carreau, A., El Hafny-Rahbi, B., Matejuk, A., Grillon, C. & Kieda, C. Why is the partial
788   oxygen pressure of human tissues a crucial parameter? Small molecules and hypoxia. *J
789   Cell Mol Med* **15**, 1239-1253 (2011).
790
791 40. O'Dwyer, D.N., Dickson, R.P. & Moore, B.B. The Lung Microbiome, Immunity, and the
792   Pathogenesis of Chronic Lung Disease. *J Immunol* **196**, 4839-4847 (2016).
793
794 41. Halder, R.C. *et al.* Self-glycerophospholipids activate murine phospholipid-reactive T
795   cells and inhibit iNKT cell activation by competing with ligands for CD1d loading. *Eur J
796   Immunol* **49**, 242-254 (2019).
797
798 42. Sullivan, B.A. *et al.* Mechanisms for glycolipid antigen-driven cytokine polarization by
799   Valpha14i NKT cells. *J Immunol* **184**, 141-153 (2010).
800
801 43. Parekh, V.V. *et al.* Glycolipid antigen induces long-term natural killer T cell anergy in
802   mice. *J Clin Invest* **115**, 2572-2583 (2005).
803

804   44.   Fujii, S., Shimizu, K., Kronenberg, M. & Steinman, R.M. Prolonged IFN-gamma-
805   producing NKT response induced with alpha-galactosylceramide-loaded DCs. *Nat*
806   *Immunol* **3**, 867-874 (2002).
807
808   45.   Sag, D., Krause, P., Hedrick, C.C., Kronenberg, M. & Wingender, G. IL-10–producing
809   NKT10 cells are a distinct regulatory invariant NKT cell subset. *Journal of Clinical*
810   *Investigation* **124**, 3725-3740 (2014).
811
812   46.   Netea, M.G. *et al.* Trained immunity: A program of innate immune memory in health and
813   disease. *Science* **352**, aaf1098 (2016).
814
815   47.   Picelli, S. *et al.* Smart-seq2 for sensitive full-length transcriptome profiling in single
816   cells. *Nat Methods* **10**, 1096-1098 (2013).
817
818   48.   Trapnell, C., Pachter, L. & Salzberg, S.L. TopHat: discovering splice junctions with
819   RNA-Seq. *Bioinformatics* **25**, 1105-1111 (2009).
820
821   49.   Schmieder, R. & Edwards, R. Quality control and preprocessing of metagenomic
822   datasets. *Bioinformatics* **27**, 863-864 (2011).
823
824   50.   Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**,
825   2078-2079 (2009).
826
827   51.   Anders, S., Pyl, P.T. & Huber, W. HTSeq--a Python framework to work with high-
828   throughput sequencing data. *Bioinformatics* **31**, 166-169 (2015).
829
830   52.   Love, M.I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion
831   for RNA-seq data with DESeq2. *Genome Biol* **15**, 550 (2014).
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Data Availability Statement

Sequence data that support the findings of this study will be deposited in the Gene

Expression Omnibus and the accession codes will be provided prior to publication.

ATAC-seq sequence data associated figures: Figure 1; Figure 2a, b, c; Figure 3 a, c;

Figure 4a; Figure 5 a, b, c; Figure 6b.

RNA-seq sequence data associated figures: Figure 2d; Figure 3b; Figure 4 b, c, d, e;

Figure 5 d, e, f; Figure 6a; Supplementary Figure 2; Supplementary Figure 3;

Supplementary Figure 4 c, d.

There are no restrictions on data availability. Additional information and materials will

be made available upon request.

