1 TITLE

2 Downregulation of Let-7 miRNA promotes Tc17 differentiation and emphysema via de-

- 3 repression of RORyt
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24 ABSTRACT

- 25 Environmental air irritants including nanosized carbon black (nCB) can drive systemic
- 26 inflammation, promoting chronic obstructive pulmonary disease (COPD) and emphysema
- 27 development. The *let-7* family of miRNAs is associated with IL-17-driven T cell inflammation, a
- 28 canonical signature of lung inflammation. Recent evidence suggests the let-7 family is

29 downregulated in patients with COPD, however, whether this repression conveys a functional 30 consequence on emphysema pathology has not been elucidated. Here we show that overall expression of the let-7 miRNA clusters, let-7b/let-7c2 and let-7a1/let-7f1/let-7d, are reduced in the 31 lungs and T cells of smokers with emphysema as well as in mice with cigarette smoke (CS)- or 32 33 nCB-elicited emphysema. We demonstrate that loss of the let-7b/let-7c2-cluster in T cells predisposed mice to exaggerated CS- or nCB-elicited emphysema. Furthermore, ablation of the 34 let-7b/let-7c2-cluster enhanced CD8⁺IL17a⁺ T cells (Tc17) formation in emphysema development 35 in mice. Additionally, transgenic mice overexpressing let-7 in T cells are resistant to Tc17 and 36 37 CD4⁺IL17a⁺ T cells (Th17) development when exposed to nCB. Mechanistically, our findings reveal the master regulator of Tc17/Th17 differentiation, RAR-related orphan receptor gamma t 38 (RORyt), as a direct target of let-7 miRNA in T cells. Overall, our findings shed light on the let-39 7/RORyt axis with let-7 acting as a molecular brake in the generation of Tc17 cells and suggests 40 a novel therapeutic approach for tempering the augmented IL-17-mediated response in 41 emphysema. 42

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44 INTRODUCTION

Chronic obstructive pulmonary disease (COPD) ranks as the third leading cause of mortality and is projected to account for over a billion deaths by the end of the twenty-first century (GBD Chronic Respiratory Disease Collaborators, 2020; *Findings from the Global Burden of Disease Study 2017*, 2019; Laniado-Laborín, 2009). Currently, there are no treatment options to reverse emphysema, the most clinically significant variant of COPD, which often is progressive despite smoking cessation (Bhavani et al., 2015; Anthonisen et al., 2002).

51 Inhalation of fine particulate matter smaller than 2.5 microns (PM_{2.5}) found in outdoor and 52 indoor air pollution as well as tobacco smoke are risk factors for COPD development (Adeloye et al., 2022; Eisner et al., 2010; Hu et al., 2010). We have previously shown that nano-sized carbon
black (nCB), a noxious chemical constituent of PM_{2.5} found in the lungs of smokers, activates
macrophages and dendritic cells orchestrating a pathogenic T cell-dependent inflammatory
response and emphysema in mice (W. Lu et al., 2015; You et al., 2015; Shan et al., 2009; C.-Y.
Chang et al., 2022).

Research over the last decade has pointed to the importance of dysfunctional 58 inflammatory T cells in human COPD lung tissue and animal models of emphysema (Grumelli et 59 al., 2004; Xu et al., 2012; Williams et al., 2021). Aberrant T cells are implicated in impaired host 60 defense, exaggerated inflammation, and loss of self-tolerance in COPD (Williams et al., 2021; 61 Chen et al., 2023; Hogg et al., 2004; Maeno et al., 2007; Xu et al., 2012). In this regard, we and 62 others have demonstrated the role and pathogenicity of activated IFN-y and IL-17-secreting 63 64 subsets of CD4⁺ and CD8⁺ T lymphocytes including Th1, Th17, and Tc1 cells in clinical isolates 65 and in mice with COPD (W. Lu et al., 2015; You et al., 2015; Shan et al., 2009; S.-H. Lee et al., 2007; Kheradmand et al., 2023). The IL-17-secreting Th17 cells are particularly important as they 66 promote the destruction of lung epithelium and recruitment of macrophages and neutrophils which 67 then release proteolytic enzymes such as matrix metalloproteinases (MMPs) involved in the 68 69 degradation of the lung structural matrix (Barnes, 2016; Hoenderdos & Condliffe, 2013). We previously demonstrated that intranasal inhalation of nCB in mice is sufficient to induce 70 emphysema by stimulating lung T cell activation by dendritic cells and macrophages. Moreover, 71 72 we found that genetic ablation of IL-17A can attenuate nCB- or cigarette smoke-induced alveolar 73 destruction and airway inflammation (Shan et al., 2012; You et al., 2015). More recently, IL-17A and IL-17F secreting CD8⁺ T cell (Tc17) subpopulation has been shown to play a critical role in 74 the pathogenesis of several autoimmune and inflammatory disorders (Globig et al., 2022; Huber 75 et al., 2013; Srenathan et al., 2016). 76

Both Th17 and Tc17, require the fate-deterministic transcription factor RAR-related orphan receptor gamma t (RORyt, encoded by *Rorc*) for differentiation and production of IL-17A (Ivanov et al., 2007). RORyt is the best-studied positive transcriptional regulator of IL-17A and IL-17F (Ivanov et al., 2006). In accordance with the importance of IL-17A transcription, RORyt expression has also been reported to be elevated in COPD patients and in mouse models of COPD (Chu et al., 2011; Li et al., 2015). However, the upstream pathophysiologic mechanisms that contribute to the induction of RORyt and differentiation of Tc17 cells in COPD have not been well elucidated.

84 We previously reported that *miR-22* inhibits HDAC4, promoting antigen-presenting cell 85 activation (APC) in the lungs and inducing Th17-mediated emphysema in response to CS or nCB in mice (W. Lu et al., 2015). Additional miRNAs that control APC and/or T cell driven IL-17A+ 86 87 inflammation have been identified by others including the *let*-7 miRNA family (Mai et al., 2012; 88 Angelou et al., 2020). MicroRNA expression-based studies have shown frequent downregulation 89 of members of the let-7 miRNA family, including let-7a, let-7b, let-7c, let-7d, let-7e, and let-7f in human emphysematous lung tissue and in murine models of emphysema, but the mechanism(s) 90 of action remain ill-defined (Christenson et al., 2013; Pottelberge et al., 2011; Conickx et al., 2017; 91 Izzotti et al., 2009). Let-7 microRNA genes are encoded across eight loci either as single genes 92 93 or as polycistronic clusters which have confounded their analysis in vivo (Rodriguez et al., 2004). Previous studies used Lin28b transgenic overexpression in T cells to block the maturation and 94 processing of the let-7 miRNA family. They showed an inhibitory role of let-7 family in Th17-driven 95 response in the murine model of experimental autoimmune encephalomyelitis (EAE) attributed in 96 97 part to regulation of IL-1 receptor 1 and IL-23 receptor (Angelou et al., 2020).

