Notch4 signaling limits regulatory T-cell-mediated tissue repair and promotes severe lung inflammation in viral infections

Graphical abstract

Highlights
- Notch4 expression on Treg cells is associated with COVID-19 disease severity
- Notch4 inhibition suppresses lung inflammation in proxy viral mouse models
- Notch4 limits amphiregulin-dependent lung Treg cell tissue repair functions

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In brief
Harb, Benamar, et al. find that interleukin-6 increases Notch4 expression on lung regulatory T cells, which, in turn, restrains production of the tissue repair cytokine amphiregulin and promotes severe lung inflammation. Their findings have implications for treatment of COVID-19 and other respiratory viral infections.

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Notch4 signaling limits regulatory T-cell-mediated tissue repair and promotes severe lung inflammation in viral infections

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SUMMARY

A cardinal feature of COVID-19 is lung inflammation and respiratory failure. In a prospective multi-country cohort of COVID-19 patients, we found that increased Notch4 expression on circulating regulatory T (Treg) cells was associated with disease severity, predicted mortality, and declined upon recovery. Deletion of Notch4 in Treg cells or therapy with anti-Notch4 antibodies in conventional and humanized mice normalized the dysregulated innate immunity and rescued disease morbidity and mortality induced by a synthetic analog of viral RNA or by influenza H1N1 virus. Mechanistically, Notch4 suppressed the induction by interleukin-18 of amphiregulin, a cytokine necessary for tissue repair. Protection by Notch4 inhibition was recapitulated by therapy with Amphiregulin and, reciprocally, abrogated by its antagonism. Amphiregulin declined in COVID-19 subjects as a function of disease severity and Notch4 expression. Thus, Notch4 expression on Treg cells dynamically restrains amphiregulin-dependent tissue repair to promote severe lung inflammation, with therapeutic implications for COVID-19 and related infections.

INTRODUCTION

The current pandemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus has resulted in massive morbidity and mortality in the United States and globally (Cucinotta and Vanelli, 2020). Although many infected subjects are asymptomatic or have a mild form of the disease, a subset suffers from more severe disease with pneumonia and marked hypoxia, leading to acute respiratory distress syndrome (Berlin et al., 2020; Richardson et al., 2020; Zhou et al., 2020a). In many of those individuals, the disease proves fatal despite intensive respiratory support. Uncontrolled activation of the immune response, leading to a cytokine storm, is a key risk factor for mortality (Henderson et al., 2020; Lucas et al., 2020; Vabret et al., 2020). The molecular mechanisms governing lung disease severity are not yet well understood. Notably, innate immune
cell hyperactivation plays a critical role in the pathogenesis of severe coronavirus disease 2019 (COVID-19) (Del Valle et al., 2020; Vabret et al., 2020; Zhou et al., 2020b), a finding also recapitulated in emerging mouse models (Winkler et al., 2020). Among the innate immune cytokines, interleukin-6 (IL-6) has been proposed to play a pathogenic role because of its increased serum concentrations in subjects with severe COVID-19 and reports of favorable clinical responses to anti-IL-6 receptor (IL-6R) monoclonal antibody (mAb) therapy (Copaescu et al., 2020; The REMAP-CAP Investigators, 2021; Salama et al., 2021; Toniati et al., 2020; Xu et al., 2020). Other studies, however, have failed to confirm such a benefit (Hermeine et al., 2021; Rosas et al., 2021; Salvarani et al., 2021; Veiga et al., 2021).

An IL-6-dependent pathway subverts lung regulatory T (Treg) cells to promote tissue inflammation in severe asthma by increasing Treg cell expression of the receptor Notch4 (Harb et al., 2020; Xia et al., 2015, 2018). In this setting, Notch4 acts via downstream pathways, including Hippo and Wnt, to disrupt Treg cell regulation of the Th helper type 2 (Th2) and Th17 adaptive immune responses. In case studies, treatment of individuals with severe asthma with the anti-IL-6R mAb tocilizumab decreased Notch4 expression on circulating Treg cells and improved disease outcomes (Esty et al., 2019).

The NOTCH4 locus is associated with critical illness in COVID-19 (Pairo-Castineira et al., 2021). Given this and the evidence supporting a pathogenic role for high levels of IL-6 in COVID-19, we examined the effect of inducible Notch4 expression on Treg cells in lung viral infection, including COVID-19. We found increased Notch4 expression in subjects with COVID-19 as a function of disease severity. In mouse models of respiratory viral infections, Notch4 enabled virus-induced tissue inflammation by mechanisms distinct from those involved in its regulation of adaptive immunity in allergic airway inflammation. Rather, Notch4 expression inhibited Treg-cell-mediated regulation of innate immune responses and promotion of tissue repair. The protective function of Notch4 inhibition involved increased production by Treg cells of the epidermal growth factor-like cytokine amphiregulin, which plays a critical role in mediating tissue repair by Treg cells in lung viral infections (Arpaia et al., 2015). These findings identify Notch4 as an effector of COVID-19 disease severity and point to interventions along the Notch4-amphiregulin axis as a viable therapeutic strategy to restore immune regulation in severe viral respiratory infections, including COVID-19.

RESULTS

Treg cell Notch4 expression is independently predictive of mortality from COVID-19

to determine the association between Notch4 and disease severity in individuals with COVID-19, we recruited three cohorts of people with COVID-19 as well as healthy control individuals from Boston, Massachusetts (n = 38 and n = 10, respectively); Genoa, Italy (n = 44 and n = 10); and Istanbul, Turkey (n = 36 and n = 20) (Table S1). The subjects were segregated into three disease severity groups (mild, moderate, and severe) based on the need for hospitalization and advanced respiratory support as well as a convalescent group, following criteria detailed in the STAR Methods. Older male individuals with a history of malignancy, cardiac disease, or endocrine disease had more severe
were suppressed upon Notch4 inhibition, consistent with decreased inflammation (Figure 2I). A similar increase was also noted for a number of other cytokines, including IFNγ, IL-1α, IL-1β, TNF-α, IFNβ, MCP1, GM-CSF, IL-17, oncostatin M, leukemia inhibitory factor, and CXCL5, most of which were also suppressed by Notch4 antagonism (Figure S3A). Further analysis revealed that Notch4 inhibition suppressed lung tissue neutrophil infiltration induced by poly(I:C) treatment and reversed the increase in lung M1 macrophages while increasing M2 macrophages (Figure 2J). In vitro co-cultures of poly(I:C)-treated macrophages with lung Treg cells derived from poly(I:C)-treated mice revealed that Foxp3<sup>YFP<sup>Cre<sup>Notch4<sup>D/D</sup> but not Foxp3<sup>YFP<sup>Cre<sup>Treg cells reversed the M1 skewing and promoted M2 macrophage differentiation (Figure 2K). These results confirmed a critical role of Treg cell Notch4 expression in the evolution of lung inflammation induced by poly(I:C).

