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In vivo inhibition of tryptophan catabolism reorganizes the tuberculoma and augments immune-mediated control of *Mycobacterium tuberculosis*

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Mycobacterium tuberculosis continues to cause devastating levels of mortality due to tuberculosis (TB). The failure to control TB stems from an incomplete understanding of the highly specialized strategies that *M. tuberculosis* utilizes to modulate host immunity and thereby persist in host lungs. Here, we show that *M. tuberculosis* induced the expression of indoleamine 2,3-dioxygenase (IDO), an enzyme involved in tryptophan catabolism, in macrophages and in the lungs of animals (mice and macaque) with active disease. In a macaque model of inhalation TB, suppression of IDO activity reduced bacterial burden, pathology, and clinical signs of TB disease, leading to increased host survival. This increased protection was accompanied by increased lung T cell proliferation, induction of inducible bronchus-associated lymphoid tissue and correlates of bacterial killing, reduced checkpoint signaling, and the relocation of effector T cells to the center of the granuloma. The enhanced killing of *M. tuberculosis* in macrophages in vivo by CD4⁺ T cells was also replicated in vitro, in cocultures of macaque macrophages and CD4⁺ T cells. Collectively, these results suggest that there exists a potential for using IDO inhibition as an effective and clinically relevant host-directed therapy for TB.

macaque | tuberculosis | granuloma | IDO | T cell

There is an urgent need to improve antitubercular treatment strategies. Tuberculosis (TB) continues to result in close to two million deaths worldwide on an annual basis, and is the single biggest killer of AIDS patients (1). Additionally, ~10% of newly diagnosed patients exhibited disease with some resistance to anti-TB drugs, ranging from multidrug-resistant to extensively drug-resistant TB (2). The failure to control TB stems from the lack of relatively poor understanding of both pathogenesis and the host factors that contribute to the susceptibility of TB disease. However, nonhuman primates (NHPs) recapitulate the complete breadth of the lung pathology and granulomatous responses that are emblematic of human disease (3). The granuloma is the site of host–*Mycobacterium tuberculosis* interactions, which either result in acute infection or the control of infection in a latent state (4). *M. tuberculosis* modulates these immune interactions to inhibit mycobacterial killing and therefore promote long-term survival of the bacilli.

The expression of indoleamine 2,3-dioxygenase (IDO) is dramatically enhanced in macaque granulomata (5). IDO catabolizes Tryptophan (Trp) to kynurenine (Kyn) and other metabolites, and acts to suppress the immune response, particularly the CD4⁺ T cell production of IFN- γ (6). Induction of host IDO is a nascent strategy to starve pathogens of Trp, an essential amino acid (7). However, *M. tuberculosis* can synthesize its own Trp de novo (8), potentially an adaption for its survival during Trp catabolism by

IDO in host phagocytes. Therefore, IDO production has little effect on mycobacterial metabolism and yet impacts protective host immune responses.

Here we demonstrate that increased IDO1 expression correlates with higher bacterial burden. Furthermore, IDO is particularly enriched in the macrophage-rich inner layer of the granuloma (5). This spatial expression may prevent lymphocytes, which are predominant in the external layers of the granuloma, from reaching the infected phagocytes, and this inhibition may further promote bacterial survival. We therefore hypothesize that the highly organized granulomas seen in NHPs and humans may be advantageous to *M. tuberculosis* due to this spatial exclusion

Significance

Mycobacterium tuberculosis induces the expression of the indoleamine 2,3-dioxygenase (IDO) enzyme, which catabolizes tryptophan. Tryptophan metabolites potentially suppress host immunity. The present study demonstrates that blockade of IDO activity reduces both clinical manifestations of tuberculosis (TB) as well as microbial and pathological correlates of the human TB syndrome in macaques. In granulomas, T cells localize in the periphery, and are unable to access the core, where bacilli persist. Inhibiting IDO activity altered granuloma organization such that more T cells translocated to the lesion core and exhibited highly proliferative signatures. Our results identify a highly efficient immunosuppressive mechanism at play in the granuloma environment that aids in *M. tuberculosis* persistence. The ability to modulate this pathway with safe and approved compounds could, however, facilitate chemotherapy-adjunctive host-directed therapy approaches for the control of TB.

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The authors declare no conflict of interest.

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Data deposition: The data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) database, <https://www.ncbi.nlm.nih.gov/geo> [accession nos. GPL10183 (macaque) and GPL7202 (murine)].

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of immune-protective lymphocytes. As such, the IDO pathway represents a potential target for host-directed therapy (HDT) to augment the control of TB.

Inhibitors of IDO activity [e.g., 1-methyl-tryptophan (1-MT, D-1MT)] are being evaluated as anticancer drugs. In this study, we demonstrated that D-1MT-mediated IDO inhibition resulted in somewhat increased *M. tuberculosis* killing, improved clinical signs of disease, increased lymphoid follicles and proliferation of pulmonary lymphocytes, and was associated with a drastic reorganization of the granuloma that allowed lymphocyte trafficking into the macrophage-tropic internal layers. These results lend significant credence to the utilization of IDO inhibitors as an HDT strategy adjunctive to anti-*M. tuberculosis* chemotherapy (9).

Results

IDO1 Is Expressed in a *M. tuberculosis* Burden-Dependent Manner in Infected Phagocytes and Experimental Hosts. We first studied whether IDO levels are induced in a *M. tuberculosis* burden-dependent manner. We found that IDO expression is induced in *M. tuberculosis*-infected murine (C3HeB/FeJ) bone marrow-derived macrophages (BMDMs) (Fig. 1A) and rhesus macaque BMDMs (Fig. 1B and Fig. S1) in vitro and in lungs of *M. tuberculosis*-infected C3HeB/FeJ mice (Fig. 1C and D). Furthermore, IDO expression levels were highly correlated with lung CFUs ($P = 0.02$, $r^2 = 0.68$) (Fig. 1E). We have recently shown that most animals with latent TB infection (LTBI) that were subsequently coinfecting with simian immunodeficiency virus (SIV), reactivated (10). In coinfecting animals, IDO levels largely