Here we found that *let-7* miRNA, notably the *let-7a3/let-7b* and *let-7a1/let-7f1/let-7d* clusters, are suppressed in the T cells isolated from lungs of emphysema patients. Consistently, the analogous murine *let-7b/let-7c2-* (*let-7bc2*) and *let-7a1/f1/d1-* (*let-7afd*) clusters were similarly downregulated in pre-clinical emphysema models. We engineered mouse models with the

specific loss-of-function (LOF) mutations of the let-7bc2- or let-7afd-clusters (let-7bc2^{LOF} and let-102 103 7afd^{LOF}, respectively) in T cells as well as an inducible *let-7g* gain-of-function (GOF) (*let-7^{GOF}*) model to determine the T cell-intrinsic role of let-7 miRNA in emphysema pathogenesis. Deletion 104 105 of let-7 miRNA in T cells worsened alveolar damage elicited by inhalation of CS or nCB, and 106 increased infiltration of immune cells in the airways, including IL-17-producing CD8⁺ T (Tc17) cells. Mechanistically, we found that *let-7* controls type 17 differentiation by directly targeting the 107 108 lineage-determining transcription factor, RORyt. In support of this conclusion, let-7^{GOF} mice were resistant to nCB-mediated induction of RORyt and Tc17 responses. Thus, we show a previously 109 110 unappreciated role for let-7 miRNA as a repressor of RORyt and a molecular brake to the IL-17mediated T cell inflammation in emphysema. 111

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113 **RESULTS**

114 The *let-7bc2*- and *let-7afd-clusters* are downregulated in lungs and T cells in COPD.

115 To explore the involvement of let-7 in emphysema, we scrutinized the genomic locations and 116 transcriptional annotation of let-7 members frequently downregulated in lung T cells isolated from smoker's lungs as well as mouse models of emphysema. This combined approach showed close 117 118 linkage and high conservation of two Let-7 clusters encoded from long intergenic non-coding RNA (linc)-like precursors in humans and mice (Figure 1A). To shed light on whether these Let-7 119 120 clusters are downregulated in patients with COPD, we analyzed a published (GSE57148) lung RNA-seq dataset obtained from COPD (n=98) and control (n=91) subjects (Kim et al., 2015). Our 121 analysis identified significant downregulation of the Mirlet7ahg and Mirlet7bhg gene cluster 122 123 transcripts in COPD compared to control subjects (Figure 1B). We carried out quantitative PCR 124 (qPCR) detection of Let-7a, which is encoded by both clusters, in lung tissue samples of smokers with emphysema and non-emphysema controls, detecting significant downregulation of Let-7a in 125

emphysema samples relative to controls (Figure 1C). Because *Let-7* has been shown to participate in IL-17⁺ T cell responses (Angelou et al., 2020; Guan et al., 2013; Newcomb et al., 2015), we next sought to determine if the expression pattern of *Mirlet7ahg* and *Mirlet7bhg*-derived *Let-7* members are impaired in purified CD4⁺ T cells from emphysematous lungs. In support of our original hypothesis, the CD4⁺ T cell expression of *Let-7a*, *Let-7b*, *Let-7d*, and *Let-7f* were all inversely correlated with more severe emphysema distribution in the lungs as determined by CT scan (Figure 1D).

Next, we elucidated *let-7a1/let-7f1/let-7d-* and *let-7b/let-7c2-*clusters expression (herein referred to as *let-7afd* and *let-7bc2* respectively) in murine models of CS- or nCB-induced emphysema respectively (Figure 1E). Paralleling our observations in human COPD and emphysema, mice with CS- or nCB-induced emphysema exhibited reduced expression levels of *pri-let7a1/f1/d* and *pri-let7b/c2* transcripts in the lung and from isolated lung CD4⁺ and CD8⁺ T cells (Figure 1F-H). Collectively, our expression results indicate suppression of *let-7afd* and *let-7bc2-*clusters in the lung and T cells in human and pre-clinical models of emphysema.

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141 Conditional deletion of the *let7bc2*-cluster in T cells enhances nCB- or CS-induced 142 emphysema.

To investigate the *in vivo* requirement of the *let-7bc2*-cluster within T cells, we generated conditional ready floxed mice (*let-7bc2^{flox/flox}*). We then crossed *let-7bc2^{flox/flox}* mice with *CD4-Cre* mice to generate *let-7bc2^{flox/flox}*; *CD4-Cre* LOF mice (denoted as *let-7bc2^{LOF}* mice hereafter) (Figure 2A). This approach allowed us to conditionally delete the *let-7bc2*-cluster in all T cells derived from the CD4⁺CD8⁺ double-positive (DP) stage (P. Lee et al., 2001; Shi & Petrie, 2012). We confirmed that *let-7bc2^{LOF}* mice exhibit robust conditional deletion of the *let-7bc2*-cluster in DP thymocytes and peripheral T cells (Figure 2B and data not shown). Our *let-7bc2^{LOF}* adult mice were born at the expected Mendelian frequency and did not show any overt histopathologic or inflammatory changes in lungs histopathology up to 1 year of age in comparison to $let-7bc2^{t/f}$ control mice (Figure 2-figure supplement 1A-C). Furthermore, quantification of major immune populations and T cell subsets by flow cytometry in $let-7bc2^{LOF}$ were comparable to control mice under baseline conditions and with moderate aging (Figure 2-figure supplement 1C,D).

We next exposed *let-7bc2^{LOF}* and *let-7bc2^{t/f}* control mice to nCB or CS and examined the 155 lungs under the context of experimental emphysema. Histomorphometry measurements of mean 156 linear intercept (MLI) from hematoxylin and eosin (H&E)-stained sections revealed that the 157 enlargement of alveolar spaces sustained from either nCB- or CS-exposure was exaggerated in 158 *let7bc2^{LOF}* mice relative to controls (Figure 2C-E). Chronic inflammation in emphysema is 159 characterized by the recruitment of macrophages and neutrophils to the lung tissue and airways 160 (Peleman et al., 1999; Senior & Anthonisen, 1998). Internally consistent with MLI measurements, 161 162 *let-7bc2^{LOF}* mice treated with nCB showed significantly increased airway infiltration of macrophages and neutrophils in BAL fluid as compared to wild-type control animals (Figure 2F). 163 Concomitant with these findings, expression levels of *Mmp9* and *Mmp12*, which are secreted by 164 macrophages and neutrophils to degrade elastin and mediate alveolar damage, were elevated in 165 airways of let7bc2^{LOF} mice exposed to CS versus controls (Figure 2G). As expected, let-7bc2^{LOF} 166 mice treated with nCB exhibit significantly less pri-let7b/c2 transcript expression in isolated lung 167 T cells relative to wild-type control mice (Figure 2-figure supplement 2A and data not shown). 168 169 Collectively, our data suggests that the *let-7bc2*-cluster within T cells protects by dampening 170 airway destruction and inflammation because the absence of this cluster worsens the severity of 171 experimental emphysema in mice.