Different Notch receptors control Treg cell function (Charbonnier et al., 2015; Ostroukhova et al., 2006; Perumalsamy et al.,...
Figure 2. Protective effect of Notch4 inhibition in poly(I:C)-induced lung injury
(A and B) Flow cytometry analysis (A) and cell frequencies, absolute numbers, and MFI (B) of Notch4 expression in lung, mediastinal lymph node (medLN), and spleen Treg and Teff cells of Foxp3YFPCre mice treated with PBS or poly(I:C) once daily for 6 days.
(C) Notch4 expression on lung, medLN, and spleen Treg cells of Foxp3YFPCre and Foxp3YFPCreNotch4D/D mice treated with PBS or poly(I:C) together with an isotype control or anti-Notch4 mAb.
(D and E) Weight index (D) and peak weight loss (E) of Foxp3YFPCre and Foxp3YFPCreNotch4D/D mice treated with PBS or poly(I:C) together with an isotype control or anti-Notch4 mAb.
(F) Hematoxylin and eosin-stained sections of lung tissues (200× magnification).
(G) Inflammation scores.
(H) AHR in response to methacholine. RI, responsiveness index (a measure of airway resistance).
(I and J) BAL fluid IL-6 concentrations (I) and graphical representation of lung tissue neutrophils and M1 and M2 macrophages.
(K) M1 and M2 macrophage frequencies in cultures of poly(I:C)-treated lung macrophages incubated with Treg cells from the indicated poly(I:C)-treated mice. (L) Flow cytometry analysis of IL-6Ra expression in lung Notch4+ or Notch4+ Treg cells of Foxp3YFPCre mice treated with poly(I:C). (M) In vitro induction of Notch4 expression in Treg cells from the lungs or spleens of poly(I:C) or PBS-treated Foxp3YFPCre mice. Each symbol represents one mouse (n = 5–15 per group).
Numbers in flow plots indicate percentages. Error bars indicate SEM. Statistical tests: Student’s t test (B), one-way ANOVA with Dunnett’s post hoc analysis (E, G, and I–K), and two-way ANOVA with Sidak’s post hoc analysis (C, D, H, and L). ***p < 0.001, ****p < 0.0001. Data were pooled from two or three independent experiments.
However, the role of Notch4 in licensing lung tissue inflammation by poly(I:C) was highly specific in that Treg cell-specific deletion of the other Notch genes, including Notch1, Notch2, and Notch3, failed to protect against tissue inflammation. In contrast, Treg cell-specific deletion of Rbpj, encoding the Notch canonical pathway transcription factor RBPj, largely reproduced the protective effect of Notch4 deletion (Figures S2A–S2F). Downstream of Notch4, our previous studies have implicated the Hippo and Wnt pathways in Treg cell regulation of Th17 and Th2 responses in allergic airway inflammation, respectively (Harb et al., 2020). Poly(I:C) treatment potently induced expression of the Hippo pathway effector Yap in lung tissue Treg cells, whereas expression of the Wnt pathway effector β-catenin was unchanged (Figures S2G and S2H). Treg cell-specific deletion of Yap1 and Wwtr1, encoding the Hippo pathway effectors Yap and Taz; Ctnnb1, encoding the Wnt pathway effector β-catenin; or all three genes failed to protect against poly(I:C)-induced inflammation. These findings indicate that Notch4 regulation of the acute inflammatory responses to viral infection proceeds by distinct mechanisms (Figures S2I–S2N).

We have previously identified a key role of IL-6 in upregulating Notch4 expression on Treg cells in asthmatic inflammation (Harb et al., 2020). Consistent with these results, Notch4+ lung Treg cells from poly(I:C)-treated mice expressed higher levels of IL-6 receptor alpha chain (IL-6Rα) compared with their Notch4− counterparts (Figure 2L). To further elucidate the mechanisms of Notch4 induction in Treg cells, we conducted in vitro studies to examine the capacity of poly(I:C) and cytokine treatment to upregulate Notch4 expression in Treg cells isolated from PBS or poly(I:C)-treated mice. The results showed that poly(I:C) treatment of lung but not splenic Treg cells increased Notch4 expression in synergy with IL-6 but not IL-33 (Figure 2M). In vivo, Treg cell-specific deletion of Il6ra attenuated poly(I:C)-induced Notch4 expression on lung Treg cells and the attendant tissue inflammatory response, including the decline in body weight, increase in AHR, influx of neutrophils, and alteration in macrophage populations (Figures S3B–S3G). These results indicate that IL-6 and additional signals contribute to Notch4 upregulation on lung Treg cells in poly(I:C)-treated mice.