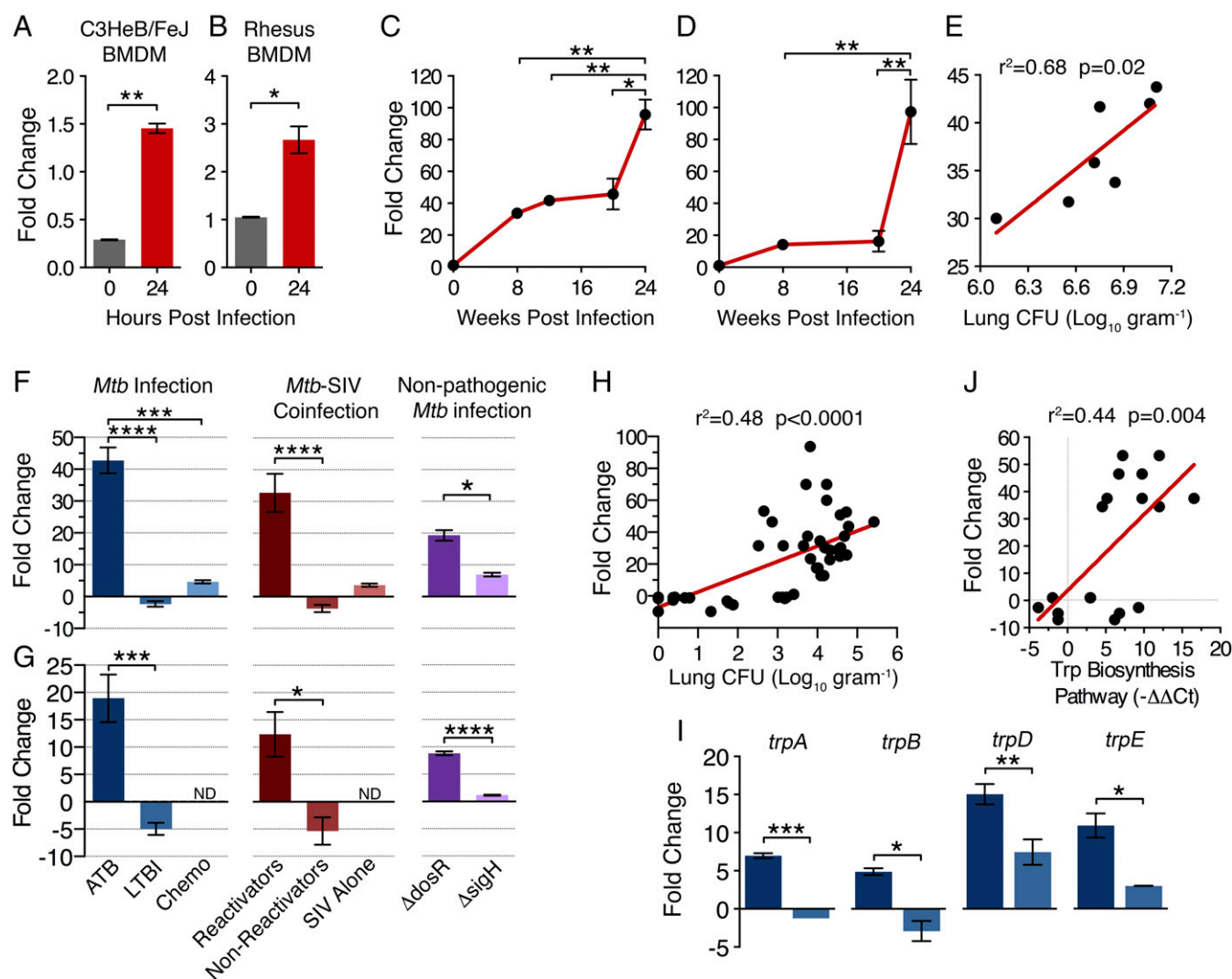


Fig. 1. Expression of IDO1 in vitro as well as in vivo experimental models of *M. tuberculosis* infection. IDO levels detected by qRT-PCR at 0 (gray) and 24 h (red) after *M. tuberculosis* infection relative to uninfected BMDMs from three biological replicates (A) C3HeB/FeJ mice (70) and (B) rhesus macaques (71). The average relative expression ($2^{-\Delta\Delta Ct}$) of IDO in C3HeB/FeJ mice lungs at weeks 8, 12–20, and 24 in respect to postday 1 (base line) *M. tuberculosis*-infected lungs by qRT-PCR (C) and microarray (D) (70). Linear regression ($r^2 = 0.68$, $P < 0.05$) plot of IDO1 expression correlates to bacillary load in C3HeB/FeJ mice lungs at weeks 8 and 12 obtained is from C (E). IDO expression in the lung of rhesus macaques with ATB (dark blue bars), LTBI (intermediate blue bars), chemotherapeutic treatment of ATB (light blue bars), or nonpathogenic *M. tuberculosis* infection (dark and light purple bars) by qRT-PCR (F) and microarray (G). IDO expression in *M. tuberculosis*-infected (dark blue bars), LTBI-coinfecting SIV lungs either exhibited a reactivation (dark brown bars) or nonreactivation phenotype (light brown bars) (10). IDO expression in lungs of rhesus macaques infected with nonpathogenic *Mtb* Δ dosR (dark purple bars) or *Mtb* Δ sigH (light purple bars) (11, 13). Linear regression ($r^2 = 0.48$, $P < 0.0001$) plot of IDO expression correlates to bacterial burdens in the lungs of rhesus macaques with ATB (24–37 d postinfection) and LTBI (166–180 d postinfection) (H). Expression of Trp biosynthetic pathway genes in ATB (dark blue) and LTBI (light blue) animals (I) and their linear regression with IDO expression levels in ATB and LTBI animals ($r^2 = 0.41$, $P < 0.005$) (J). Data are means \pm SEM, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$ using (A, B, and I) Student's *t* test, (E, H, and J) linear regression analysis, or (C, D, F, and G) one-way ANOVA.

D-1MT Treatment Improves the Clinical Outcomes and Reduces Lung Tissue Pathology. Macaques recapitulate several aspects of human TB including ATB and LTBI (5, 11–26), HIV coinfection-mediated reactivation TB (10, 15), as well as immune protection (5, 21). We tested the importance of IDO signaling in vivo in acutely infected macaques by treating the animals with D-1MT, a specific inhibitor of IDO activity. Treatment was initiated 1 wk after *M. tuberculosis* infection (Fig. S2). The progression of TB was significantly altered in treated macaques, as reflected by clinical outcomes (Fig. 2). Whereas all of the control animals had to be killed within 5 wk of *M. tuberculosis* infection, D-1MT-treated animals survived until 8 wk, exhibited significantly delayed kinetics, and lower levels of serum C reactive protein (CRP) compared with controls (Fig. 2A). Similarly, treated animals exhibited limited weight loss over time compared with control animals (Fig. 2B). This finding was consistent with the low bacterial burdens detected in treated animals (Fig. 2C–E). CFUs were determined from bronchoalveolar lavage (BAL) in two groups each at week 1 (the time when treatment was initiated), week 3 (i.e., 2 wk after treatment), and at the end point, at which time *M. tuberculosis* CFUs were also assessed in the lung tissues. The control animals exhibited significantly higher *M. tuberculosis* burdens ($P < 0.05$) in BAL at week 3 and in the terminal lung samples compared with the D-1MT-treated animals. BAL data are shown for at least three animals (Fig. 2C). However, the CFU levels in the BAL did not differ between the two groups at

week 1, before initiating treatment, indicating that the initial infections were similar (Fig. 2C). The total bacterial burdens in terminal lungs (Fig. 2D) and bronchial lymph node (BLN) (Fig. 2E) were significantly lower in D-1MT-treated animals than in the control animals (>1 log, $P < 0.05$). The bacterial burdens were also lower in liver, kidney, spleen in D-1MT-treated animals than controls (Fig. 2E). D-1MT-treated animals presented with fewer granulomas (Fig. 2F) relative to control animals (Fig. 2G) and exhibited significantly lower ($P < 0.005$) lung pathology (Fig. 2H). Hence, animals treated with D-1MT not only had better clinical outcomes (Fig. 2A and B) and reduced pathology (Fig. 2F and H), but also exhibited reduced bacterial burdens (Fig. 2C–E). Together, these results underscore our contention that, although active TB developed in all animals, the disease in D-1MT-treated animals progressed more slowly and to a lesser extent.

D-1MT Treatment Reduces the IDO Enzymatic Activity. The central area of the BAL cytospin that contained regular, monolayer-distributed cells, as confirmed by H&E staining (Fig. S2), was used for Kyn staining on samples obtained from D-1MT-treated and control animals at week 3. Kyn is one of the end products of IDO enzymatic activity. Numerous studies have implicated it in the immunosuppressive function of this signaling pathway (27). It is also known to be a ligand for the aryl hydrocarbon receptor signaling pathway (28). Confocal microscopy revealed greater levels of Kyn accumulation in controls, relative to D-1MT-treated animals (Fig. 3A). Furthermore, quantification revealed a highly significant ($P = 0.0001$) fourfold reduction in the average number of Kyn⁺ cells in D-1MT-treated animals (Fig. 3B). We also quantified absolute levels of Kyn and Trp in the plasma, a second measure of IDO activity by ELISA using pure standards, and calculated the Kyn/Trp ratio as an indirect measure of IDO activity (Fig. 3C). The two groups had virtually indistinguishable Kyn/Trp ratios at week 1 (i.e., before the initiation of treatment). In week 3 plasma samples, however, a significantly different ($P < 0.001$) Kyn/Trp ratio was observed between two groups. Both results suggest that D-1MT treatment inhibits IDO enzyme activity (> 95% reduction) (Fig. 3C). The effect of D-1MT on IDO enzymatic activity could also be observed in the treated group of animals at later stages (up to week 8) during the infection (Fig. S2B). These results establish that the changes in disease progression in D-1MT-treated animals were correlated with inhibition of IDO.

Effect of the in Vivo Modulation of IDO Signaling on T Cell Phenotype. We phenotyped mononuclear cells isolated from dematricized lung and BAL from the end point. Using these samples, we assessed temporal changes in both T cell numbers and T cell phenotypes in the lungs. BAL data at the end point was compared between two groups (Fig. 3 *D–H*), as previously described (10–13, 16, 20–23). The quantification of memory subsets was established for T cell populations based on CD28 and CD95 coexpression for which a representative flow cytometry plot and

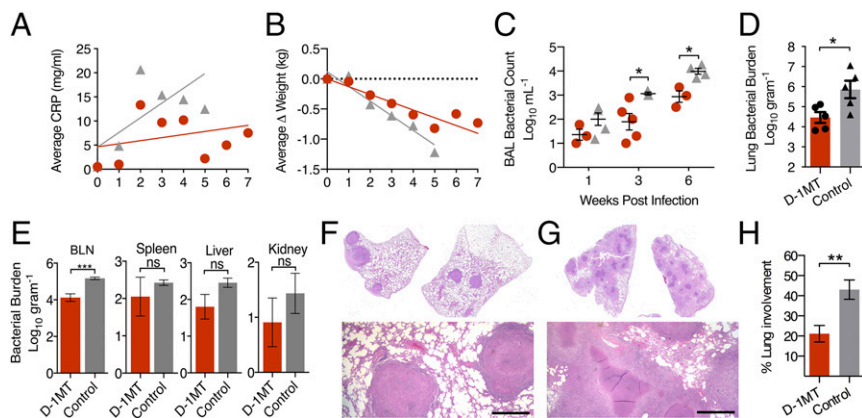


Fig. 2. Clinical, microbiology and pulmonary pathology measures of infection and disease in control and D-1MT-treated macaques. Linear regression of serum CRP ($\mu\text{g/ml}$) between two groups (A). Linear regression of weight change over the course of time (weeks postinfection) between two groups: D-1MT-treated (orange circle), control (gray circle) (B). (C–E) Bacterial burdens detected by CFU assay in BAL (C), per gram of lung tissues (D), and per gram tissue for each BLN, spleen, liver, and kidney (E). Subgross H&E staining of lung sections from D-1MT (F) and control animals (G). (Scale bars, 250 μm .) Morphometric measure of TB-related total lung pathology (H). At least three systematic random microscopic fields from each lung, representing all lung lobes, from at least two of the animals in every group, were used for the morphometric analysis of histopathology. Data are means \pm SEM, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ using (C) one-way ANOVA with Bonferroni post correction or (D, E and H) Student's *t* test; ns, not significant.