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173 The *let-7bc2* miRNA cluster negatively regulates T_c17 inflammation in emphysema.

174 We sought to identify the T cell-intrinsic mechanisms that underlie the exaggerated inflammation observed in emphysematous *let-7bc2^{LOF}* mice. We focused on the IL-17-mediated 175 T cell response because it promotes neutrophil and macrophage recruitment in the lungs 176 (Beringer et al., 2016; Veldhoen, 2017; Shan et al., 2012). Previously, we established the induction 177 178 of CD4⁺IL17⁺ (Th17) cells along with CD4⁺IFNγ⁺ (Th1) cells in mice with chronic nCB exposure (You et al., 2015), however whether nCB similarly induces CD8⁺IL17A⁺T cells (Tc17) or cytotoxic 179 180 T cells (Tc1) had not been studied. The flow cytometric profiling of lung T cells revealed enriched proportions and counts of Tc1/Tc17 as well as Th1/Th17 cells in wild-type mice upon treatment 181 182 with nCB (Figure 3A,B). These findings suggests that nCB elicits both the type 17 and type 1 T cell responses, consistent with CS and elastase pre-clinical models of emphysema (Zhang et al., 183 2019). 184

185 We next interrogated the regulatory role of the *let-7bc2*-cluster in the type 17 and type 1 responses generated from exposure to nCB. Interestingly, *let-7bc2^{LOF}* mice showed increased 186 CD8⁺IL17A⁺ Tc17 cells relative to nCB control animals. In contrast, CD8⁺IFNy⁺ and GZMA⁺ Tc1 187 populations remained unperturbed with absence of the *let-7bc2*-cluster, suggestive of a more 188 refined regulatory role on Tc17 differentiation (Figure 3A,B). There were no significant differences 189 in either Th1 or Th17 cells when comparing nCB-treated let-7bc2^{LOF} to wild-type controls, 190 indicating the *let-7bc2*-cluster was dispensable for their generation (Figure 3C). Regulatory T cells 191 form a dynamic axis with Tc17/Th17 cells and act as a counterbalance to lung inflammation in 192 193 emphysema (Duan et al., 2016; Jin et al., 2014). Therefore, we examined whether Tc17 cell alterations were driven by the let-7bc2-cluster acting on regulatory T cells (Tregs). The let-7bc2^{LOF} 194 mice showed no significant difference in the Tregs subset relative to controls in our model (Figure 195 196 3D). Together, our data support the notion that deletion of the *let-7bc2*-cluster is insufficient to 197 provoke Tc17 cell generation under homeostatic conditions. However, under the context of chronic

inflammation in emphysema, the loss of *let-7bc2*-cluster is intrinsic for the potentiation of T cells
 towards Tc17 differentiation.

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The *let-7* family directly inhibits RORγt expression governing Tc17 differentiation in emphysema.

We utilized the TargetScan predictive algorithm to identify putative *let-7* miRNA targets 203 that are known to control the IL-17-mediated T cell response (Agarwal et al., 2015). This analysis 204 205 revealed that the 3'UTR region of Rorc, encoding RORyt, contains an evolutionarily conserved and complementary motif for the let-7 miRNA family (Figure 4A). Thus, we examined if let-7bc2-206 207 cluster loss in T cells would stimulate and enhance RORyt. Initially, we carried out flow cytometric quantification for RORyt in thymocyte, splenic, and lung T cells of naïve control and let-7bc2^{LOF} 208 209 mice up to 6-months of age. Our interrogation of RORyt mean fluorescent intensity (MFI) by flow 210 cytometry showed induction of RORyt in single-positive CD8⁺ and CD4⁺ thymocytes, as well as 211 peripheral splenic CD8⁺ and CD4⁺ T cells (Figure 4B). However, RORyt levels appeared unchanged in purified lung CD8⁺ T cells and CD4⁺ T cells of naive *let-7bc2^{LOF}* mice, alluding to a 212 compensatory effect in homeostatic lung T cells (Figure 4B). Since we and others have shown 213 that miRNAs are frequently associated with stress-dependent phenotypes, we posited that 214 emphysematous let-7bc2^{LOF} T cells are poised towards induction of RORyt and production of IL-215 17⁺ subsets after challenge with nCB. Indeed, nCB-emphysematous *let-7bc2^{LOF}* mice exhibited 216 enhanced RORyt protein levels in both CD8⁺ and CD4⁺ T cells relative to control mice with 217 emphysema (Figure 4C). 218

Because we had found that the *let-7afd*-cluster is downregulated in T cells isolated from COPD lungs in human and mice, and that the *let-7* family operates with some functional redundancy, we generated mice with conditional deletion of the *let7afd*-cluster in T cells (*let-7afd*^{*iff*};

CD4-Cre). The let-7afd[#]; CD4-Cre (let-7afd^{LOF}) mice aged up to 6-months did not exhibit overt 222 223 lung histopathology and inflammatory changes (Figure 4-figure supplement 1A-F). Of particular interest, ablation of the let-7afd-cluster enhanced levels of RORyt in thymic and peripheral T cells 224 225 of mice (Figure 4D). Overall, this indicates that independent let-7 clusters restrain RORyt 226 expression levels from thymic development to peripheral T cells under homeostatic conditions. 227 Next, we determined whether loss of *let-7afd*-cluster in T cells likewise sensitizes mice towards 228 induction of RORyt in nCB-emphysema. Intranasal administration of nCB provoked increased RORyt expression in lung T cells of *let-7afd^{LOF}* mice compared to control mice (Figure 4E), 229 supporting overlapping functionality between the let-7bc2- and let-7afd-clusters in repression of 230 RORyt within T cells. 231