Notch4 promotes lung inflammation induced by H1N1 influenza A virus

To extend these findings to an RNA virus model, we analyzed the role of Notch4 expression on Treg cells in licensing lung tissue inflammation in a mouse model of H1N1 influenza A virus infection (Woodham et al., 2020). In studies where mice were infected with H1N1 virus at 4 × 10⁴ plaque-forming units (PFUs)/mouse, the weight loss induced by the infection was abrogated by prior treatment with a neutralizing anti-Notch4 mAb or upon Treg cell-specific deletion of Notch4 (Figures 3A and 3B). Notch4 antagonism suppressed the virus-induced increase in BAL fluid IL-6 concentration (Figure 3C). It also suppressed induction by viral infection of a number of other inflammatory cytokines, similar to what was noted for with poly(I:C) treatment (Figure S4A). It also reversed the lung tissue inflammatory response in infected mice (Figure 3D). Antagonism of Notch4 expression did not result in increased viral loads, as measured on days 7 and 12 after infection (Figure 3E). Analysis of Notch4 expression on lung Treg cells in the respective mouse groups revealed that H1N1 infection increased Notch4 expression, an effect abrogated by treatment with an anti-Notch4 mAb or by Treg cell-specific Notch4 deletion (Figure 3F). Both interventions greatly attenuated lung tissue neutrophil influx, restored the alveolar macrophage population, and reversed skewing of tissue macrophages away from the pro-inflammatory M1 phenotype toward an anti-inflammatory M2 phenotype (Figures S4B–S4D). Notch4 inhibition did not affect the frequencies of IFNy+CD4+ or IFNy+CD8+ T cells or IFNyγ+ macrophages infiltrating the lungs of infected mice, whereas those of IFNyγ− innate lymphoid cells 1 (ILC1s) were decreased. Nevertheless, the absolute numbers of all four populations were decreased sharply, consistent with the markedly attenuated inflammatory response (Figures S5A–S5F). Notch4 inhibition also decreased the frequencies and absolute numbers of lung tissue IL-17+ CD4 and CD8 T cells (Figures S5G and S5H).

To determine the capacity of Notch4 antagonism to rescue active disease, mice were infected with the same dose of H1N1 virus and were treated with an isotype control mAb or with an anti-Notch4 mAb following onset of infection. The results revealed that treatment of mice with the anti-Notch4 mAb on day 4 or on days 4 and 7 after infection rescued mice from death, whereas only day 4 and 7 treatment suppressed the weight loss and innate immune activation associated with infection (Figures 3G and 3H). Both anti-Notch4 mAb treatment regimens suppressed the increase in BAL fluid IL-6 and IFNy+ concentrations induced by the viral infection (Figure 3I). We further compared different anti-Notch4 mAb treatment regimens for their capacity to rescue mice from a lethal dose 75% (LD75) of H1N1 virus (at 7 × 10⁴ PFU/mouse). Treatment with the anti-Notch4 mAb on days 2, 6, and 10 was associated with decreased mortality (22%). In contrast, treatment with an isotype control mAb or with an anti-IL-6Rα mAb failed to protect the mice from exacerbated mortality (62% and 72% mortality, respectively) (Figure 3J). These results indicate that therapy with an anti-Notch4 mAb protects mice from active influenza virus infection.

To extend the above results to the setting of a humanized immune system mouse model, we analyzed the capacity of neutralizing anti-human Notch4 mAbs to rescue disease in non-obese diabetic (NOD)-Prkdcsod1I2rgbrwys/Sz (NSG) mice reconstituted with human peripheral blood mononuclear cells (PBMCs) and infected with the H1N1 virus (Verma et al., 2017). Neutralizing mAbs specific for Notch4, but not other Notch proteins, were derived by immunizing mice with a recombinant N-terminal human Notch4 protein fragment (amino acids 1–637) derived by immunizing mice with a recombinant N-terminal human Notch4 protein fragment (amino acids 1–637) (Figures S6A and S6B). Treatment of mice with one neutralizing anti-human Notch4 mAb (clone 4H1), but not an isotype control mAb, protected against H1N1 virus infection-induced weight loss and tissue inflammation (Figures 4A–4D). Another neutralizing antibody (clone 3B11) was partially protective. Both antibodies inhibited Notch4 expression on lung Treg cells (Figure 4E) and inhibited macrophage skewing, neutrophil infiltration, and production of the cytokines IL-6 and IFNy+ (Figures 4F–4I). The antibody treatment did not affect virus clearance, as measured by virus copy numbers in lung tissue (Figure 4J). These results confirm that Notch4 regulates the magnitude of the human inflammatory response to H1N1 virus infection.
response to H1N1 infection and that it can be targeted successfully for therapeutic intervention.

**Protection by Notch4 antagonism is amphiregulin dependent**

To better understand the mechanisms by which Notch4 deficiency protected against lung inflammation, we analyzed the transcriptomes of lung Treg cells of Foxp3<sup>YFP<sup>Cre</sup></sup> and Foxp3<sup>YFP<sup>Cre</sup>Notch4<sup>Δ/Δ</sup></sup> mice treated with poly(I:C) for 6 days. The results revealed that lung Treg cells of poly(I:C)-treated Foxp3<sup>YFP<sup>Cre</sup></sup> mice exhibited an activated effector Treg cell signature, with upregulation of many canonical Treg cell transcripts, including Ctla4, <i>Ikzf2</i>, <i>Il10</i>, and <i>Tigit</i> and the TNF receptor superfAMILY members <i>Tnfrsf4</i>, <i>Tnfrsf9</i>, and <i>Tnfrsf18</i> (Arpaia et al., 2015; Figures 5A and 5B). Poly(I:C) treatment also imparted an exhausted T cell-like signature with increased <i>Pdcd1</i>, <i>Ilcos</i>, <i>Lag3</i>, and other related transcripts that may impair their suppressive function (Lowther et al., 2016). The function of Treg cells in lung tissue repair in H1N1 virus infection involves production of the epidermal growth factor (EGF) protein amphiregulin (Amr), which is a ligand for epidermal growth factor receptor (EGFR). Although the RNA and protein expression of several key canonical markers was increased concordantly in Foxp3<sup>YFP<sup>Cre</sup></sup> lung Treg cells, exceptions included the transcription factor Helios, encoded by <i>Ikzf2</i>, whose expression was decreased despite increased transcript levels (Figure 5D). Further analysis localized the loss of Helios expression to the Notch4<sup>+</sup> fraction of Foxp3<sup>YFP<sup>Cre</sup></sup> lung Treg cells, suggesting an expansion of Helios low Notch4<sup>+</sup>-induced Treg cells, similar to our observation in the asthma model (Harb et al., 2020), or loss of Helios expression leading to an increased potential for destabilization (Thornton et al., 2019; Figure 5E).