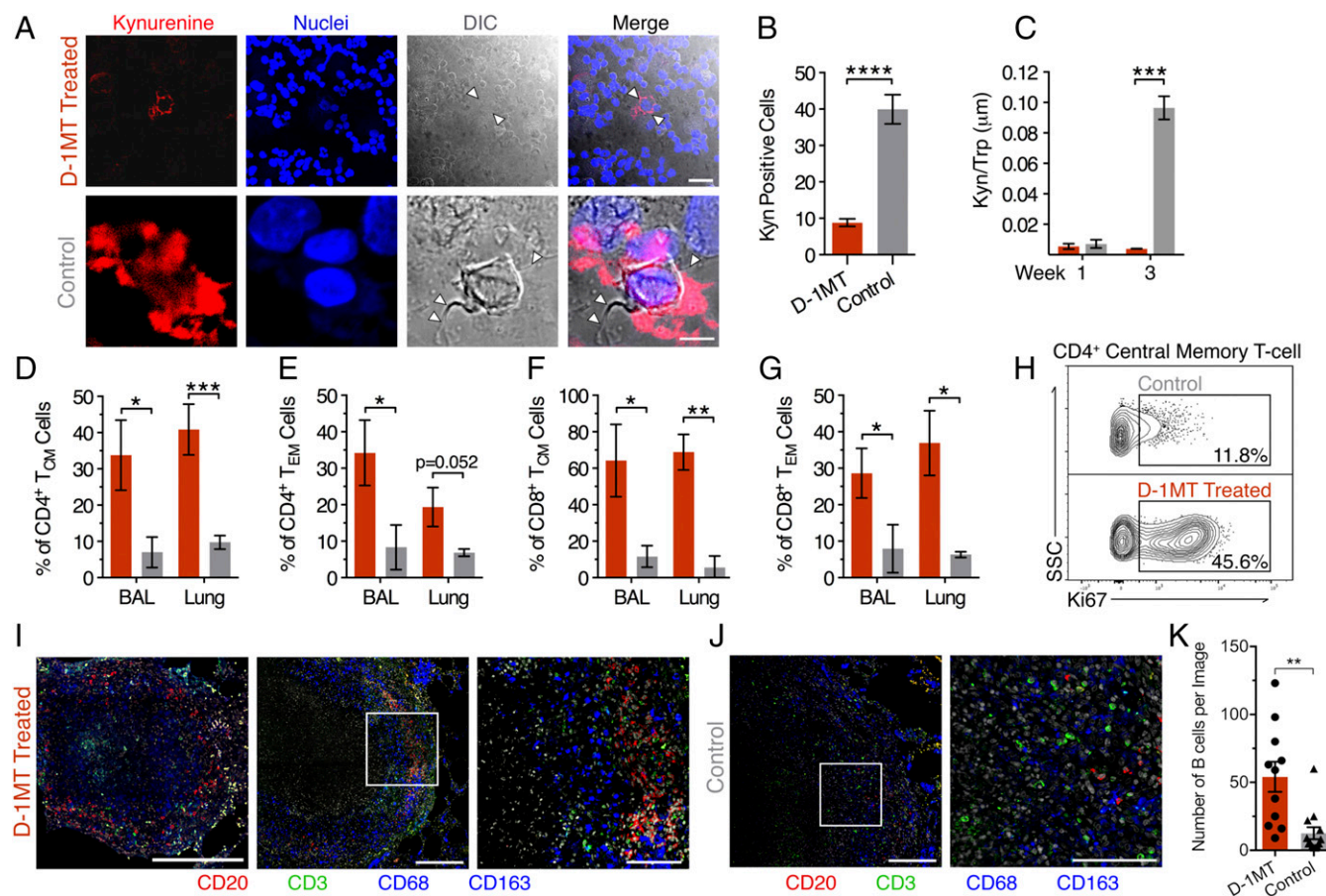


Fig. 3. Assessing the IDO enzymatic activity in *M. tuberculosis*-infected macaques in vivo and its impacts on T and B cell phenotypes. BAL staining 3 wk after *M. tuberculosis*-infection; red, Kyn; blue, nuclei; gray, DIC marked with white arrowheads pointing toward the lining that appears a cell membrane indicates Kyn deposition within a cell. [Scale bars, 100 μ m (Upper); 20 μ m (Lower).] (A) Kyn quantification (B) and Kyn/Trp ratio by ELISA (C). In A, images are shown at different scale with more number of cells in a field from D-1MT-treated animals. Phenotype of memory T cells in BAL and lung samples at necropsy with respect to proliferation as measured by Ki67 positivity in D-1MT-treated (orange) and control animals (gray) (D–H). A representative flow-density plot from lungs of memory T cells expressing Ki67 (H). Costaining with CD20 and CD3 exhibits iBALT in D-1MT-treated (I), control animals (J): red, CD20⁺ B cells; green, CD3⁺ T cells; blue, macrophages. [Scale bars, 20 μ m (I, Left and Right, and J, Right); 40 μ m (I, Middle and J, Left).] White box indicates CD3⁺ T cells (I) and CD20⁺ B cells (J) found in iBALT follicle. Quantification of B cells in the multiple lesions from both groups: D-1MT-treated (orange circle) and control (gray circle) (K) (means \pm SEM). * P < 0.05, ** P < 0.01, *** P < 0.001, **** P < 0.001 using a (B and K) Student's *t* test or (C) two-way ANOVA or (D–G) repeated-measures *t* test.

gating strategy are shown in Fig. S3. Comparisons were also made to T cell phenotypes in peripheral blood (Fig. S4) and immune cell numbers in blood, BAL, and lung (Figs. S4 and S5). We observed significant differences in the percentage of these cells that expressed the highly specific proliferation marker Ki67 (29–32). Thus, the percentage of both central memory (Fig. 3D and F) and effector memory (Fig. 3E and G) cells was higher in BAL as well as lungs of D-1MT-treated animals compared with controls, with enhanced CD4⁺ T_{CM} proliferation, detected by Ki67, in the treated group (Fig. 3H). Moreover, this difference in T cell proliferation between the two groups could also be observed in peripheral blood ($P = \sim 0.05$) (Fig. S4). Similarly, the Ki67⁺ status of central memory CD4⁺, CD8⁺, and effector memory CD8⁺ cells was also significantly enhanced ($P < 0.05$) in the peripheral blood of D-1MT-treated animals relative to control animals (Fig. S4). However, no differences were observed between the two groups of animals in the total number of CD4⁺ or CD8⁺ cells in blood (Fig. S4E–G), in BAL before or after D-1MT treatment (Fig. S5A–D) or in the lung (Fig. S5E–G), except that significantly higher levels ($P < 0.05$) of CD8⁺ T_{EM} cells were present in D-1MT animals at the end point (Fig. S5H). As it is well established that Trp catabolism orchestrated by IDO1 inhibits T cell proliferation (33, 34), mediated directly by end products of this pathway (34), we propose that inhibition of T cell proliferation by IDO1 is one of

the primary mechanisms of Trp catabolism-mediated immune dysfunction in the context of *M. tuberculosis* infection.

D-1MT Induces Inducible Bronchus-Associated Lymphoid Tissue Formation.

We next analyzed the potential effects of D-1MT treatment on inducible bronchus-associated lymphoid tissue (iBALT) formation. The presence of granuloma-associated iBALT is correlated with protection from *M. tuberculosis* infection (13). Paraffin-embedded lung samples collected at the time of necropsy were assayed for iBALT by histopathology and immunofluorescence staining with CD3 (detects T cells) and CD20 (detects B cells) antibodies, followed by confocal microscopy and image analysis (13). The presence of B cells and their follicular organization were greater in D-1MT-treated animals (Fig. 3I) relative to control animals (Fig. 3J). The total number of B cells enumerated in multiple lesion sections of lung was significantly higher ($P = 0.0013$) for D-1MT-treated animals compared with controls (Fig. 3K). These results further support our previous observations that protection from *M. tuberculosis* infection directly correlates with the presence of granuloma-associated iBALT (10, 13, 19, 22).

IDO Inhibition in Vivo Causes Broad-Spectrum Improvement in Granuloma Function. We assessed if IDO inhibition improved the function of granulomas in effectively controlling *M. tuberculosis*