To confirm that the *let-7* family negatively regulates Tc17 cell differentiation, at least in part, 232 cell autonomously in CD8⁺ T cells, we purified naïve CD8⁺ T cells from *let-7bc2^{LOF}* and control 233 234 mice spleens and cultured these cells in vitro in the presence of Tc17 polarizing (TGFβ, IL-6, anti-IFNy, IL-23, and IL-1β) or Tc1 polarizing (IL-2) conditions (Flores-Santibáñez et al., 2018). Our 235 flow cytometric analysis confirmed the enhanced commitment of *let-7bc2*-cluster deficient CD8⁺ 236 T cells towards Tc17 cells and IL-17A⁺ production relative to control CD8⁺ T cells (Figure 5A,B). 237 238 Moreover, enhanced Tc17 cell differentiation mirrored the increased IL-17A detected in the supernatant from *in vitro* polarized cells as quantified by ELISA (Figure 5C). Parallel assessment 239 of Tc1 differentiation did not detect a difference in CD8⁺IFN γ ⁺ cells (Figure 5A and Figure 5D). 240 Altogether, these data recapitulated our *in vivo* findings that the *let-7bc2*-cluster negatively 241 242 regulates Tc17 response but is dispensable in Tc1 cells. Finally, to determine whether Tc17 differentiation is likewise controlled by the *let-7afd*-cluster, we cultured naive CD8⁺ splenocytes 243 from *let-7afd^{LOF}* and controls under Tc17 conditions. As we had observed with *let-7bc2^{LOF}*, 244 absence of the let-7afd-cluster in T cells further enhanced differentiation towards Tc17 cells as 245 quantified by flow cytometry and ELISA (Figure 5F,G). 246

Next, we focused on *Rorc* as a potential direct target of *let-7*, which could mechanistically 247 mediate enhanced Tc17 differentiation in *let7bc2^{LOF}* mice. Towards this objective, we tested 248 whether *let-7bc2^{LOF}* or *let-7afd^{LOF}* naïve CD8⁺ T cells show elevated RORyt expression under 249 250 either Tc0 or Tc17 differentiation conditions. In agreement with enhanced Tc17 differentiation, 251 RORyt expression was differentially and significantly upregulated under both Tc0 and Tc17 differentiation conditions in let-7 LOF cells relative to controls (Figure 5E.H). To determine 252 253 whether let-7 directly represses Rorc mRNA levels we cloned the 3'UTR of Rorc into luciferase constructs. These reporter assays with let-7b expressing cells independently confirmed that let-254 255 7b represses Rorc (Figure 5I, left). Furthermore, deletion of the putative let-7 binding sequence (Figure 4A) abrogated repression by *let-7b* (Figure 5I, right), thus confirming *Rorc* as a functional 256 target of *let-7* miRNA. Overall, these *in vitro* experiments readily recapitulated an upstream 257 regulatory role of *let-7* in Tc17 differentiation, mediated in part, via direct suppression of RORyt. 258

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260 Enforced expression of *let-7* tempers RORγt T cell expression levels in experimental 261 emphysema.

To explore a potential protective role of let-7 miRNA in experimentally-induced 262 263 emphysema, we generated mice which allowed for selective induction of *let-7* activity in T cells 264 using the published rtTA-iLet7 mice crossed to CD4-Cre (herein referred to as let-7^{GOF}; Figure 6A) (Angelou et al., 2020; Belteki et al., 2005; Pobezinskaya et al., 2019; Wells et al., 2017; Zhu et 265 al., 2011). The rtTA-iLet7 mouse model has been utilized to promote ~2-3-fold rise in total let-7 266 activity in T cells (Angelou et al., 2020; Wells et al., 2017, 2023; Angelou et al., 2020). Steady-267 268 state *let*-7^{GOF} and control (*rtTA-iLet7*) mice were examined for compromised RORyt protein levels 269 within thymocytes and peripheral T cells. Providing further evidence of *let-7*-dependent regulation of Rorc, protein levels of RORyt were suppressed in CD8⁺ and CD4⁺ T cells of *let*-7^{GOF} mice 270 relative to controls (Figure 6B). To determine whether enforced expression of let-7 offered 271

protection from experimental emphysema, *let-7^{GOF}* and control mice were treated with nCB and 272 then examined for changes in lung pathology and T cell type 17 responses. The *let-7^{GOF}* mice did 273 not exhibit any signs of lung inflammation or pathologic remodeling at baseline (Figure 6C,D and 274 275 data not shown) Histopathologic analysis revealed a comparable degree of lung alveolar distension via morphometric measurements of MLI in nCB-treated let-7^{GOF} mice versus controls 276 suggesting that enforced let-7 expression is insufficient to protect the lung from emphysema 277 (Figure 6C,D). On the other hand, evaluation of the IL-17⁺ response and RORyt levels in 278 emphysematous lung T cells demonstrated that, in contrast to control nCB-treated mice, let-7^{GOF} 279 280 mice exhibited dampened lung Tc17 and Th17 cell populations and were resistant to the induction of RORyt after nCB-exposure (Figure 6E.F). Taken together, our let-7 LOF and GOF models 281 demonstrate the necessity and sufficiency of let-7 miRNA to act as a molecular brake to the type 282 17 T cell response through the direct regulation of RORyt, further our data suggests that nCB- or 283 284 CS-mediated suppression of this braking mechanism furthers inflammation and exacerbates emphysema severity (Figure 6G). 285

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287 DISCUSSION

MiRNA expression-based studies of COPD patients and mice exposed to CS have 288 289 reported downregulation of let-7 miRNA expression in lung tissues (Conickx et al., 2017; Christenson et al., 2013b; Schembri et al., 2009). We and others explored the consequence of 290 loss of let-7 expression/activity with synthetic oligonucleotides, sponges, lentiviral antisense 291 knockdown, or via ectopic delivery of *Lin28b* (Polikepahad et al., 2010; Viswanathan et al., 2008; 292 293 Piskounova et al., 2011), but studies pinpointing the role of individual let-7 clusters as potential 294 drivers of lung inflammation and COPD within T cells remained elusive. In the present study, we established that the let-7 miRNA family members encoded by the let-7bc2- and let-7afd-clusters 295 296 are downregulated in T cells from lungs of emphysema patients and emphysematous mice that were exposed to CS or nCB. Correspondingly, we demonstrated that *in vivo* genetic ablation of *let-7bc2-cluster* further sensitized mice to lung tissue destruction and emphysema upon treatment with nCB or CS. Mechanistically, our studies suggests that *let-7bc2-*cluster prevents the emergence of CD8⁺ T cell differentiation into Tc17 cells during emphysema in part, by directly silencing of *Rorc*.