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factor-like cytokine amphiregulin (Arpaia et al., 2015). Treg cells are the main source of amphiregulin in the lungs, whereas Treg cell-specific deletion of Areg, the gene encoding amphiregulin, worsens disease outcome (Arpaia et al., 2015). Analysis of lung Treg cells revealed that, despite markedly increased Areg transcripts in Foxp3YFPCre compared with Foxp3YFPCreNotch4D/D Treg cells following poly(I:C) treatment (Figure 6A), amphiregulin protein expression failed to increase in Treg cells and BAL fluid of Foxp3YFPCre mice. However, it was increased markedly in lung Treg cells and BAL fluid of Foxp3YFPCreNotch4A/A mice and in Foxp3YFPCre mice treated with an anti-Notch4 mAb (Figures 6A–6C). In contrast, amphiregulin expression in lung tissue T eff cells was unaffected by Notch4 antagonism (Figure 6D). Similar results were also found in the H1N1 infection model (Figures 6D and 6E). Consistent with these results, amphiregulin expression was found to be differentially enriched in Notch4+ versus Notch4− lung Treg cell in poly(I:C)-treated mice (Figure 6F). Similar results were also found in lung Treg cells of influenza H1N1 virus-infected mice (data not shown).

Induction of amphiregulin expression in lung Treg cells is mediated primarily by the action of IL-18 with an ancillary effect by IL-33 (Arpaia et al., 2015). We examined the expression of IL-18Rα, IL-6Rα, and IL-33R on lung Treg cells isolated from poly(I:C)-treated mice. Although amphiregulin expression in these Treg cells was induced minimally by IL-18 treatment, it was increased upon co-treatment with the anti-Notch4 mAb (Figure 6I). These results suggest that Notch4 inhibits amphiregulin expression in Treg cells at least in part by antagonizing its upregulation by IL-18.

To establish the role of amphiregulin in protection against lung inflammation induced by Notch4 antagonism, and in light of previous studies demonstrating a protective effect of amphiregulin treatment in respiratory infections (Jamieson et al., 2013), we examined the capacity of recombinant amphiregulin therapy to
rescue poly(I:C)-induced lung inflammation. Treatment of Foxp3YFPCre mice with recombinant amphiregulin largely abrogated the weight loss and the inflammatory responses induced by poly(I:C) treatment in association with restoration of intact epithelial barrier function (Figures 7A–7D). Recombinant amphiregulin also reversed skewing of lung macrophages toward an M1 phenotype upon their in vitro treatment with poly(I:C) (Figure S6 H), mirroring the same effect of Foxp3YFPCreNotch4D/D Treg cells (Figure 2 J).

Reciprocally, we analyzed the effect of co-treatment with an amphiregulin peptide spanning the amino-terminal heparin binding domain, which is necessary for amphiregulin activation of the epidermal growthfactor receptor (EGFR) (Johnson and Wong, 1994), on the protective effects of anti-Notch4 mAb treatment or Treg cell-specific Notch4 deletion in poly(I:C)-induced lung injury, resulting in exacerbated weight loss, tissue inflammation, neutrophil infiltration, and increased M1 versus M2 macrophage skewing (Figure S6E). The anti-amphiregulin mAb co-treatment also reversed restoration by Notch4 deficiency of airway epithelial barrier integrity, as measured by increased leakage of high-molecular-weight dextran instilled in the airways into the blood stream (Figure S6 F).

Consistent with the above results, analysis of the sera of subjects with COVID-19 revealed increased amphiregulin concentrations in subjects with mild disease compared with...
those of healthy controls, which declined in the sera of individuals with moderate and severe disease in a manner inversely proportional to Notch4 expression (Figure 7J). This inverse correlation between amphiregulin and Notch4 was particularly pronounced when comparing Notch4 and amphiregulin expression specifically in circulating Treg cells (Figure 7K). In contrast, there was no correlation between Notch4 and amphiregulin expression on circulating Teff cells (Figure 7K). Overall, these results are consistent with suppression of amphiregulin production by Treg cells as a key mechanism of Notch4 inhibitory function in viral infections.

**DISCUSSION**

In this study, we addressed the role of a tissue-specific immunoregulatory mechanism involving inducible Notch4 expression on Treg cells in mediating severe lung tissue inflammation in COVID-19 and related viral infections. We found that Notch4 was increased on circulating Treg cells of individuals with COVID-19 as a function of disease severity and associated with heightened mortality, indicating that this mechanism is operative in SARS-CoV-2 infection and may be critically involved in the pathogenesis of acute respiratory failure in this disorder. Furthermore, by employing conventional and humanized
immune system mouse models of respiratory viral infections, we found that the evolution of severe viral lung inflammation was contingent on induction of Notch4 on lung Treg cells, which acted as a molecular switch to alter their regulatory and tissue repair activities. Thus, Notch4 emerges as a critical regulator of disease severity in different respiratory viral infections.

Notch4 was increased on tissue Treg cells very early in lung inflammation and acted to promote the innate immune response.
at a time when adaptive immunity had not yet been mobilized effectively. In particular, the downstream mechanisms by which Notch4 promoted innate immune cell activation in viral infection were different from those involved in promoting the T1,2 and T1,17 cell-adaptive immune responses in asthma: the Wnt and Hippo pathways, respectively (Geng et al., 2017; Harb et al., 2020). Thus, Treg cell-specific deletion of Yap1 and Wwtr1, encoding the Hippo pathway mediators Yap and Taz, or Ctnnb1, encoding the Wnt pathway effector protein β-catenin, showed little effect on disease induced by poly(I:C) treatment. This bifurcation in the mechanisms by which Notch4 promotes innate versus adaptive immunity points to distinct functions served by this pathway in the respective immune responses. In the context of an acute virus-mediated injury, Notch4 allows evolution of an innate immune response instigated by lung epithelium-derived danger signals that is unencumbered by tonic Treg cell suppression (Whitsett and Alenbach, 2015), consistent with the previously noted role of Treg cells in coordinating early protective immunity to viral infection (Lund et al., 2008). This physiological function of Notch4 becomes detrimental in the context of severe respiratory viral infections, resulting in uncontrolled pathological activation of innate immunity, leading to damaging lung tissue injury.