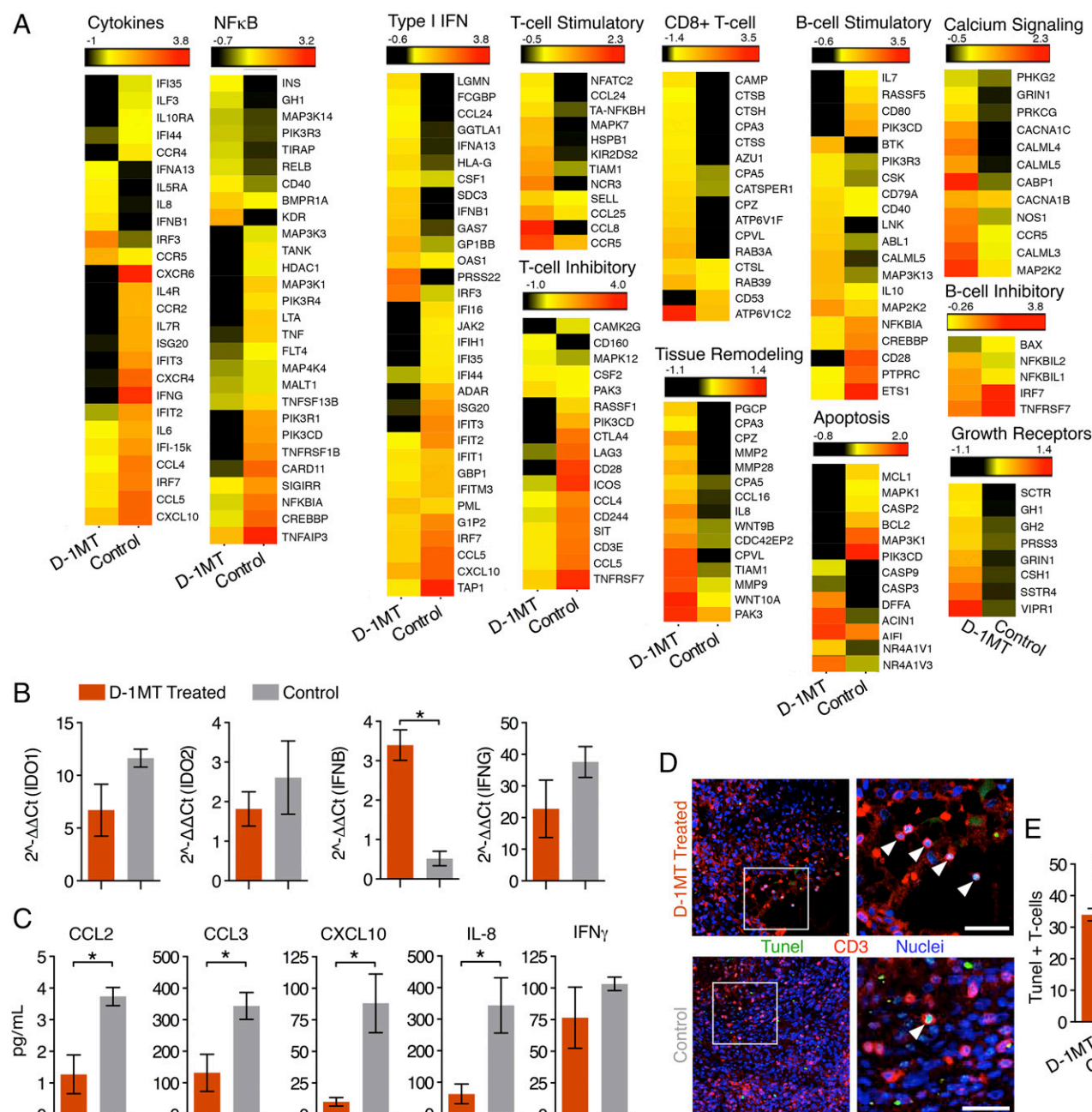


Fig. 4. Impact of inhibiting IDO on lung gene expression. Selected modules derived from significantly enriched pathways based on the method described elsewhere (70) in BAL microarray datasets are shown. The horizontal colored bar on top of each module for a category represents a range in gene-expression magnitude in logarithmic base2. Heat-map clusters: "black" to "yellow" to "red," lower (fold-change ~ 1.5 cut-off) to higher expression (4). The change in gene expression ($2^{-\Delta\Delta C_t}$) by RT-PCR (B), cytokine assay (C) in lung homogenates of D-1MT-treated (orange) and control animals (gray) relative to uninfected lung samples as base line. GAPDH was used as an internal reference. Bars with no statistics shown are nonsignificant between two groups (e.g., IFN γ ($P = 0.3381$)). Immunofluorescence-based detection of T cell apoptosis by TUNEL assay. The arrowheads (white) in each magnified image indicate apoptotic cells [scale bars, 20 μ m (Right); magnification, 20 \times (Left)] (D). Data obtained by counting multiple fields with T cells positive for TUNEL staining using a Leica confocal microscope (Leica Microsystems) (E). The data (means \pm SEM) from animals from both groups were used for analysis; * $P < 0.05$, **** $P < 0.001$ using a Student's t test.

inhibition permits lymphocytes with cytotoxic phenotype to migrate to the center of the tuberculoma and assist in the control of *M. tuberculosis* replication. It is possible that some of these cells may be classic CD8 $^{+}$, but the role of other CD3 $^{+}$ populations, such as NKT cells and mucosal-associated invariant T cells, cannot be ruled out. These results indicate that intragranulomatous T cell function is radically altered by D-1MT-mediated inhibition of IDO activity.

We conclude that blockade of IDO signaling leads to significantly better control of *M. tuberculosis* infection and reduces the

signs of TB disease by promoting the proliferation of memory T cell subtypes and by enhancing the ability of granulomas to kill *M. tuberculosis*. Because of the possibility that disruption of granuloma following D-1MT treatment might lead to increased dissemination of *M. tuberculosis* to extrapulmonary tissues, we performed CFU assays in BLN, liver, kidney, and spleen at the time of necropsy. The CFU counts in these organs revealed lesser bacterial burdens than controls; however, these numbers were statistically insignificant in liver, kidney, and spleen but drastically reduced in BLN in

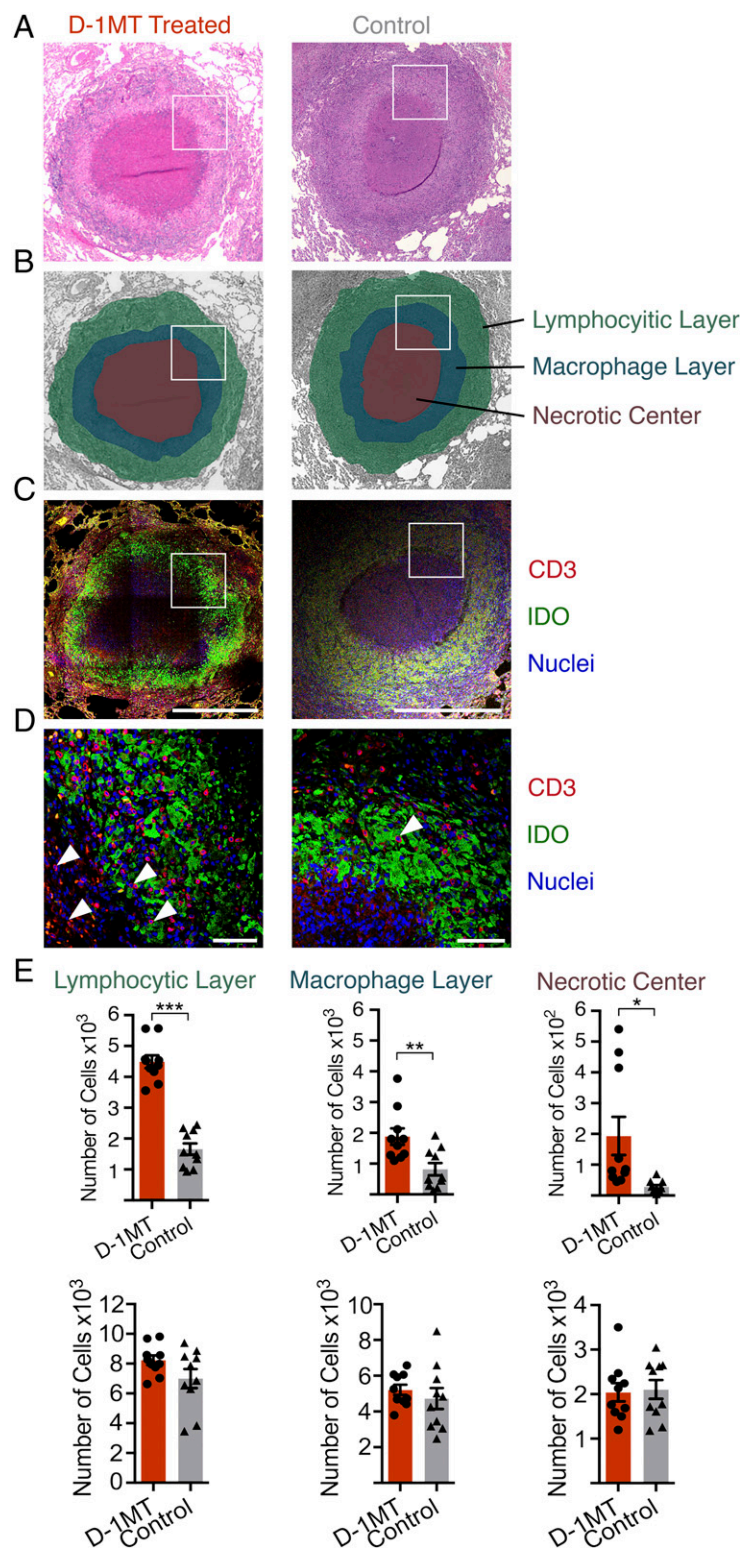


Fig. 5. Extensive relocation of T cells to the internal regions of the macaque granulomata after inhibition of IDO-signaling. H&E staining of a representative lesion from D-1MT-treated (Left) and control (Right) groups is shown (A). A schematic representation of the granulomata shown in A is drawn in B, distinctly differentiating the lymphocytic and macrophage layers from the necrotic center. The expression of IDO was measured as a function of its presence in either of the three intragranulomatous compartments (necrotic, macrophage, or lymphocytic layer) by immunostaining; IDO (green), CD3 (red), and nuclei (blue) (C). A magnification of the white square area in C is shown in D, with white arrowheads pointing to CD3⁺ cells in red. The number of CD3⁺ cells (E, Upper) as well as total nuclei (E, Lower) in multiple granulomata in D-1MT-treated (orange with circular data points) and control (gray with triangle data points) animals enumerated in the lymphocytic, macrophage, and necrotic center compartments are shown. For quantification, 10 fields from each compartment were counted under a fixed magnification (corresponding to an area of 0.05 mm²) using a multispectral imaging camera (CRi Nuance). The data are means \pm SEM, * P < 0.05, ** P < 0.01, *** P < 0.001 using a Student's t test. [Scale bars, 20 μ m (C, also applies to A and B); 5 μ m (D).]

comparison with controls (Fig. 3F). Thus, CFU measurements ruled out that disruption of granuloma by D-1MT treatment does not cause an increase in bacterial dissemination to extrapulmonary tissues, but indeed, these animals have over all lesser bacterial burdens.