302 Tc17 cells are vital for defense against viral, fungal and bacterial infections and they have also been associated with inflammation in various human diseases such as multiple sclerosis, 303 304 inflammatory bowel disease, and cancer (Huber et al., 2013; Globig et al., 2022; Corgnac et al., 2020). In accordance with the potential pathogenic role of Tc17 cells as drivers of COPD, several 305 studies detected increased cell numbers in airways and tissues of COPD patients as well as lungs 306 of smoke-exposed animal models (Y. Chang et al., 2011; Zhou et al., 2020; Duan et al., 2013). 307 308 Other researchers also detected increased Tc17 subpopulations in tissues of COPD patients with 309 infectious microbial exacerbations. In our earlier work to define the adaptive T cell immune responses in nCB induced COPD, we predominantly focused on the pathogenic role of Th17 cells, 310 but did not examine Tc17 cells (You et al., 2015). Here we expand upon our prior observations, 311 revealing that chronic exposure to nCB and elicitation of emphysema mice orchestrates the 312 313 emergence and accumulation of Tc17 cells which may act in parallel with Th17 cells to promote tissue damage. 314

Prior research has shown the importance of both transcriptional and post-transcriptional regulatory control of RORyt expression in T cells (Ciofani et al., 2012; Donate et al., 2013; Medvedev et al., 1997). Altogether, our *in vivo* studies establish *let-7* as a new important link associated with regulation of RORyt and lung Tc17 differentiation in COPD. Our data also showed that *in vivo* conditional genetic ablation of individual *let-7* clusters in T cells stimulates a rise in RORyt protein expression in single-positive thymocytes and peripheral CD8⁺ and CD4⁺ T cells while enforced *let-7* activity leads to partial repression of RORyt in T cells. Despite these 322 alterations in RORyt expression in our let-7 T cell LOF mice, the mice did not exhibit spontaneous gross phenotypes in thymus, spleens, or lungs at baseline nor did they exhibit changes in 323 Tc17/Th17 subpopulations. This may be due to the subtle and modest expression thresholding of 324 325 RORyt detected in mice and/or residual let-7 expression in T cells. On the other hand, and in agreement with our Tc17 and experimental emphysema data, we observed enhanced RORyt 326 expression in lungs of *let-7*^{LOF} mice after treatment with nCB. We corroborated the importance of 327 let-7 activity in Tc17 differentiation of ex vivo cultured CD8⁺ T cells, as well as in the direct 328 posttranscriptional control of RORyt, suggesting that this defect, is in part, direct and cell 329 330 autonomous. We did not ascertain whether deletion of let-7afd-cluster is an equally or more effective modulator of experimentally induced emphysema than the *let-7bc2*-cluster. Nonetheless, 331 we predict that under different cell stress contexts, the functions of let-7 clusters do not fully 332 overlap due to differential thresholding of mRNAs. 333

334 Prior studies have elucidated the relative and absolute quantities of individual *let-7* family members in murine thymocytes and peripheral T cells which range from ~2-30% (Pobezinskaya 335 et al., 2019: Pobezinsky et al., 2015). Moreover, the same group reported that all let-7 miRNAs 336 are coordinately downregulation following antigen stimulation through the T cell receptor (Wells 337 338 et al., 2017). Another recent study discerned a role for the IncRNA, CCAT1 (colon cancerassociated transcript 1) as a molecular decoy or sponge in human bronchial epithelial cells which 339 drives downregulation of *let-7c* following cigarette smoke extract exposure (L. Lu et al., 2017). 340 Thus, it seems likely that complex synergistic transcriptional and post-transcriptional mechanisms 341 342 contribute to downregulation of *let-7* activity in emphysematous T cells.

It is also important to note that *let-7* has been reported to exert potent effects by titrating the levels of multiple gene targets in mechanisms that contribute to Th17 inflammatory response and influence diverse set of processes including T cell activation, proliferation, differentiation, and cell homing (Angelou et al., 2020; Beachy et al., 2012; Bronevetsky et al., 2016; Pobezinskaya et

al., 2019; Pobezinsky et al., 2015; Wells et al., 2017). A particular feature of these studies has 347 348 been the utilization of Lin28b transgenic mice to block maturation and activity of entire let-7 family to promote a let-7 LOF function phenotype (Angelou et al., 2020; Piskounova et al., 2011; 349 Pobezinskaya et al., 2019; Wells et al., 2023; Zhu et al., 2011). Furthermore, Lin28b was recently 350 351 reported to also influence transcriptome-wide ribosome occupancy and global miRNA biogenesis (Tan et al., 2019). Thus, it is likely that Lin28b transgenic overexpression could give rise stronger 352 phenotypes than we observed in our single cluster *let-7*^{LOF} mice. Nonetheless, unbiased omics-353 based methods will be useful to determine if other gene targets beyond RORyt synergistically 354 355 potentiate the in vivo Tc17-response and emphysema phenotype in context of deletion of let-7bc2cluster. 356

357 Tc17 cells play a major role in microbial infections, providing a potent anti-viral response 358 (Hamada et al., 2009; Yeh et al., 2010), while viral infection has been an established factor in 359 COPD exacerbations (Hewitt et al., 2016; Wedzicha, 2004). It will be interesting to determine whether loss of let-7bc2- or let-7afd-cluster activity in the T cell compartment contributes to COPD 360 disease susceptibility in the context of viral exposure. Our experiments with let-7 GOF were 361 partially successful in limiting the emergence of Tc17 and Th17 in nCB-elicited emphysema. Let-362 363 7^{GOF} mice exhibited a reduction in RORyt expression levels and type 17 responses but were not protected from alveolar remodeling following nCB exposure. A potential limitation of the let-7^{GOF} 364 transgenic model is that it expresses only the *let-7g* sequence which may render it less potent 365 than the corresponding two mature forms transcribed from the let-7bc2-cluster. Additional studies 366 367 will be required to ascertain whether other interventions that enhance let-7 activity in T cells are successful in preventing or reversing COPD. 368

369

370 MATERIALS AND METHODS

371 **Mice**

372 Conditional knockout-ready floxed let-7bc2 and let-7afd mice were generated using CRISPR gene 373 editing in an isogenic C57BL/6 genetic background and were sequence verified for rigor. Mice 374 were PCR genotyped from ear samples with primers flanking loxP sites (Supplementary Table 1). The let-7bc2^{flox/flox}; CD4-cre and let-7afd^{flox/flox}; CD4-cre mice were PCR genotyped. The R26-375 376 STOP-rtTA; Col1a1-tet0-let-7 (rtTA-iLet7) mice were obtained from JAX Jax Stocks 023912 and 05670 and then bred to CD4-Cre were PCR genotyped with established JAX primers (Belteki et 377 al., 2005; Zhu et al., 2011). Control rtTA-iLet7 and the let-7^{GOF} mice were fed ad libitum with 378 200mg/kg of doxycycline-containing chow (Bio-Serv S3888) at weaning age primers (Belteki et 379 380 al., 2005; Zhu et al., 2011). Syngeneic littermates served as controls for all mouse experiments. All mice were bred in the transgenic animal facility at Baylor College of Medicine. All experimental 381 protocols used in this study were approved by the Institutional Animal Care and Use Committee 382 of Baylor College of Medicine animal protocol (AN-7389) and followed the National Research 383 384 Council Guide for the Care and Use of Laboratory Animals.