Analysis of Notch4 expression on Treg cells in the context of respiratory viral infection revealed its restriction to lung tissue Treg cells, suggesting a lung tissue origin of circulating Notch4+ Treg cells in individuals with COVID-19. Induction of Notch4 on lung Treg cells was in part IL-6 dependent, as evidenced by in vitro studies showing that co-treatment of lung but not splenic Treg cells with IL-6 and poly(I:C) increased Notch4 expression. These results are consistent with partial suppression of poly(I:C)-induced Notch4 expression and tissue inflammation upon Treg cell-specific deletion of Ibral. They are also consistent with the positive correlation of increased Notch4 expression in individuals with COVID-19 with serum IL-6 concentrations. Notwithstanding these findings, Notch4 but not IL-6 predicted mortality in the affected population. Direct comparison of genetic and functional interventions that target Notch4 versus IL-6R pathways revealed the superiority of the former approach in mediating protection against poly(I:C) and influenza H1N1 virus-induced lung injury. This difference may reflect previously noted additional positive functions of IL-6 in protecting against severe respiratory viral infections, separate from its role in Notch4 induction (Dienz et al., 2012; Pyle et al., 2017; Yang et al., 2017).

A key mechanism by which Notch4 impairs lung tissue Treg cell function involved amphiregulin, whose expression is enriched in tissue-resident Treg cells, especially under conditions of active tissue repair (Arpaia et al., 2015; Burzyn et al., 2013; Schiering et al., 2014; Zais et al., 2013, 2015). Amphiregulin protein expression is increased markedly in poly(I:C)-treated and H1N1 influenza virus-infected mice upon Treg cell-specific Notch4 deletion or treatment with an anti-Notch4 mAb. The protective function of Notch4 antagonism in viral lung injury was reproduced by treatment with recombinant amphiregulin and abrogated by co-treatment with an amphiregulin-blocking peptide or neutralizing antibody. Amphiregulin may thus serve as a key effector mechanism by which lung tissue Treg cells suppress danger signals emanating from the epithelium and other innate immune cells, including macrophages. A previous study by Arpaia et al. (2015) has shown that Treg cells are the predominant source of amphiregulin in the course of H1N1 infection in the lungs. Furthermore, amphiregulin expression specifically in Treg cells is critical for lung tissue repair in the context of H1N1 infection, highlighting the privileged role of Treg cell-derived amphiregulin in this process (Arpaia et al., 2015). Amphiregulin expression in Treg cells is induced primarily by IL-18 and secondarily by IL-33 (Arpaia et al., 2015). Our study demonstrated that Notch4 inhibits the capacity of IL-18 to upregulate amphiregulin expression in lung Treg cells, providing a mechanism for suppression of amphiregulin protein expression by Notch4. Amphiregulin mobilization upon Notch4 antagonism would then allow recovery from virus-induced lung injury.

Our results identify the Notch4-amphiregulin nexus as a putative target of therapy in viral respiratory infections, including SAR-CoV-2 and influenza. The remarkable capacity of anti-Notch4 mAb therapy to abrogate poly(I:C) and H1N1 influenza virus-induced disease morbidity and mortality in conventional and humanized mice makes Notch4 an attractive candidate for intervention in severe respiratory viral infections. That Notch4 also plays an essential role in promoting tissue inflammation in asthma further denotes it as a hub common to different inflammatory responses in the lungs that may serve as a target of therapy. Furthermore, the essential role of amphiregulin in mediating the therapeutic outcome of Notch4 inhibition in viral lung injury points to the amphiregulin-EGFR pathway as an additional locus of intervention. The full spectrum of Notch4-licensed diseases and the role of different downstream pathways in such disorders will require further intensive investigation.

Limitations of study

There are limitations to this study that should be noted. The individuals with COVID-19 were part of an observational cohort of adults who were predominantly of European and Turkic ethnicities. The study was not specifically designed or powered to examine differences in Notch4 expression among affected individuals of different racial and ethnic backgrounds, nor did it extend to pediatric subjects with COVID-19 or people with other lower respiratory viral infections. The mouse studies employed proxies of SARS-CoV2 infection, including poly(I:C) treatment and influenza virus infection. They were relatively short in duration and thus do not explore additional immune-regulatory mechanisms that may be operative in long-term sequelae of COVID-19. These limitations highlight the urgent task of elucidating the full range of tissue-inflammatory licensing mechanisms operative in COVID-19 and related viral infections as a requisite step for designing precision therapies to restore immune tolerance and effective tissue repair in these disorders.

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Supplemental information can be found online at https://doi.org/10.1016/j.immuni.2021.04.002.

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AUTHOR CONTRIBUTIONS

DECLARATION OF INTERESTS

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Matsui, K., gulin-induced mitogenic signaling by the epidermal growth factor receptor. J. Biol. Chem. 279, 37265–37272.


### STAR METHODS

#### KEY RESOURCES TABLE

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**Critical commercial assays**

- recombinant Amphiregulin | R&D | Cat# 989-AR-100/CF |
- Dynabeads Mouse T-Activator CD3/CD28 | Thermo Fischer | Cat# 11452D |
- Poly(I:C) HMW | Invivogen | Cat# tlr-pic-5 |
- recombinant IL-6 | Peprotech | Cat# 500-P56 |
- recombinant IL-33 | Peprotech | Cat# 210-33 |
- recombinant IL-18 | R&D | Cat# 9139-IL-010/CF |
- Notch4-His protein | Sino-Biologicals | Cat# 11869-H08B |
- complete Freund’s adjuvant | Sigma Chemical | Cat# F5881-10ML |
- Mouse IL-6 Quantikine ELISA Kit | R&D | Cat# M6000B |

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RESOURCE AVAILABILITY

Lead contact
Further information and requests for resources and reagents should be directed to and will be fulfilled by the lead contact, Talal A. Chatila (talal.chatila@childrens.harvard.edu)

Materials availability
All unique/stable reagents generated in this study are available from the Lead Contact with a completed Materials Transfer Agreement.

