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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Human clinical data captured using the Datafax system
Data analysis	Flow Cytometry data analyzed by FlowJo, Statistical analysis all conducted using GraphPad Prism.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Provide your data availability statement here.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No prior sample size calculations were performed for human studies. For the blood analysis, similar sample numbers were used as in previous studies reporting statistical differences between blood ILC populations (Kloverpris et al. Immunity 2015). For lung analysis, samples represent those collected over a 3 study period. For animal studies, sample sizes were chosen following empirical statistical power analysis based on previous pilot studies (Khader et al. 2007 Nat Immunol, Griffiths et al, 2016 etc).
Data exclusions	No human blood samples were excluded from analysis. Human lung samples were excluded if <10,000 viable CD45+ve leukocytes were detected by flow cytometry following sample processing. This was based on previous experience with lung tissue and was done prior to additional analysis steps. 6 lung sample in total were excluded on this basis.
Replication	For animal studies, all attempts at replication were successful.
Randomization	Human subjects divided into those with active TB, previous TB or non-TB controls as reported in the manuscript. For animal studies, no method of randomization was used.
Blinding	Blinding was not possible for human subjects due to the nature of sample collection and processing. For animal studies, J.R-M. was blinded during the histological analyses.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	All the antibodies used in human and mouse experiment is reported in methods in the "Flow cytometry" sections.
Validation	All antibodies commercially available flow cytometry antibodies for staining primary human or mouse samples and validated by the manufacturer. All antibodies titrated in house and compatibility with the flow panel confirmed by FMO staining.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	The description of research animals used is reported in the methods in the "Mice" section.
Wild animals	*Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*

Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*

Human research participants

Policy information about studies involving human research participants

Population characteristics	For human PBMC samples - CUBS: n= 50; Median age 35 years (IQR 29-45); 66% female; 54% HIV infected; 80% on ARV at time of sampling; all drug susceptible TB infected subjects treatment naive at the time of sampling; all subjects with drug resistant TB on first line TB therapy at the time of sampling. FRESH: n=18; Median age 20 years (IQR 18-23); 100% female; all HIV negative by nucleic acid test; non-pregnant, non-anemic and with no signs and symptoms of chronic illness (reported in Dong et al, Lancet HIV 2017, https://doi.org/10.1016/S2352-3018(17)30146-7) For human TB lung samples n=30; Median age 39 years (IQR 31-61); 43% female; 57% HIV positive all on ART therapy, all subjects with previous TB on precautionary Rifafour TB treatment at the time of surgery. Treatment of active TB cases varied on a case by case basis depending on drug susceptibility and patient status. TB pathology confirmed by pathologist. Non-TB lung Samples n=5; Median 31 (IQR 24-55); 45% female, all HIV negative, negative TB status/cancer diagnosis confirmed by pathologist.
Recruitment	Human PBMC samples CUBS (TB infected): Participants are recruited from hospitals, primary health care clinics, HIV testing and counseling sites, HIV treatment clinics, universities and other relevant health care sites in KwaZulu Natal, South Africa. The relevant authorizations and approvals for each site was acquired before implementation of this protocol. Participants were identified by the research nurse based the eligibility criteria. The enrolling research team member then discussed the purpose of the study with the participant and they are asked to read and sign the consent form prior to recruitment. Clinical data was collected from participants and medical chart review. If HIV status is not known, participants may be referred for HIV counseling and testing. Participants who were on site were reimbursed R80 for participation. If the participants were required to travel to return for subsequent sample collection, they were reimbursed R150. FRESH (TB negative, HIV negative): Eligible women were HIV uninfected, aged 18-23 years, sexually active, not pregnant, non-anaemic, without other barriers to participation (serious chronic illness, enrollment in another study, or family responsibilities), and gave written consent to enrollment. More details of cohort can be found in Dong et al Lancet HIV 2017 (https://doi.org/10.1016/S2352-3018(17)30146-7) LUNG: Particpants are recruited from two sites based in Durban, South Africa; namely Inkosi Albert Luthuli Central Hospital (IALCH) and King Dinizulu Hospital Complex (KHDC). Collaborating surgeons identified individuals who are scheduled to have thoracocentesis and/or surgical procedures where lung tissue is excised. The enrolling research team member then contacted the potential participants to discuss the purpose of the study. This is conducted in the language that the participant is most comfortable with. The participant is asked to read and sign the consent form prior to recruitment. In the event that consent may not be acquired prior to the surgical procedure (e.g. emergency surgery), consent is obtained post-operatively. A copy of the informed consent document is given to the participants to keep. Participants are not reimbursed.

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Sample preparation is described in methods in the "Flow cytometry" section.
Instrument	Human cells were acquired on a 4 laser BD Fortessa flow cytometer (CUBS and FRESH blood samples) or a 5 laser FACSARIA Fusion (Lung, chemokine and apoptosis experiment samples) within 24 hours of processing. Mouse samples were acquired in Becton Dickinson (BD) Fortessa flow cytometer using FACS Diva software.
Software	All Human and mouse FACS data were analysed using FlowJo (TreeStar).
Cell population abundance	For sorting of human lung ILCs, a test lung sample was sorted and purity checked by re-acquiring sorted ILC population. Purity of

Cell population abundance	test sort was >95%. Subsequent sorts were not checked for purity due to low cell numbers, however, cell sorter (FACS ARIA) performance assessed before each sorting run using CST beads as per manufacturers instructions.
Gating strategy	For human flow cytometry experiments' singlets were gated based by plotting FSC-H vs FSC-A and then sub-gated on lymphocyte using FSC vs SSC characteristics. ILC populations were then identified using the antibody panels described in the text and in Extended figure 1. Positive gates where set using unstained control cells. For mouse experiments, gating strategy is reported in the text and also in the extended figure 3. Percentages of different cell types were gated based on both published strategies for APC cell types (Griffiths et al, 2016; Treerat et al, 2017) and ILC subsets gating is shown in Extended figure 3. Total cells per subset/lung were back calculated based on lung cell numbers.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.