385

386 Human emphysema tissue samples and T cell isolation

Lung tissues were obtained from a total of 19 non-atopic current or former smokers with significant 387 388 (>20 pack-years, one pack-year equals to smoking one pack of cigarettes per day each year) history of smoking who were recruited into studies from the chest or surgical clinics at Michael E. 389 390 DeBakey Houston Veterans Affairs Medical Center hospitals (Supplementary Table 2) (Shan et 391 al., 2009). Emphysema and non-emphysema control patients were diagnosed from CT scans 392 according to the criteria recommended by the National Institutes of Health-World Health 393 Organization workshop summary (Pauwels et al., 2001). Human single-cell suspensions were 394 prepared from surgically resected lungs as previously described (Yuan et al., 2020; Grumelli et 395 al., 2004). Briefly, fresh lung tissue was minced into 0.1 cm pieces in petri dishes and treated with 396 2 mg/mL of collagenase D (Worthington) for 1 hour at 37°C. Digested lung tissue was filtered 397 through a 40-µm cell strainer (BD Falcon) followed by red blood cell lysis using ACK lysis buffer

(Sigma-Aldrich) for 3 minutes to yield a single-cell suspension. CD4⁺ T cells were selected from
resultant suspensions by labeling with bead conjugated anti-CD4 for enrichment by autoMACs
(Miltenyi Biotec). Studies were approved by the Institutional Review Board at Baylor College of
Medicine and informed consent was obtained from all patients.

402

403 Human lung transcriptome data

A publicly available RNA-seq dataset from a Korean cohort GSE57148 was selected for the analysis (Kim et al., 2015). The raw FASTQ files of paired end reads representing the transcriptome of control and cases were retrieved from the GEO database at the National Centre for Biological Information (NCBI) through accession number GSE57148 and analyzed with R package for differential expression.

409

410 Cigarette smoke exposure model of pulmonary emphysema

To promote emphysema, mice were exposed to cigarette smoke using our custom designed whole-body inhalation system (Morales-Mantilla et al., 2020). In total, mice were exposed to four cigarettes (Marlboro 100's; Philip Morris USA) per day, five days a week, for four months as previously described (Shan et al., 2012).

415

416 nCB exposure model of pulmonary emphysema

Nano-sized particulate carbon black was prepared and administered as previously described (You et al., 2015; W. Lu et al., 2015). Dried nCB nanoparticles were resuspended in sterile PBS to a concentration of 10 mg/ml. Fifty µl of reconstituted nCB (0.5 mg) were intranasally delivered to deeply anesthetized mice on a schedule of three times a week for four weeks (total delivered dose of 6 mg). Lung histomorphometry and airway inflammation were assessed four weeks after the final nCB challenge. For histomorphometric analysis, mice lungs were fixed with 10% neutral-buffered formalin solution via a tracheal cannula at 25-cm H₂O pressure followed by paraffin

embedding and tissue sectioning and stained with hematoxylin and eosin. Mean linear intercept
(MLI) measurement of mouse lung morphometry were done as previously described (Shan et al.,
2014; Morales-Mantilla et al., 2020). Briefly, this was done in a blinded fashion to mice genotypes
from ten randomly selected fields of lung parenchyma sections. Paralleled lines were placed on
serial lung sections and MLI was calculated by multiplying the length and the number of lines per
field, divided by the number of intercepts (Morales-Mantilla et al., 2020).

BALF was collected by instilling and withdrawing 0.8 ml of sterile PBS twice through the
trachea. Total and differential cell counts in the BALF were determined with the standard
hemocytometer and HEMA3 staining (Biochemical Sciences Inc, Swedesboro, NJ) using 200 μL
of BALF for cytospin slide preparation (Morales-Mantilla et al., 2020; W. Lu et al., 2015).

434

435 Cell isolation from murine lung tissue

436 Mouse lung tissue were cut into 2-mm pieces and digested with collagenase type D (2 mg/ml; Worthington) and deoxyribonuclease (DNase) I (0.04 mg/ml; Roche) for 1 hour in a 37°C 437 incubator. Single-cell suspensions from lung digest, spleen, and thymus were prepared by 438 mincing through 40-µm cell strainers then washing and resuspension in complete RPMI media. 439 440 Mouse lung and spleen single-cell suspensions were additionally overlaid on Lympholyte M cell separation media (Cedarlane) as indicated in the manufacturer's protocol to purify lymphocytes. 441 For murine *let-7* expression studies, lung single-cell suspensions were labeled with anti-CD4⁺ or 442 anti-CD8⁺ magnetic beads and separated by autoMACS (Miltenyi Biotec), or CD4⁺CD8⁺ double 443 444 positive cells purified from thymus single-cell suspensions by flow-cytometric sorting on FACS 445 Aria (BD Biosciences).

446

447 In vitro polarization of CD8⁺ T cells

448 CD8⁺ naïve T cells were isolated from spleen using Mojosort Mouse CD8 Naïve T cell isolation
449 Kit (Biolegend) and adjusted to a concentration of 1.0x10⁶ cells/mL. Purified cells were activated

with plate-bound anti-CD3 (1.5 μ g/mL) and complete RPMI media containing anti-CD28 (1.5 μ g/mL) and β -mercaptoethanol (50nM) for Tc0 polarization, or further supplemented with Tc1 [IL-2 (10ng/mL)] or Tc17 [TGF β (2ng/mL), IL-6 (20ng/mL), anti-IFN γ (10 μ g/mL), IL-23 (20ng/mL), and IL-1 β (5ng/mL)] polarization conditions for 72 hours (Flores-Santibáñez et al., 2018).

454

455 **ELISA**

Supernatant was collected from *in vitro* polarized murine CD8⁺ T cells and centrifuged to remove
cellular debris (W. Lu et al., 2015). Cytokine levels of IL-17A and IFNγ were quantified from
collected supernatant using Mouse IL-17A Uncoated ELISA and Mouse IFN gamma Uncoated
ELISA (Invitrogen) Kits, respectively, per the manufacturer's instructions with colorimetric analysis
by the Varioskan LUX microplate reader (ThermoFisher).