Data and code availability
The data presented in the manuscript, including de-identified patient results, will be made available to investigators following request to the corresponding author. Any data and materials to be shared will be released via a material transfer agreement. RNA sequencing datasets have been deposited in the Gene Expression Omnibus, GSE159584: A Regulatory T Cell Notch4 Switch Governs Lung Inflammation in Viral Infections.
EXPERIMENTAL MODEL AND SUBJECT DETAILS

Human subjects
We recruited three prospective cohorts of patients with COVID-19 from the following institutions: (1) Massachusetts General Hospital in Boston, Massachusetts, USA; (2) San Martino Hospital in Genoa, Italy; (3) Istanbul Medical Faculty Hospitals in Istanbul, Turkey. The patient demographics are shown in Table S1. Inclusion criterion included a clinical syndrome consistent with COVID-19 disease and a positive SARS-CoV-2 test from a nasal swab based on RT-PCR. Severity of illness was defined as follows: (1) Mild for patients who did not require inpatient hospitalization; (2) Moderate for patients requiring inpatient hospitalization and who did not require therapies for acute respiratory failure such as high flow oxygen (defined as a flow rate of more than 15 l per minute), non-invasive positive pressure ventilation, mechanical ventilation, and who did not require therapies for other types of organ failure such as renal replacement therapy or shock; (3) Severe for patients with organ failure requiring supportive therapies typically administered in the intensive care unit such as high flow oxygen, non-invasive positive pressure ventilation, mechanical ventilation, vasopressors, renal replacement therapy; (4) Convalescent for patients who have recovered from their acute illness and discharged from the hospital. A cohort of country-matched healthy controls were also recruited (Table S1).

Clinical data including patient characteristics, therapies received, and clinical outcomes was abstracted from the medical record into a password-protected REDCap (Research Electronic Data Capture) database. A peripheral blood draw was obtained at the time of enrollment and weekly thereafter (if available) for flow cytometry and cytokine analysis.

Study approval
Recruitment of Boston study participants was approved by the Institutional Review Board at Massachusetts General Hospital and Boston Children’s Hospital. Recruitment of Genoa study participants was approved by the Institutional Review Board at Genoa University. Recruitment of Istanbul study participants was approved by the Institutional Review Board at Istanbul University. All animal studies were reviewed and approved by the Boston Children’s Hospital office of Animal Care Resources and Massachusetts General Hospital office of Animal Care Resources.

Mice
The following mouse strains were obtained from the JAX Laboratories: Foxp3<sup>YFP</sup>/Cre<sup>YFPCre</sup> (B6.129(Cg)-Foxp3<sup>tm4(YFP/icre)Art</sup>/J) (Rubtsov et al., 2008), Il6<sup>fl/fl</sup> (B6.129S1-Ly5.1<sup>tm6</sup>1Drea/J) (McFarland-Mancini et al., 2010), Notch1<sup>fl/fl</sup> (B6.129X1-Notch1<sup>tm2RkoGrid</sup>/J) (Yang et al., 2004), Notch2<sup>fl/fl</sup> (B6.129S-Notch2<sup>tm3Gdi/h</sup>/J) (McCright et al., 2006), Notch3<sup>fl/fl</sup> Wwtr1<sup>fl/fl</sup> (B6.129(Cg)-Wwtr1<sup>tm1Hmc</sup>/J) and Yap1<sup>fl/fl</sup> (B6.129P2(Cg)-Yap1<sup>tm1.1Dupa</sup>/J) (Reginiensi et al., 2013; Zhang et al., 2010), NOD-Prkdc<sup>scid</sup>/Il2rg<sup>tm9</sup>/Sz/Nsg (Vera et al., 2017), and (Ctnnb1<sup>fl/fl</sup>) (B6)(Cg)-Ctnnb1<sup>tm1Knw</sup>/J) (Messerschmidt et al., 2016) mice. Notch4<sup>fl/fl</sup> (Notch4<sup>tm1c(NCOM)Mgc</sup>) were obtained from the Canadian mutant mouse repository. Rbpj<sup>fl/fl</sup> (B6.129P2-Rbpj<sup>tm1Hepf</sup>/HonRbrc) were kind gifts of Pamela Stanley and Tasuku Honjo, respectively (Han et al., 2002; Shi and Stanley, 2003). Notch3 floxed allele mice (Notch3<sup>fl/fl</sup>) were derived by Crispr/Cas9 targeting with LoxP sequences inserted in introns 4 and 9 to target exons 5-9 by Cre-mediated excision.

METHOD DETAILS

Regulatory T cell co-cultures with macrophages
Macrophages cells were isolated from lungs of Poly I:C-treated mice. Macrophages were isolated based on CD45<sup>+</sup> F4/80<sup>+</sup> MHCII<sup>+</sup> cells. Macrophages were then co-cultured (at 1:1 concentration) with lungs Treg cells from Poly I:C-treated mice. Cells were treated with Poly I:C at a concentration of 10ug/ml for three days. After 72h, M1 (F4/80<sup>+</sup> MHCII<sup>+</sup> CD68<sup>+</sup>) and M2 (F4/80<sup>+</sup> MHCII<sup>+</sup> CD163<sup>+</sup> CD206<sup>+</sup>) polarization was measured by flow cytometric analysis.

In vitro macrophages-Amphiregulin co-cultures
Macrophages cells were isolated from the lungs of Poly I:C treated Foxp3<sup>YFP</sup>/Cre<sup>YFPCre</sup> mice. These cells were incubated with recombinant Amphiregulin (R&D) (10 g/ml). Macrophages were isolated at 1:1 concentration with lungs Treg cells from Foxp3<sup>YFP</sup>/Cre<sup>YFPCre</sup> or Foxp3<sup>YFP</sup>/Cre<sup>Notch4<sup>fl/fl</sup></sup> mice Poly I:C-treated mice. Cells were treated with Poly I:C at a concentration of 10ug/ml for three days. After 72h, M1 (F4/80<sup>+</sup> MHCII<sup>+</sup> CD68<sup>+</sup> CD80<sup>+</sup>CD86<sup>+</sup>) and M2 (F4/80<sup>+</sup> MHCII<sup>+</sup> CD163<sup>+</sup> CD206<sup>+</sup>) polarization was measured by flow cytometric analysis.

In vitro Notch4 induction
Lung and spleen Treg cells from Poly I:C or PBS-treated Foxp3<sup>YFP</sup>/Cre<sup>YFPCre</sup> mice were isolated by cell sorting (Sony Sorter, MA900). Treg cells were seeded at 1 x 10<sup>6</sup> cells with 96-well plates then stimulated with CD3/CD28 Dynabeads (ThermoFisher) in presence of Poly I:C (10 μg/ml) alone or in combination with recombinant IL-6 and IL-33 (10 μg /ml; Peprotech) for 72h. Notch4 expression on Foxp3<sup>+</sup> Treg cells was then assessed by Flow cytometry.