Inhibition of IDO Signaling in Macrophage: CD4⁺ T Cell Cocultures Restricts Mycobacterial Growth. We cocultured *M. tuberculosis*-infected rhesus macrophages where IDO expression had been

silenced, with *M. tuberculosis*-specific CD4⁺ T cells in vitro, and measured bacterial burden (Fig. S1) used were from rhesus macaques with acute TB infection. The siRNA specifically affected IDO1 (Fig. S1 F and J) and not IDO2 (Fig. S1 F and K) expression. IDO1 silencing resulted in a greater control of *M. tuberculosis* replication when macrophages were cocultured with CD4⁺ T cells but not in macrophages alone (Fig. S1E). The silencing of IDO1 resulted in increased levels of IFN- β (Fig. S1 F

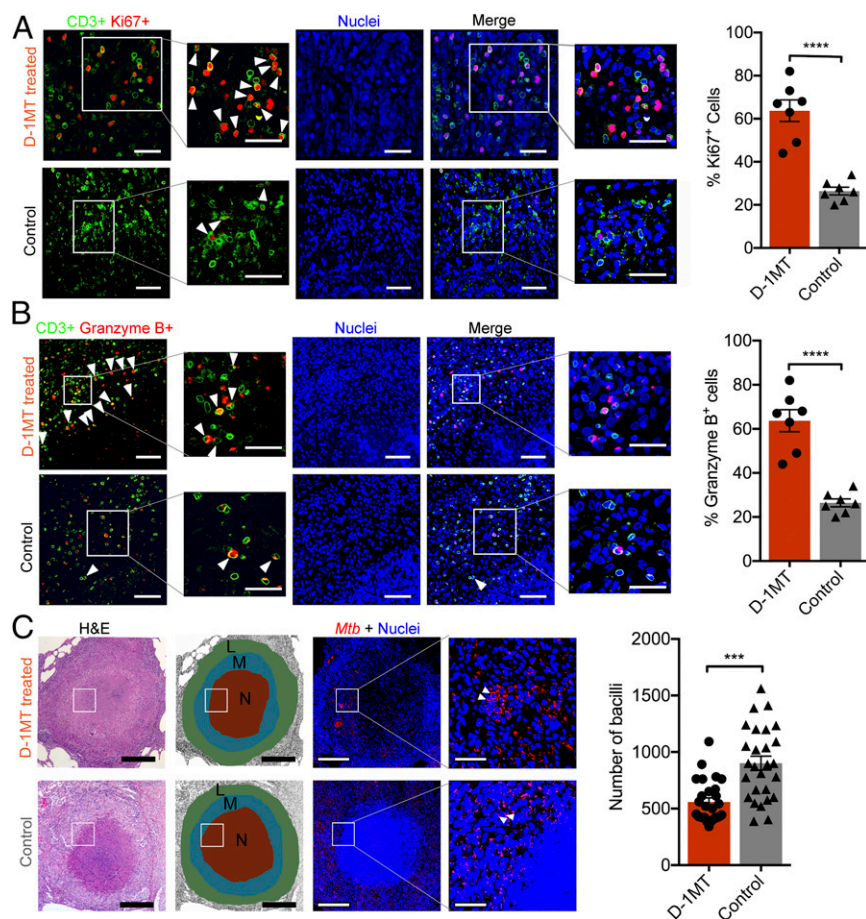


Fig. 6. Granuloma performance in D-1MT-treated and control animals. Immunohistochemistry staining of lung sections for CD3⁺ T cells; (A) Ki67 (red), (B) granzyme B (red) with CD3 in green and nuclei (TOPRO3) stained in blue (A and B) and *M. tuberculosis* (red) staining (C). Multiple granzyme B⁺ cells can be observed in the necrotic center of granuloma from D-1MT-treated animals and are marked with white arrowheads. The far-right images in each panel are close-ups of the boxed region. (Scale bars, 150 μ m.) The total number of cells positive for both CD3 and Ki67 as well as CD3 and granzyme B in A and B, respectively, as well as total nuclei in each panel were counted in multiple granulomata for each group and plotted. The graphs (far right in each panel) show percentages of cells positive for Ki67 (A) and granzyme B (B). The H&E staining of a representative lung lesion from D-1MT-treated (Upper) and control animals (Lower). [Scale bars, 20 μ m (C, H&E); 150 μ m (C, immunostaining).] A schematic representation of the granulomata and demarcation (L, lymphocytic layer; M, macrophage layer; N, necrotic center) in C is shown as described and is also applicable to A and B. The far-right image in C is the close-up of the boxed region and the graph shows the enumeration of bacilli in both groups (C). *** $P < 0.001$, **** $P < 0.0001$ using a Student's t test. Data are means \pm SEM, D-1MT treated (orange circle), controls (gray circle).

and L), while the expression of IFN- γ (Fig. S1 F and M) and the internal control GAPDH (Fig. S1 F) was not perturbed.

Discussion

M. tuberculosis utilizes the host granulomatous response to persist in the face of strong immunity (51), by modulating both innate (52) and adaptive (53) immune responses. The fate of *M. tuberculosis* infection is decided in the granuloma; some lesions affect elite control of *M. tuberculosis* replication via enhanced killing, but others fail, resulting in uncontrolled replication and spread. Therefore, the potential to modulate granulomatous responses in favor of bacterial killing by enhancing natural immunity using HDT exists (54, 55). These HDT approaches can channel the chronic immune dysregulation displayed by granulomas that fail, resulting in counterproductive lung pathology, into productive responses characterized by sterilization of granulomas.

M. tuberculosis can overcome the restriction imposed by IDO and the resulting Trp insufficiency, by biosynthesizing this amino acid (8). IDO potentially suppresses CD4⁺ T cells via a variety of mechanisms, including limiting their proliferation (56), induction of immunoregulatory APCs, and by promoting the differentiation of Th0 cells into Tregs (57, 58). Thus, high IDO activity has been correlated with pathogen burden and sepsis during infection (59),

especially with intracellular pathogens (60), including *M. tuberculosis* (61). Here, inhibition of IDO activity by a potent yet safe inhibitor in macaques led to a slightly better control of *M. tuberculosis* replication, and somewhat reduced pathology and disease severity, accompanied by increased proliferation of CD4⁺ and CD8⁺ memory and effector populations, and the inhibition of lung marker T cell exhaustion and dysfunction. This was associated with reorganization of the granulomata, with T cells otherwise present in the peripheral region of lesions being able to gain greater access to the core region.

It has recently been shown that mycobacterial infection results in the reprogramming of macrophages in the granuloma to a flattened, epithelial phenotype (62). This results in macrophage interdigitation and tighter granulomas. Inhibition of canonical epithelial pathways in the zebrafish model of *Mycobacterium marinum* infection resulted in the dysregulation of the granuloma, along with immune cell access to the lesion core, and reduced bacillary burdens (62). These results, taken together with our study, suggest that the ability of pathogenic mycobacteria to replicate within host lungs is intricately linked to lesion organization, and disruption of this process represents an attractive future strategy for the control of TB.

Our results have implications both for the fundamental understanding of why granulomas are unable to achieve their full potential during *M. tuberculosis* infection and for providing clues to

likely targets of productive HDT against TB, including IDO. These results suggest that the complex and highly ordered architecture of the primate (and human) lung tuberculoma may in fact be beneficial to the pathogen by preventing contact between T cells and pathogen-containing APCs. It may, however, be possible to alter granuloma architecture by inhibiting IDO signaling, and thereby allowing T cells access to the lesion core while also fostering the development of the follicular organization of B cell-containing iBALT. Such lesions appeared to overcome checkpoint inhibition and T cell dysfunction, greatly promoting bacterial killing.

Inhibition of IDO signaling *in vivo*, as well as *in vitro*, enhanced the expression of the type I IFNs, although the expression of all type I downstream genes (e.g., IFIT1, IFIT2, IFIT3, and so forth) was not induced. These results are not surprising, given that IDO can be induced by both IFN- γ as well as type I IFN. This regulation of IDO by type I vs. type II interferons is context- and cell-type-dependent (63). It appears that type I IFN plays a major role in triggering IDO expression in primate alveolar macrophages in the context of *M. tuberculosis* infection, and therefore, inhibition of IDO enzymatic activity likely causes induction of type I IFN gene expression via feedback (63, 64). Whereas type I IFN is an important antiviral mechanism (65), its induction correlates with increased lung pathology and exacerbated disease upon *M. tuberculosis* infection (66). As such, approaches targeting type I IFN signaling have been successfully attempted in experimental models of TB (66). Our data suggest that the concurrent silencing of IDO signaling and type I IFN signaling could lead to a more profound control of TB in macaque (and human) lungs. Furthermore, testing the potential of such HDT alone, as well as concurrently with anti-TB chemotherapy, could pave the way for future clinical applications. Our results suggest that therapeutic strategies aimed at eliminating or reducing the levels of cells with IDO induction following *M. tuberculosis* infection, such as myeloid-derived suppressor cells in the lung, may also result in reduction of TB. Finally, we have not discussed as part of this report the conundrum that IDO expression on nonhematopoietic cells following *M. tuberculosis* infection may indeed have a protective effect for the host, as has been shown in the murine model (67). Moreover, several novel IDO inhibitors are being generated (e.g., Indoximod), and it may be possible in future studies to test if they are preclinically superior to D-1MT in suppressing IDO activity.

Materials and Methods

In Vivo. Ten rhesus macaques were infected with a high dose of *M. tuberculosis* CDC1551 (~200 CFU) via the aerosol route, as described previously (10–16, 23). Five animals were randomly chosen to be in the treatment group and were D-1MT-treated daily, via the oral route with an IDO enzymatic activity inhibitor, D-1MT (45 mg/kg body weight) 1 wk after *M. tuberculosis* infection. The remaining animals served as controls.