859 **Figures**

Fig. 1. Subsets of thymic iNKT cells have differences in chromatin accessibility. a.
Scatterplot of mean ATAC-seq counts per peak comparing differentially accessible
regions of chromatin for pairs of thymic iNKT cell subsets. Colors indicate differentially
accessible regions defined by limma/voom (details in Methods). The numbers of
differentially expressed genes are indicated. b. ATAC-seq coverage at the indicated
gene loci with a range of 0-600 for all samples. Grey bar in the upper left panel (*Ifng*)
locus indicates enhancer region. c. Left, *k*-means clustering of relative ATAC-seq
density (counts per million mapped reads/kb, log$_2$ fold change from the mean) identifies
eight groups of accessible regions that varied similarly (rows), 3 sets for NKT1, 2 for
NKT2 and 3 for NKT17. Columns indicate number of replicates, 3 or 4. d. Motifs
enriched in enriched in clusters of accessible regions. All motifs with a HOMER log p-
value less than –15 and found in 10% or more regions in at least one cluster are shown.

Fig. 2. Imprint of tissue location is minor compared to subset. a. Scatterplot of
mean ATAC-seq counts per peak comparing differentially accessible regions of
chromatin for pairs of iNKT cell subsets in spleen. Colors indicate differentially
accessible regions defined by limma/voom (details in Methods). b. Boxplot of
normalized average ATAC-seq counts per peak from the indicated samples (labeled at
bottom) at differentially-accessible regions that distinguish thymic iNKT cell subsets.
Box indicates interquartile range with whiskers +/−1.5 times this range and outlier points
indicated. c, d. PCA display of ATACseq (c) and RNA-seq (d) data from the indicated
iNKT cell subsets from the different tissues. e. Heat map of normalized reads from
RNA-seq for genes (19) differentially regulated in thymus versus peripheral iNKT cell
subsets, within all subsets, n > 2-fold difference, p = 0.1.

Fig. 3. Lung-specific transcriptome and epigenome. a. PC1 by PC3 display of ATAC-seq data showing distribution of iNKT cell subsets from different tissues. b. Heat map of relative RNA expression of selected AP-1 and ATF family genes in iNKT subsets from the indicated sites. c. chromVAR computed deviation in ATAC-seq signal (Z-score) at regions containing indicated transcription factor motifs. Motifs with a p-value less than 1e-25 are shown and families and representative members are labeled. Samples are indicated at the bottom, iNKT cell subsets from the lung are boxed to highlight lung-enriched motifs. d. Total CTLA-4 expression in permeabilized iNKT cells from the indicated tissues. Representative cytogram of total iNKT cells (left) and percent CTLA-4$^+$ cells within each subset from the different organs (right). Symbols depict individual mice, error bars depict SD. Data are combined from five experiments, n = 8 mice, statistical significance assessed via Kruskal-Wallis test. e. Total CTLA-4 expression in permeabilized total iNKT cells from indicated tissues. Symbols depict individual mice, error bars depict SD, n = 8 mice from two independent experiments. Statistical significance assessed via one-way ANOVA.

Fig. 4. Lung signature extends to other lung populations. a. chromVAR computed deviation in ATAC-seq signal (Z-score) at regions containing indicated transcription factor motifs between the indicated cell populations from spleen and lung. Motifs with a p-value less than 1e-25 are shown and families and representative members are labeled. Tissue source of the samples indicated at the bottom of the diagram; columns indicate number of replicates. b. PCA of RNA-seq data comparing lymphoid cell types isolated from lung and spleen. c. Heat map depicting the lung gene signature from Supplementary Fig. 3 with normalized transcript levels from RNA-seq data from the indicated cell types from lung and spleen. d. RNAseq read tracks in the *Bhlhe40*, *Tnfaip3* and *Fosl2* loci in samples from lung and spleen from indicated cell types. e. GSEA of pre-ranked comparisons of genes differentially expressed in lung iNKT cell subsets comparing each cell type within the lung to its counterpart in the spleen.