461

462 Flow cytometric analysis

Cells used for in vitro or in vivo cytokine analysis were stimulated with PMA (20ng/mL; Sigma 463 Aldrich), Ionomycin (1µg/mL; Sigma Aldrich), and Brefeldin A (2µg/mL; Sigma Aldrich) for 4 hours 464 prior to flow staining (W. Lu et al., 2015). For intracellular staining, cells were fixed and 465 466 permeabilized using the Mouse FOXP3 Buffer Set (BD) per the manufacturer's protocol. The fluorophore-conjugated antibodies used in this study were as follows: Live/Dead Fix Blue 467 (Invitrogen), CD3 PerCPCy5.5 (Biolegend), TCRb PE/Cy7 (Biolegend), CD4 PB (Biolegend), CD4 468 AF700 (Biolegend), CD8 BV650 (Biolegend), CD25 BV421 (Biolegend), FOXP3 AF488 469 (Biolegend), ROR gamma T PE (Invitrogen), TCF1 AF647 (Cell Signaling Technologies), TCF1 470 PE (Biolegend), IFNy AF647 (Biolegend), IL17A FITC (Biolegend), IL17A PE (ebioscience). 471 Representative flow cytometric gating and quantification strategy for detection of lung Th1/Th17 472 473 and Tc1/Tc17 cell populations is shown in Supplementary Figure 3. Samples were analyzed using 474 BD LSR II flow cytometer (BD Biosciences) and FlowJo software (TreeStar).

475

476 **RNA Isolation and Quantitative RT-PCR**

RNA was isolated using miRNeasy (Qiagen) or RNeasy Mini Kit (Qiagen) in conjunction with the 477 RNase-Free DNase (Qiagen) according to the manufacturer's instructions. cDNA of miRNAs and 478 479 mRNAs were synthesized using TagMan Advanced miRNA cDNA Synthesis Kit (ThermoFisher) 480 and High-Capacity cDNA Reverse Transcription Kit Real-Time PCR system (Applied Biosystems). 18S and snoRNA-202 were used to normalize mRNA and miRNA expression respectively (W. Lu 481 et al., 2015). Quantitative RT-PCR data were acquired on 7500 Real-Time PCR System or 482 StepOne Real-Time PCR System (Applied Biosystems) with the following TagMan probes: hsa-483 484 let-7a-5p [478575 mir], hsa-let-7b-5p [478576 mir], hsa-let-7d [478439 mir], hsa-let-7f [478578 mir], pri-let7a1/f1/d [44411114, arfvmhy], pri-let7b/c2 [4441114, areptx2], Mmp9 485 [Mm00442991], Mmp12 [Mm00500554]. 486

487

488 Luciferase reporter assays

Genomic fragment containing the murine Rorc 3'UTR was cloned into psiCHECK2 luciferase 489 reporter plasmid (Promega). This construct was also used to generate the let-7 'seed' deletion 490 mutant derivative using the QuikChange Multi Site Mutagenesis Kit (catalog 200514-5, 491 492 Stratagene). 3T3 mouse embryonic fibroblasts (MEFs) were transfected using Oligofectamine 493 (Invitrogen) with 100 ng of psiCheck-2 plasmid containing wild-type or mutant 3'UTR, along with the miRNA control or *let-7b* duplex (Dharmacon) at a final concentration of 6 nM (Gurha et al., 494 495 2012) (Supplementary Table 1). Reporter activity was detected with the Dual-Luciferase Reporter 496 Assay System (Promega).

497

498 Statistical analysis

499 Statistical analyses were performed using GraphPad Prism 10.0.1 software. Statistical 500 comparison between groups was performed using the unpaired Student's t-test, two-way analysis 501 of variance (ANOVA) with Tukey's or Sidak's correction, and Mann-Whitney Test when indicated.

A P-value less than 0.05 was considered statistically significant; ns indicates not significant. Statistical significance values were set as *P < 0.05, **P < 0.01, ***P < 0.001, and ****P < 0.0001.

504 Data are presented as means ± SEM. P-value and n can be found in the main and supplementary

505 figure legends.

506

507 **COMPETING INTEREST STATEMENT**

508 The authors declare no competing interests.

509

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517

518 AUTHOR CONTRIBUTIONS

- 519 P.E., X.H., D.B.C, F.K., and A.R. conceptualized experiments and interpreted results. P.E., X.H.,
- 520 M.J.S., H.T., M.A.P., and S.L.L. acquired the data, M.J.R. provided bioinformatics analyses. P.E.
- and A.R. wrote the manuscript.

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Figure 1. Repression of *Let-7* miRNA gene clusters in lung T cells from COPD patients and murine models of emphysema. (A) Schematic representation of the polycistronic transcripts for the *Let-7a1/Let-7f1/Let-7d-* and *Let-7b/Let-7a3-*clusters in humans and *let-7a1/let-7f1/let-7f1/Let-7d-* and *Let-7b/Let-7a3-*clusters in humans and *let-7a1/let-7f1/let-7f1/let-7f1/let-7f1/let-7f2-* and *let-7b/let-7c2-*clusters in mice. (B) *In silico* analysis of *Mirlet7a1hg* and *Mirlet7bhg* from the publicly available lung transcriptome dataset from RNA-seq of COPD and control patients (GEO: GSE57148). (C) Quantitative RT-PCR (qPCR) of mature *Hsa-Let-7a* from resected lung tissue of COPD (n=15) and control subjects (n=11). (D) QPCR and regression analysis of *Hsa-Let-7a, Hsa-Let-7b, Hsa-Let-7d, and Hsa-Let-7f* expression to emphysema severity score based on CT: 0=no, 1=upper lobes only, 2=upper/middle lobes, 3=extensive pan lobular emphysema (n=19). (E) Schematic diagram of experimental emphysema in mice induced by either intranasal (i.n.) instillation of nCB or exposure to CS by whole-body inhalation (w.b.i.). (F-H) QPCR analysis for *pri-let-7a1/f1/d* and *pri-let-7b/c2* from lung tissue or lung-derived CD8⁺ and CD4⁺ T cells of mice with emphysema elicited by (F) nCB- or (G-H) CS (n=3-6 per group). Data are representative of three independent experiments displayed as mean±SEM. Mann-Whitney (B,C) or Student's t-test (F,G,H). *p < 0.05, **p < 0.01, ***p < 0.001, ****p<0.0001.