NHPs, Infection, Sampling, Killing, and Clinical Pathology. All 10 animals were negative for tuberculin skin test (TST) before infection, but tested positive 3 wk after *M. tuberculosis* infection. Blood and BAL were collected before and after *M. tuberculosis* infection and during the time-course of D-1MT treatment till necropsy. CFUs were measured in BAL 1 wk after *M. tuberculosis* infection and every 2 wk thereafter until the end point. Lung pathology was determined as described previously (11, 15). CFUs were also measured in lung and lymph node tissues derived at necropsy, as described previously (10–16, 23). Humane end points were predefined in the animal-use protocol and applied as a measure of reduction of discomfort as described earlier to kill animals as necessary (10, 11, 13). The Tulane National Primate Research Center Institutional Animal Care and Use Com-

mittee and the Tulane Institutional Biosafety Committee approved all procedures. All animal procedures were performed in strict accordance with NIH guidelines.

Immunostaining and Confocal Microscopy. H&E histology, immunostaining, and confocal microscopy were performed on formalin-fixed, paraffin-embedded tissues, as previously described (5, 10–13, 15, 19, 22, 23, 68–71). Staining for Kyn was performed on fixed (4% formaldehyde) BAL cytospun frozen slides using a Kyn-specific polyclonal antibody (ImmuSmol). For preparation of frozen BAL slides, 0.1–0.5 million BAL cells were cytospun on a positively charged glass slides (Inform; PerkinElmer) at 700 \times g for 7 min at room temperature, followed by washing two times with PBS (1 \times solution; Thermo Fisher Scientific). Slides were kept for evaporation of residual liquid for 10 min followed by addition of 4% PFA (room temperature) and incubation for overnight and stored in -80°C .

ELISA. Trp and Kyn were quantified in blood plasma samples from all animals before infection (baseline) and every week thereafter until necropsy, using a Trp and Kyn ELISA kit strictly as per the manufacturer's instructions (ImmuSmol).

Flow Cytometry. Flow cytometry was performed on whole blood, BAL, and lung samples from all animals, as previously described (10–13, 16, 20, 21, 23, 26). Briefly, memory subsets were established for T cell populations based on CD28 and CD95 coexpression (72), as previously described (11), and subdivided based on CD3 $^{+}$, CD28 $^{+}$, CD95 $^{+}$ subsets being defined as central memory, and CD3 $^{+}$, CD28 $^{-}$, CD95 $^{+}$ being defined as effector memory. Various antibodies and their amount used for staining are described in Table S2.

Cytokine Assay. Cytokine assays were performed in lung samples derived at time of necropsy from D-1MT-treated and control animals, as well as from naïve (not infected with *M. tuberculosis* and untreated) lungs (as baseline) following the procedures described earlier (11, 23, 68–71).

Quantitative Real-Time RT-PCR and Transcriptomics. Total RNA from BAL obtained at baseline and 3-wk after *M. tuberculosis* infection of two representative animals from each group, was amplified using MessageAmp II aRNA Amplification Kit (Thermo Fisher Scientific) and processed for microarray and qRT-PCR, as described previously (11, 13).

In Vitro Culturing. Monocyte derived macrophages (MDMs) were generated from macaque blood and cocultured with CD4 $^{+}$ s, as described previously (73). A subset of MDMs was treated with IDO1-specific siRNA 24 h before *M. tuberculosis* infection (multiplicity of infection = 10:1) (Table S1) to inhibit IDO1 expression, as described previously (71). Samples were collected at 0 and 24 h post-infection (71) and used for CFU assay, qRT-PCR, and immunocytochemistry.

Statistics. Unless otherwise stated, statistical analyses were performed with Prism v7 (GraphPad). For statistics, either Mantel–Cox (log-rank) survival analysis, Student's *t* test, or a *t* test with repeated-measures or two-way or one-way ANOVA with Bonferroni multiple comparisons was performed. When required, a goodness-of-fit in linear regression was performed for the statistical analysis between two groups.

More details can be found in *SI Materials and Methods*.

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Supporting Information

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SI Materials and Methods

In Vivo. Ten rhesus macaques were infected with a high dose of *Mycobacterium tuberculosis* CDC1551 (~200 CFU) via the aerosol route, as described previously (1–8). Five animals were randomly chosen to be in the treatment group and were D-1MT-treated daily, via the oral route with an IDO enzymatic activity inhibitor, D-1MT (45 mg/kg body weight) after week 1 of *M. tuberculosis* infection. D-1MT has been previously used to assess the impact of IDO on SIV disease progression in macaques (9). The remaining five animals served as controls.

NHPs, Infection, Sampling, Killing, and Clinical Pathology. All animal procedures were approved by the Institutional Animal Care and Use Committee of the Tulane National Primate Research Center (TNPRC) and were performed in strict accordance with NIH guidelines. The TNPRC is accredited by the Association for the Assessment and Accreditation of Laboratory Animal Care and is routinely monitored by the US Department of Agriculture. Infection was performed as described previously using an aerosol exposure modality specifically configured for macaques (1–8). All 10 animals were negative for tuberculin skin test before infection, but tested positive 3 wk after *M. tuberculosis* infection. Blood and BAL samples were collected before and after *M. tuberculosis* infection and during the time-course of D-1MT treatment till necropsy. Serum CRP, a marker for systemic inflammation, correlated with extent of disease in both groups based on the parameters described previously (1–3). CFUs were measured in BAL 1 wk after *M. tuberculosis*-infection and every 2 wk thereafter until and including the end point. Lungs were stereologically sectioned and pathology was determined as described previously (3, 6). CFUs were also measured in lung and lymph node tissues derived at necropsy, as described previously (1–8). For various assays, lung samples obtained from naïve, TST-negative rhesus macaques from the TNPRC colony were used as baseline. Humane end points were predefined in the animal-use protocol and applied as a measure of reduction of discomfort, as described earlier to kill animals as necessary (1–3). Macaques were killed based on Institutional Animal Care and Use Committee-approved guidelines. To minimize any experimental variation, tissues, blood, and BAL samples collected at each time point and during necropsy were immediately processed without storage for downstream applications, such as flow cytometry, CFU determination, and so forth.

Immunostaining and Confocal Microscopy. H&E histology, immunostaining, and confocal microscopy were performed on formalin-fixed, paraffin-embedded tissues as previously described (1–3, 6–8, 10–16). Staining for Kyn was performed on fixed (4% formaldehyde) BAL cytospun frozen slides using a Kyn-specific polyclonal antibody (ImmuSmol). For preparation of frozen BAL slides, 0.1–0.5 million BAL cells were cytospun on a positively charged glass slides (Inform; PerkinElmer) at 700 × g for 7 min at room temperature followed by washing two times with PBS (1× solution; Thermo Fisher Scientific). Slides were kept for evaporation of residual liquid for 10 min followed by addition of 4% PFA (room temperature) and incubation for overnight. On the following day, slides were wrapped in a foil and stored in –80 °C until used. All of the operations were performed at room temperature inside the BSL3 laminar flow. For quantification of LAG-3, K_i67, Granzyme B, and *M. tuberculosis* in the individual lesions, 10–15 fields from multiple

granulomas were counted under a fixed magnification using a multispectral imaging camera (CRi Nuance) and plotted.

ELISA. Trp and Kyn were quantified in blood plasma samples from all animals before infection (baseline) and every week thereafter until necropsy using Trp and Kyn ELISA kit strictly as per the manufacturer's instructions (ImmuSmol). The Trp and Kyn values were extrapolated from respective known standards provided in each kit and the numeric ratio (Kyn/Trp) was calculated and plotted using GraphPad.

Flow Cytometry. Flow cytometry was performed on whole blood, BAL, and lung samples from all animals as previously described (1–3, 5, 7, 8, 16–19). Briefly, memory subsets were established for T cell populations based on CD28 and CD95 coexpression (20) as previously described (3), and subdivided based on CD3⁺, CD28⁺, CD95⁺ subsets being defined as central memory, and CD3⁺, CD28[–], CD95⁺ being defined as effector memory. Various antibodies and their amount used for staining are described in Table S2.

Cytokine Assay. Cytokine assays were performed in lung samples derived at time of necropsy from D-1MT-treated and control animals, as well as from naïve (not infected with *M. tuberculosis* and untreated) lungs (as baseline) following the procedures described previously (3, 8, 10, 12, 15, 16) with minor modifications. Briefly, lung homogenates were prepared in the lysis Buffer [500 mM Tris-HCl, 0.1% (wt/vol) SDS, 0.15% sodium deoxycholate, 1× protease inhibitor mixture, 1× phosphatase inhibitor mixture (Roche)]. For preparation of lung homogenates, 1 mL lysis buffer per 0.2-g tissue was used. Lung homogenates were filtered with 0.22-μm filters (Millipore) before use in cytokine assay using Cytokine Monkey Magnetic 29-Plex Panel kit (Thermo Fisher Scientific), essentially as described previously (10).

Quantitative Real-Time RT-PCR and Transcriptomics. For host-transcriptomics, total RNA isolated from BAL obtained at the preinfection (~1-wk before infection, baseline) and 3-wk after *M. tuberculosis*-infection of two representative animals from each group was subjected to RNA amplification using MessageAmp II aRNA Amplification Kit (Thermo Fisher Scientific) and processed for microarray and qRT-PCR, as described previously (2, 3). The microarray datasets relative to baseline (as above) were subjected to statistical analysis using ANOVA, as previously described (16). The impact of gene-expression profiles in animals from both groups was compared using Ingenuity Pathway Analysis (Ingenuity Systems). The gene families with significant overrepresentation were selected for supervised clustering and pathway analyses using DAVID and as described elsewhere (2, 3). The genes of a significantly overrepresented pathway (from above) were used to generate modules. The qRT-PCR was performed on subset of genes on microarray datasets and for the detection of Trp biosynthetic gens of *M. tuberculosis* (for primer sequences, see Table S1) in triplicates on RNA derived from four animals in both ATB and LTBI groups, following the method described previously (2, 21).