Fig. 5. Antigenic experience shapes the transcriptome and chromatin landscape of iNKT cells. iNKT cells from αGalCer-injected mice either selected for PD-1 and CXCR5 expression (NKT_FH) and or negative for both markers (NKT_eff) were sorted from the spleen of mice 6 days after injection (i.v.) with αGalCer. a. Scatterplots of mean ATAC-seq counts per peak comparing antigen experienced NKT_FH and NKT_eff (top left)

or pairwise comparisons of differentially accessible regions of chromatin for each of the
sorted populations from antigen exposed mice compared to the corresponding subsets
from unimmunized mice. Data from unimmunized mice are the same as depicted in Fig.
2. Colors indicate differentially accessible regions defined by limma/voom (details in
Methods). b. ATAC-seq coverage (range of 0-600 for all samples) comparing the *Il21*
and *Cd247* loci from unimmunized splenic iNKT cell subsets, splenic NK cells, and
NKT_{FH} and NKT_{eff} from αGalCer-treated mice. NFAT ChIP-seq analysis of CD8$^+$ splenic
T cells with and without PMA/ionomycin stimulation included for comparison[54]. c. Left, *k*-
means clustering of relative ATAC-seq density (counts per million mapped reads/kb,
log$_2$ fold change from the mean) identifies ten groups of accessible regions that vary
similarly (rows), 2 sets for splenic NKT1, 2 for splenic NKT2, 2 for splenic NKT17, 6 for
NKT_{FH} and 3 for NKT_{eff}. Columns indicate number of replicates. Right, motifs enriched
in clusters of accessible regions. All motifs with a HOMER log p-value less than –15 and
found in 10% or more regions in at least one cluster are shown. d. PCA analysis of
RNA-seq data comparing NKT_{FH} to NKT_{eff} from αGalCer-immunized mice as well as to
total iNKT cells from unimmunized mice. e. PCA analyses of RNA-seq data comparing
splenic NKT1, NKT2 or NKT17 samples to spleen NKT_{FH} cells. f. Top: Plot of the
distribution of genes upregulated in mainstream GC T_{FH} vs T_{H1} in a list of genes ranked
by relative expression (directional p value) in NKT_{FH} vs splenic NKT1 cells using GSEA.
Bottom (left and right): Plots of genes differentially regulated between CD8$^+$ effector vs
memory against a directional p-ranked file comparing αGalCer-stimulated NKT_{FH} vs
NKT_{eff}. Normalized Enrichment Scores (NES) and q values were determined by the
pre-ranked GSEA algorithm. g. Expression of reporter in T-bet fate-mapping mice by
NKT_{FH} and NKT_{eff} cells 6 days-post antigen exposure, and NKT1 and NKT2 cells and
total iNKT cells from unstimulated mice; n = 6 mice per group, error bars depict SEM.
Quantification on right, statistical significance assessed via Kruskal-Wallis test.

Fig. 6. Enhanced effector or NK cell signature in antigen-exposed iNKT cells. a. ATAC-seq coverage (with a range of 0-600 for all samples) at the *Gzma*, *Gzmb* and *Spry2* loci comparing untreated splenic iNKT cells subsets, spleen NK cells, NKT_FH and NKT_eff from mice injected 6 days earlier with αGalCer. NFAT1 ChIP-seq analysis of CD8^{+} T cells with and without PMA/ionomycin stimulation included for comparison[54]. b. Flow cytometry analysis of expression of KLRG1 and CX3CR1 by the indicated populations of gated spleen iNKT cells at day 6 after antigen. Quantification on right, n = 11 mice (αGalCer challenged, KLRG1), n = 12 mice (αGalCer challenged, CXCR3), n = 6 mice (unstimulated, KLRG1), n = 8 mice (unstimulated, CXCR3), n = 11-12 mice (NKT_FH). c. Representative flow cytometry analysis of expression of NKT_eff markers CX3CR1 and KLRG1 by gated spleen PD-1^{-} KLRG1^{-} iNKT cells at day 30 or later after antigen administration. Quantification of iNKT cells expressing NKT_eff markers, challenged mice analyzed at day 30 or later on right, n = 8 mice (αGalCer challenged, NKT_FH), n = 7 mice (unstimulated). b,c. Representative data from 3-5 experiments, error bars depict SEM, statistical significance assessed via Kruskal-Wallis test.