Figure 2. Deletion of the *let-7bc2* **cluster in T cells enhances nCB- or CS-triggered emphysema.** (A) Schematic representation of CD4-Cre (*let-7bc2^{LOF}*) or *let-7bc2^{t/ff}* (Control) mice. (B) QPCR analysis of *pri-let-7b/c2* from flow-sorted live, TCR β^+ , CD4⁺CD8⁺ double-positive (DP) thymocytes of control and *let-7bc2^{LOF}* mice (n=3-5 per group). (C-G) Control and *let-7bc2^{LOF}* mice were exposed to vehicle (PBS) or nCB for 4 weeks, or alternatively air or cigarette smoke by whole body inhalation of cigarette smoke (CS) for 16 weeks. (C) Representative H&E stained lung sections from PBS-, nCB-, or CS-exposed mice as indicated on each panel (x20 magnification; scale bars, 50µm). (D-E) Mean linear intercept (MLI) measurement of lung morphometry. (F) Total and differential cell counts from bronchoalveolar lavage (BAL) fluid from controls and *let-7bc2^{LOF}* mice (n=4-7 per group). (G) *Mmp9* and *Mmp12* mRNA expression from BAL cells of air- and smoke-exposed control and *let-7bc2^{LOF}* mice (n=4-6 per group). Data are representative of at least three independent experiments displayed as mean±SEM using Student's t-test (B) or two-way ANOVA with *post-hoc* Tukey correction (D,E,F,G). *p < 0.05, **p < 0.01, ***p < 0.001, ****p<0.0001.



Figure 3. In vivo T cell ablation of the *let-7bc2*-cluster enhances Tc17 inflammatory response to nCB-emphysema. Representative flow plots with percentage and counts of live TCR β^+ (A) CD8⁺IL-17a⁺ and CD8⁺IFN γ^+ , (B) CD8⁺IFN γ^+ GzmA⁺, (C) CD4⁺IL-17a⁺ and CD4⁺IFN γ^+ , and (D) CD4⁺ Foxp3⁺CD25⁺ cells from the lungs of control (Ctrl) PBS vehicle- (n=5-6), control nCB- (n=6), and *let-7bc2^{LOF}* nCB-exposed mice. Data are representative of three independent experiments displayed as mean±SEM using ANOVA with *post-hoc* Sidak correction. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001.



Figure 4. Deletion of either the *let7bc2- or let7afd-cluster* in T cells enhances RORyt expression *in vivo.* (A) Left: Schematic representation of the murine *Rorc* 3'UTR with *let-7* miRNA binding sites as identified by TargetScan. Right: Schematic of a conserved *let-7* miRNA target sequence in the 3'UTR of *Rorc.* (B-C) Flow analysis of RORyt expression by MFI quantification in live TCR β *CD8* or CD4* T cells from indicated tissues of (B) naïve control (Ctrl) and *let-7bc2^{LOF}* mice or (C) nCB-treated lungs by representative flow plot and MFI quantification (n=5 per group). (D) RORyt expression by MFI quantification in naïve mice *let-7afd^{LOF}* mice thymus, spleen, and lungs (n=3-4 per group), or (E) nCB-exposed lungs (n=5 per group). Data are representative of at least three independent experiments displayed as mean±SEM using student's t-test. *p < 0.05, **p < 0.01, ***p < 0.001.



Figure 5. *Let-7* restricts Tc17 *in vitro* differentiation in part via direct targeting of *Rorc* mRNA. (A) Representative flow plots of live TCR β^+ CD8⁺, IL-17a⁺ and IFN γ^+ populations from Tc1 and Tc17 polarized naïve splenic CD8⁺ cells from control and *let-7bc2^{LOF}* mice and (B) quantification of CD8⁺IL-17a⁺ cells (n=5 per group). (C) ELISA of IL-17a from the supernatant of Tc1 and Tc17 polarized control and *let-7bc2^{LOF}* cells (n=5 per group). (D) Flow quantification of CD8⁺IFN γ^+ populations in Tc1 and Tc17 polarized control and *let-7bc2^{LOF}* cells (n=5 per group). (E) Representative flow plot and quantification of ROR γ t from Tc0 or Tc17 differentiated naïve splenic CD8⁺ T cells isolated from control and *let-7bc2^{LOF}* mice (n=5 per group). (F) Representative flow plots of CD8⁺IL-17a⁺ population frequency and quantification of Tc17 polarized naïve splenic CD8⁺ cells of indicated mice polarized under Tc1 or Tc17 conditions. (G) ELISA of IL-17a from control, Tc1 (n=4), control Tc17 (n=4), and *let-7afd^{LOF}* Tc17 (n=3) polarized cells. (H) Quantification of ROR γ t from Tc0 or Tc17 *in vitro* polarized naive CD8⁺ T cells from control and *let-7afd^{LOF}* mice (n=3-4 per group). (I) Control (*Rorc* WT) or binding site mutant (*Rorc* Mut) 3' UTRs of *Rorc* were cloned downstream of the renilla luciferase reporter. Plasmids were cotransfected with either a control-miR (black bars) or *let-7b* mimic (blue bars) duplex into cultured cells. Reporter activity was measured 24 hours after transfection and normalized to firefly activity. Data are representative of two (H), three independent experiments (A-G), or carried out in triplicate (I) and displayed as mean±SEM using student's t-test. *p < 0.05, **p < 0.01, ***p < 0.001.



Figure 6. Enforced *let-7* expression in T cells restrains induction of RORyt and Tc17/Th17 inflammation in lungs of nCB-exposed mice. (A) Schematic outlining our T cell-inducible *let-7g* mouse model (*let-7^{GOF}*). (B) Flow analysis of RORyt expression in live, TCR β +CD8⁺ or CD4⁺ T cells from (B) naïve control and *let-7^{GOF}* mice in thymus, spleen, and lungs (n=3-5 per group). (C) Control and *let-7^{GOF}* mice were treated with PBS vehicle or nCB then analyzed. Representative H&E-stained lung sections from PBS- and nCB-exposed mice as indicated on each panel (x20 magnification; scale bars, 50µm) (D) MLI measurements from indicated mice (n=5-6 per group). (E) Flow analysis of lungs gated on live TCR β ⁺ CD8⁺ or CD4⁺ cells for (E) IL-17a⁺ population frequency (n=3-4 per group) or (F) RORyt expression by representative flow plot and MFI quantification (n=4-5 per group). (G) Figure model for *let-7*/RORyt axis in emphysema pathogenesis. Data are representative of two (B) or three (C-F) independent experiments and displayed as mean±SEM using student's t-test (B) or two-way ANOVA with Tukey's multiple correction (D-F). *p < 0.05, **p < 0.001, ***p < 0.001.