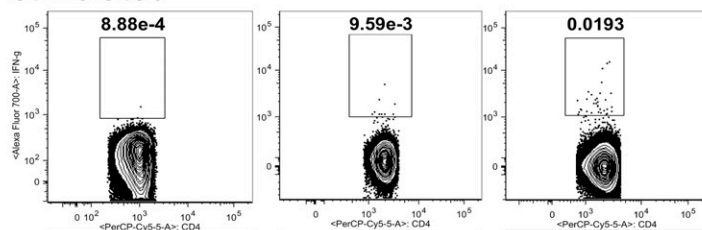
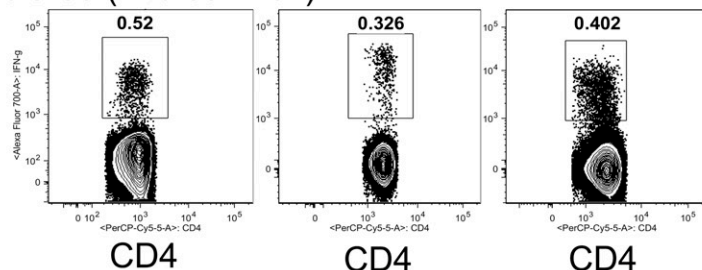
In Vitro Culturing. Macaque whole blood was collected in EDTA tubes (S-Monovette Sarstedt) and monocytes isolated by Histopaque-1077 (Sigma) density gradient centrifugation. MDMs from these samples were used in a coculture model with autologous CD4⁺ T cells (22). A negative-selection process that involves MACS (magnetic-activated cell sorting) with the NHP

CD4⁺ T cell Isolation Kit (Miltenyi Biotec) was used to isolate CD4⁺ T cells as described previously (22). A subset of MDMs was treated with IDO1-specific siRNA 24 h before *M. tuberculosis*-infection (multiplicity of infection = 10:1) (Table S1) to inhibit IDO1 expression as described previously (16). Samples were collected at 0 and 24 h postinfection (16) and used for CFU assay, qRT-PCR, and immunocytochemistry.

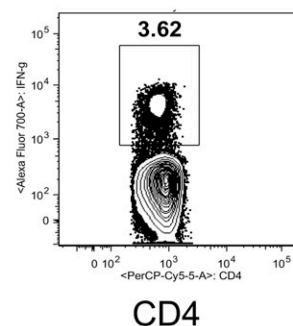
Statistics. Unless otherwise stated, statistical analyses were performed with Prism v7 (GraphPad). For statistics, either Mantel-Cox (log-rank) survival analysis, Student's *t* test or a *t* test with repeated measures or two-way or one-way ANOVA with Bonferroni multiple comparisons was performed. When required, a goodness-of-fit in linear regression was performed for the statistical analysis between two groups.

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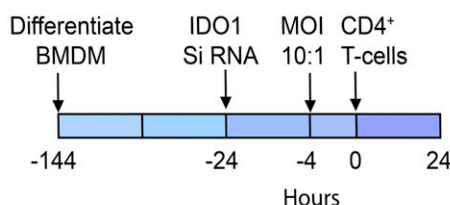
A. Non-stimulated

B. Stimulated (*Mtb* cell wall)

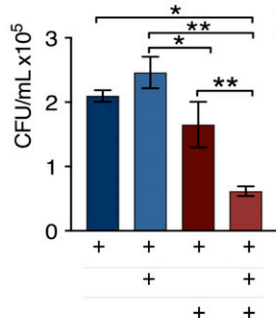
C. Stimulated (SEB)



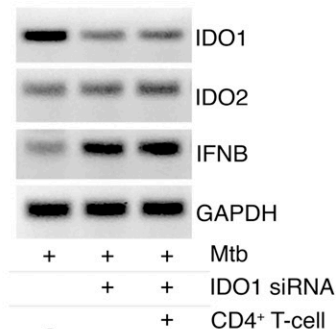
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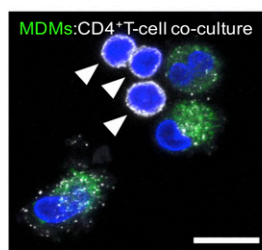
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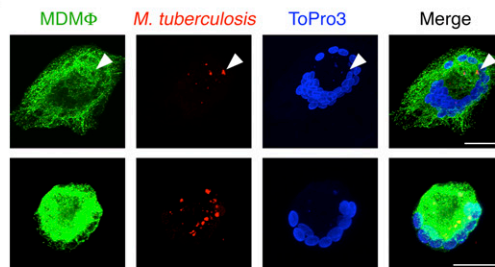
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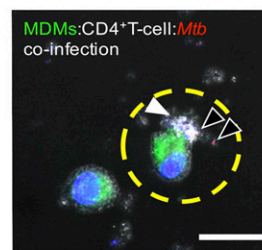
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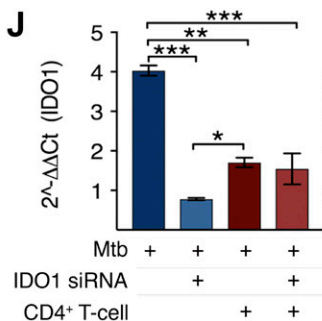
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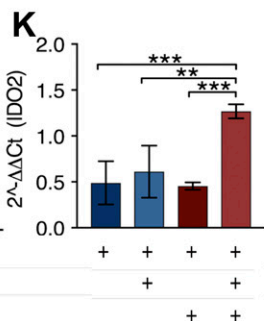
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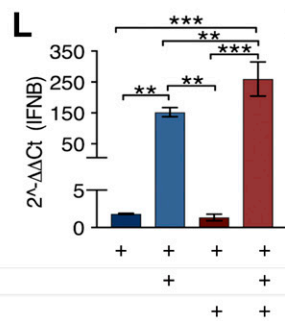
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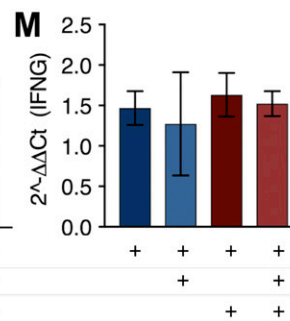


Fig. S1. Analysis of the role of IDO1 during *M. tuberculosis*-infection using MDMs:CD4⁺ T cells in an in vitro coculture model. (A–C) A representative IFN- γ response of CD4⁺ T cells. The CD4⁺ T cells from peripheral blood mononuclear cells prepared from whole blood were used to measure their functional profile, unstimulated (A), and Staphylococcal enterotoxin B (SEB)-stimulated (C) cells are negative and positive controls; *M. tuberculosis* cell wall-stimulated (B). Schematic design (D) of coculture experiment (E–M). MDMs proliferated for 120 h, followed by IDO1 silencing before *M. tuberculosis*-infection (D). CFU measurements at 24 h (E). IDO1 silencing (F and J). Confocal microscopy (G–I) showing immunocytochemical staining of CD4⁺ T cells (white, G and H) MDMs (green), nuclei (blue), and intracellular *M. tuberculosis* (red) marked with white arrowheads. A representative image of an infected macrophage with *M. tuberculosis* (stained in red and shown with black arrowheads in I) associated with T cell indicated with a white arrowhead is shown within a dotted yellow circle in a MDMs:CD4⁺ T cell coculture experiment (I). (Scale bars, 20 μ m.) IDO1 silencing, expression of IFN genes, and bacterial killing in MDMs in the presence of CD4⁺ T cells that were derived from rhesus macaques with acute TB infection (E–M). The qRT-PCR on RNA samples derived at 24 h after *M. tuberculosis* infection to detect IDO1

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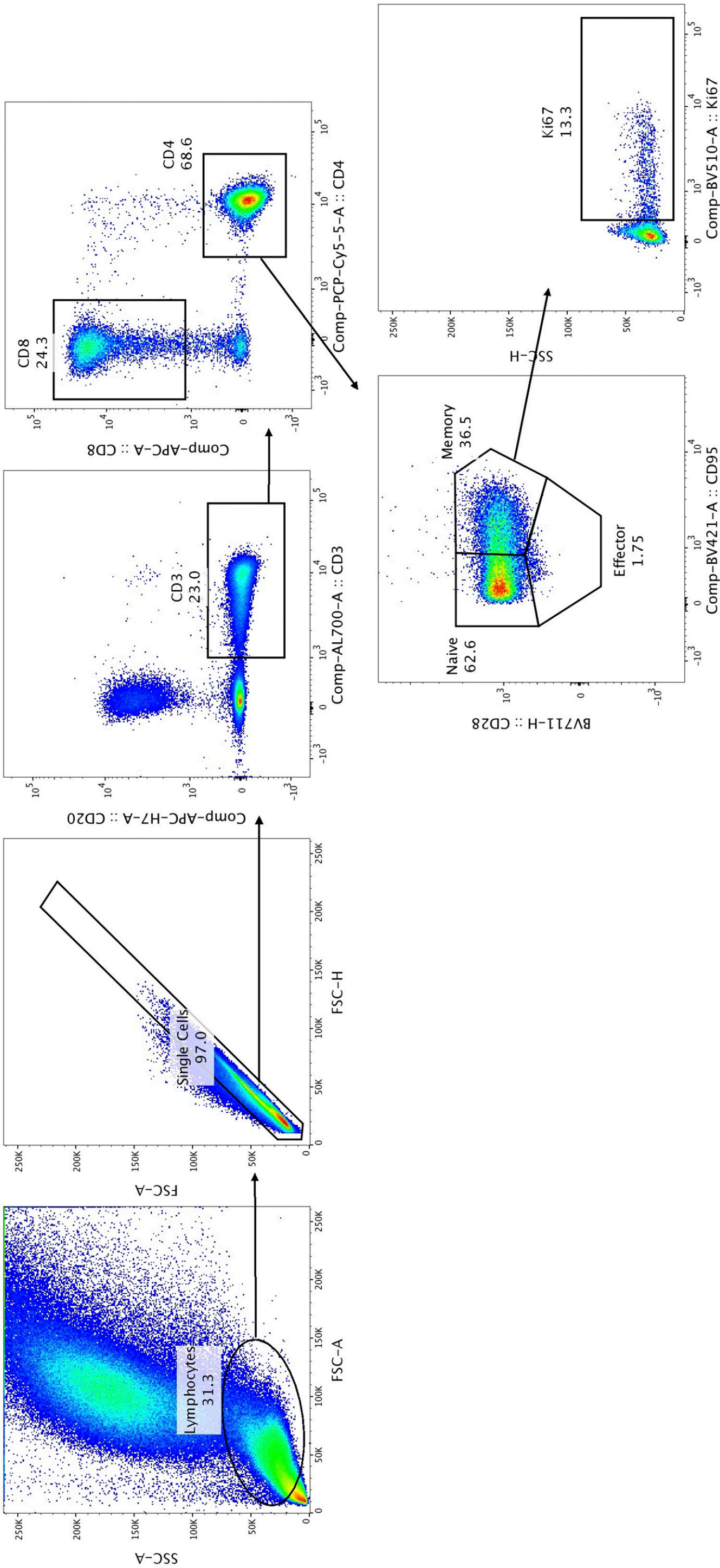