In vitro amphiregulin induction
Lung Treg cells from Poly I:C or PBS-treated Foxp3<sup>YFP</sup>/Cre<sup>YFPCre</sup> mice were seeded at 1 x 10<sup>6</sup> cells then stimulated with CD3/CD28 Dynabeads with Poly I:C (10 μg/ml) either alone or in combination with recombinant IL-18 and IL-33 (R&D systems, Peprotech, respectively, 10 μg/ml) for 72h. Amphiregulin expression was then assessed by Flow cytometry.

Mouse anti-human Notch4 monoclonal antibody generation
Notch4-deficient mice were immunized with 50 μg of recombinant Notch4-His protein (Sino-Biologicals, Wayne, PA) suspended in Dulbecco’s phosphate buffered saline (PBS; GIBCO, Grand Island, NY) and emulsified with an equal volume of complete Freund’s adjuvant...
Cytokine measurements

Phosphorulin concentrations for the whole cohort were measured using Amphiregulin ELISA kit (R&D, USA). Genoa patients IL-6 concentrations were measured using ELISA (R&D, USA) per manufacturer’s protocol. As for Amphiregulin, Amphiregulin and IL-6 and Amphiregulin ELISA different chemokine and cytokine expression by flow cytometry.

Isolation of Human peripheral blood mononuclear cells (PBMCs)

Human PBMCs were isolated from whole blood from either healthy control, mild COVID-19, moderate COVID-19 or severe COVID-19 probands via density gradient using Ficoll (GE Healthcare). PBMCs were then stored frozen in Fetal Calf Serum (FCS) (Sigma Aldrich) and 15% Dimethyl sulfoxide (DMSO) (Sigma Aldrich). The cells were later thawed for analysis of their Notch, Yap1, β-Catenin or different chemokine and cytokine expression by flow cytometry.

IL-6 and Amphiregulin ELISA

Genoa patients IL-6 concentrations were measured using ELISA (R&D, USA) per manufacturer’s protocol. As for Amphiregulin, Amphiregulin concentrations for the whole cohort were measured using Amphiregulin ELISA kit (R&D, USA).

Cytokine measurements

IL-1β, IL-6 (For Boston and Istanbul cohorts), IL-8, IFNγ, IFNβ, IFNα, CXCL10 and TNF were measured using Legendplex (Biologen) per manufacturer’s protocol. Mouse cytokine were assessed using Legendplex (Biologen) per manufacturer’s protocol on BAL samples from Poly I:C treated mice (Day 7) or on BAL samples from H1N1-infected mice (Day 12). OSM, LIF and CXCL5 were also measured on the same samples using Quantikine Elisa kits (R&D systems).

Polyinosinic-polycytidylic acid (Poly I:C) mouse model

Mice were treated intratracheally with 2.5 mg/kg of Poly I:C HMW (InvivoGen) daily for six consecutive days. The weight of the mice was recorded daily upon application of the Poly I:C. The mice were subjected to airway hyperresponsiveness at day 7, then euthanized and analyzed. For blockading amphiregulin, Mouse cytokine were assessed using Legendplex (Biologen) per manufacturer’s protocol on BAL samples from Poly I:C treated mice (Day 7) or on BAL samples from H1N1-infected mice (Day 12). OSM, LIF and CXCL5 were also measured on the same samples using Quantikine Elisa kits (R&D systems).

H1N1 influenza A virus preparation

Mouse-adapted H1N1 Influenza A virus (PR/8/34) was obtained from Charles River (Catalogue no. 10100374). Viral stocks were calculated to contain 40,000 infectious units (IU) per mouse and were diluted to a volume of 20 μl/mouse in PBS. For lethal dose (LD75), the viral stocks were calculated to contain 60,000 IU per mouse and diluted to a volume of 20 μl/mouse in PBS as well.

H1N1 Influenza A viral infection model

Mice were treated intranasally on day 0 of the experiments with either a 40,000 pfu dose of the H1N1 virus or 70,000 pfu dose, equivalent to a lethal dose 75 (LD75), as indicated. The mice were monitored on a daily basis to see signs of infection. The weights of the mice were recorded and once a mouse weight loss exceeded 20%–25%, the mouse was euthanized. The endpoint of the experiments was set at day 12, to capture the peak of inflammation. For antibody treatment experiments, mice received anti-Notch4 mAb (10 μg/ml) (clone HMN-4-14; Bio-X-Cell) or their respective isotype control mAb (clone AB-108-C; R&D systems) daily for the duration of the experiment.

Humanized mice H1N1 viral infection

NOD-Prkdc<sup>−/−</sup>/Il2rg<sup>−/−</sup>/Sz (NSG) humanized mice were reconstituted with PBMCs from healthy control. Then, mice were treated with a sublethal dose of the virus as indicated intranasally on day 0. The mice were monitored on a daily basis to see signs of infection. The weights of the mice were recorded and once a mouse weight loss exceeded 20%–25%, the mouse was euthanized. For sublethal experiments, the endpoint of the experiment was set at day 12, to capture the peak of inflammation.
Viral Load
Viral titers were determined by quantification of viral transcripts using reverse transcription (RT)-quantitative (q) PCR as previously described (Cho et al., 2012; Glenn et al., 2017; Molteo et al., 2011). The collected lung tissue was weighed, and total RNA was isolated using RNAeasy mini kit (QIAGEN). Purified RNA was converted into cDNA using the SuperScript III First-Strand Synthesis System (Invitrogen) following the manufacturer’s recommended procedures. Quantification of viral load was performed in 96-well plates and run on a QuantStudio 3 Real-Time PCR instrument (Applied Biosystems). The amplification was carried out using H1N1 nucleo-protein region specific primers: forward primer, 5’-GGGGGAAGCTCCACTAGA-3’ and reverse primer, 5’-GTTGTTGTCGTATTTGCCC-3’ in the presence of the SYBR Green Master Mix (Applied Biosystems). The PCR amplification cycle was set as 95°C for 5 min for initial denaturation, followed by 50 cycles of 95°C for 15 s, 60°C for 1 min. The standard curve was generated using 10-fold serial dilutions of constructed plasmid pcDNA3-3P (Addgene) by plotting each cycle threshold (CT) value against the log quantity of each standard plasmid copy number. Viral RNA copies were extrapolated from the standard curve using the sample CT value and represented as viral RNA copies per gram of tissue.