Fig. S3. Gating strategy for characterizing T cells in peripheral blood, BAL, or lungs. Lymphocytes were first subjected to forward scatter analysis to identify singlets, which were then gated on CD3⁺ T cells, excluding CD20⁺ B cells. T cells were then compartmentalized into CD4⁺ and CD8⁺ T cells, and memory status identified using CD28 and CD95 positivity (CD28⁺CD95⁺, central memory; CD28⁺CD95⁻, effector; and CD28⁻CD95⁻, naive). Proliferative capacity was identified using Ki67.

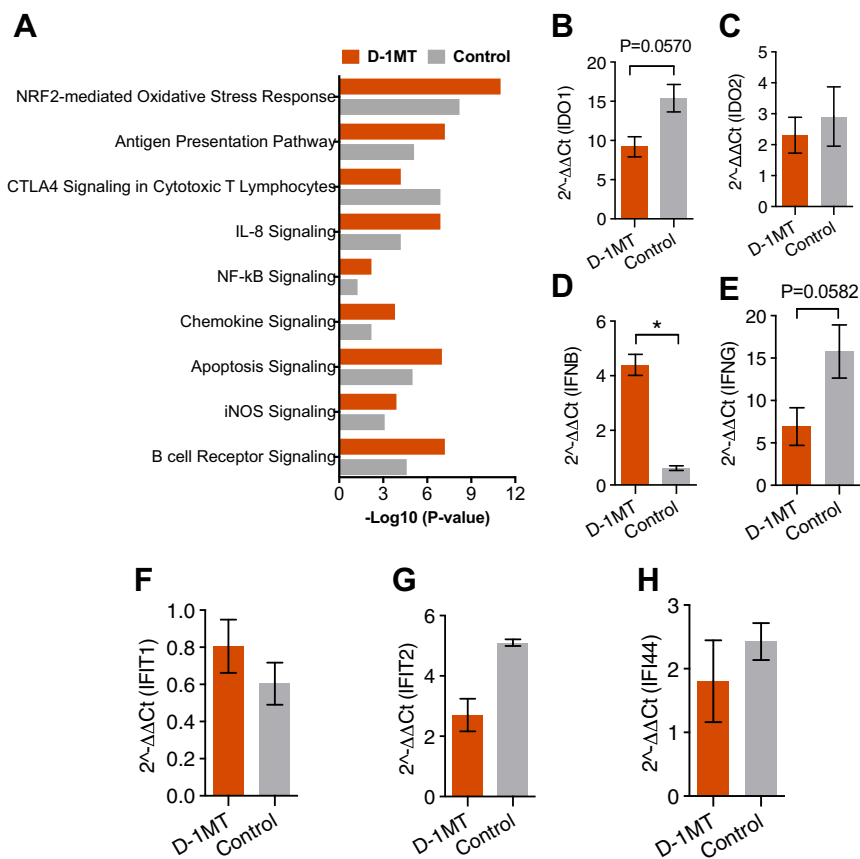


Fig. S6. Transcriptomics in BAL. (A) Microarray-based detection of cytokine signaling pathways in BAL. Gene families with significant overrepresentation as previously described (22), selected for supervised clustering and pathway analyses using DAVID are shown. RT-PCR (B–H). Relative expression ($2^{-\Delta\Delta C_t}$) of IDO1 (B), IDO2 (C), and interferons, IFN- β (D), IFN- γ (E), IFIT1 (F), IFIT2 (G), IFI44 (H) detected at week 3 postinfection; D-1MT-treated (orange) and control animals (gray). The data obtained are significant ($*P < 0.05$) for IFN- β or approaching significance for IFN- γ ($P = 0.0582$) and not IDO2, IFIT1, IFIT2, or IFI44 using a student's t test. The BAL samples of three animals from each group were included for the analyses.

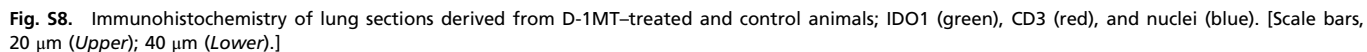
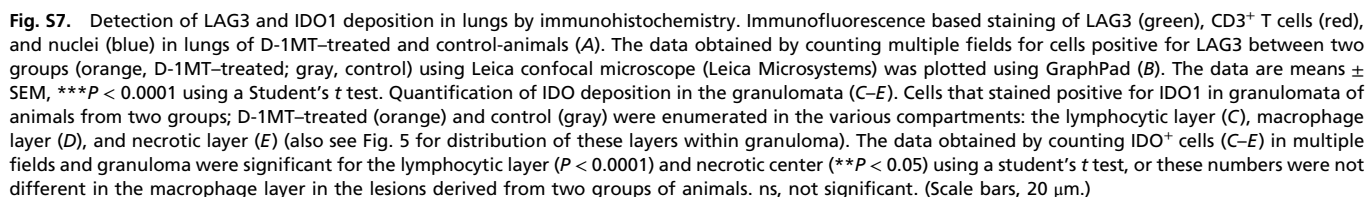


Table S1. Primers and siRNA used in the study

Gene/siRNA	Primer/siRNA sequence (5'-3')
Rh IDO1 F	GGTTTATGCAGACTGTGCTTGGCA
Rh IDO1 R	CTCCATCACGAAAGGAGAACAAAAC
Rh IDO2 F	CAGATTCTCTGAAAGAACTTCCAGAT
Rh IDO2 R	ACATGAGCTCGAAGCTGGTGAGC
Rh IFN- γ F	GACTCGAATGTCCAACGCAAAGCA
Rh IFN- γ R	CGACCTCGAAACATCTGACTCCTTT
Rh IFN- β F	ACGCTGCATTGACCATCTATGAGA
Rh IFN- β R	TTAGCAAGGAAGTTCTCCACAATAGT
Rh GAPDH F	TCAAGAAGGTAGTGAAGCAGGCGT
Rh GAPDH R	AAGAGTGGGTGTCGCTGTTGAAGT
<i>Mtb trpE</i> F	GTACCGAATTCTGCGGGTAA
<i>Mtb trpE</i> R	ACAATCGAAAAGTCCACTGC
<i>Mtb trpD</i> F	GAGGTTGGGATCGGGTTCT
<i>Mtb trpD</i> R	CCCAGAAGATTGAACACGG
<i>Mtb trpC</i> F	AATCGTTGGGTATGACAGCA
<i>Mtb trpC</i> R	GTTAACGCCAATCACCTTGG
<i>Mtb trpA</i> F	GCGGCATTGATTGGTTACTT
<i>Mtb trpA</i> R	GGAACCCCGACTTCGATAAT
<i>Mtb trpB</i> F	TAGGTGTTGAGTTGGGAAGG
<i>Mtb trpB</i> R	AGCAAGCCAAACCATTTTCG
Rh IDO1 siRNA sense	GGUAAGGUGUCAUGGAGACUU
Rh IDO1 siRNA antisense	GUCUCCAUGACUUUAUCCUU

This table reports the sequences of oligonucleotides and macaque specific IDO1 Si-RNA used in qRT-PCR and cell culture, respectively. The primers were designed from rhesus macaque-specific and *M. tuberculosis*-specific genes. F, forward primer; R, reverse primer; Rh, rhesus.

Table S2. List of antibodies

Fluorochrome	Antibody name	Source	Clone	Quantity used per sample (μL)	Catalog no.
FITC	CD69	BD Biosciences	FN50	20	555530
PerCP-Cy5.5	CD4	BD Biosciences	L200	20	552838
APC	CD8	BD Biosciences	RPA-T8	10	555369
AL 700	CD3	BD Biosciences	SP34-2	10	557917
APC-HY7	CD20	BD Biosciences	2H7	5	560853
BV421	CD95	BD Biosciences	DX2	5	562616
BV510	Ki67	BD Biosciences	B56	5	563462
BV711	CD28	BD Biosciences	CD28.2	5	563131
PE	CCR5	BD Biosciences	3A9	20	550632

The table summarizes the list of antibodies used for staining by flow cytometry experiments.