For determination of the viral load in the humanized mouse model, viral transcripts were quantitated using reverse transcription (RT)-quantitative (q) PCR as previously described (Cho et al., 2012; Glenn et al., 2017; Molteo et al., 2011). Briefly, RNA was isolated from right upper lung lobe homogenates prepared in TRIzol (Sigma-Aldrich) and 1 μg RNA as determined by a Nanodrop 2000 spectrophotometer (ThermoFisher) was converted to cDNA by reverse transcription using the protocol provided by the manufacturer (TaqMan Reverse Transcription Reagents, ThermoFisher). qPCR reactions in the presence of SYBR Green (FastStart Essential DNA Green Master Mix, Roche) were performed on a Light-Cycler 96 Instrument (Roche). Primers: Polymerase gene (PA), 5’-CGTCCAAAATTCTGCTGA-3’ (forward) and 5’-CATTGGGCTTCCATCCA-3’ (reverse).

Measurement of airway functional responses
PolyI:C-induced airway hyperreactivity (AHR) was measured, as previously described (Xia et al., 2018). Anesthetized mice were exposed to doubling concentrations of aerosolized acetyl-β-methacholine (Sigma-Aldrich) by using a Buxco small-animal ventilator (Data Sciences International). The relative peak airway resistance for each methacholine dose, normalized to the saline baseline, was calculated.

Lung histopathology staining
Paraffin-embedded lung sections were stained with hematoxylin and eosin (H&E) or Paraffin-acid-Schiff staining (PAS). The lung pathology was scored by blinded operators. Inflammation was scored separately for cellular infiltration around blood vessels and airways: 0, no infiltrates; 1, few inflammatory cells; 2, a ring of inflammatory cells 1 cell layer deep; 3, a ring of inflammatory cells 2–4 cells deep; 4, a ring of inflammatory cells of > 4 cells deep (Tachdjian et al., 2009). A composite score was determined by the adding the inflammatory scores for both vessels and airways.

Dextran Leakage Assay
25 μg of TRITC-Dextran (MW 40,000; Sigma) in 80 μl saline was instilled intratracheally in each mouse. After one hour of dextran instillation, blood from the mice were collected retro-orbitally in sodium citrate solution, and the plasma was separated by centrifugation (2000 rpm, 15 minutes at 4°C). Leakage of dextran in the bloodstream is calculated as TRITC fluorescence in the plasma compared to plasma from mock-treated mice.

Flow cytometric analysis of mouse and human cells
Technology), beta-Catenin (196624, Catalogue no: IC13292V, 1:200, R&D system), IL-4 (MP4-25D2, Catalogue no: 500828 1:200, Biolegend), IL-13 (JES10-5A2, Catalogue no: 501912, 1:200, Biolegend), CCR4 (L291H4, Catalogue no: 359417 1:300, Biolegend), CXCR3 (G025H7, Catalogue no: 353708, 1:300 Biolegend), CRTH2 (BM16, Catalogue no: 350108 1:300, Biolegend), CD127 (A019D5, Catalogue no: 351320 1:300, Biolegend), IFNγ (4S.B3, Catalogue no: 560741 1:200, BD Biosciences) and Amphiregulin polyclonal antibody (orb7378 1:200, Biorbyt), CD196 (G034E3, Catalogue no: 353423, 1:300 Biolegend) . The specificity and optimal dilution of each antibody was validated by testing on appropriate negative and positive controls or otherwise provided on the manufacturer’s website. Intracellular cytokine staining was performed as previously described (Charbonnier et al., 2015). Dead cells were routinely excluded from the analysis based on the staining of eFluor 780 Fixable Viability Dye (1:1000 dilution) (Thermofisher). Stained cells were analyzed on a BD LSR Fortessa cell analyzer (BD Biosciences) and data were processed using Flowjo (Tree Star Inc.).

**M1 and M2 gating strategy**

M1 was defined as follows: CD45+CD4– F4/80+ MHCII+ CD68+ CD80+CD86+ while M2 macrophages were defined as follows: CD45+CD4–F4/80+ MHCII+CD163+CD206+.

**Transcriptome Profiling**

Treg cells were isolated from either Foxp3<sup>YFP<sup>cre</sup></sup> or Foxp3<sup>YFP<sup>cre</sup></sup> Notch4<sup>Δ/Δ</sup> mice that were treated with Poly I:C as shown above. mRNA was isolated using QIAGEN RNeasy mini kit (QIAGEN). RNA was then converted into double-stranded DNA (dsDNA), using SMART-Seq v4 Ultra Low Input RNA kit (Clontech). dsDNA was then fragmented to 200-300 bp size, using M220 Focused-ultrasonicator (Covaris), and utilized for construction of libraries for Illumina sequencing using KAPA Hyper Prep Kit (Kapa Biosystems). Libraries were then quantified using Qubit dsDNA HS (High Sensitivity) Assay Kit on Agilent High Sensitivity DNA Bioanalyzer.

Gene-level read counts were quantified using feature Counts and the latest Ensambl mouse annotation (GRCm38.R101). Raw data were trimmed using Trimmomatic (version 0.39, default parameters), tool for Illumina NGS data. To identify differentially expressed genes, we used 3 algorithms: DESeq2 (version 1.26.0), edgeR (version 3.28.1) and Lima (3.42.2) Bioconductor packages with default parameters. Count tables were normalized to TPM (Transcripts per Million) for visualizations and QC. Sample clustering, pathway analyses and integration of the results were performed using a custom-made pipeline available upon request (Variant Explorer RNaseq).

Transcripts were called as differentially expressed when the adjusted p values were below 0.05, fold-changes over ± 1.5 and false discovery rate (FDR) were below 0.05. For our path analyses, we tested 10,715 biological pathways from KEGG and GO annotations. We filtered the results using an adjusted p value below 0.01.

**QUANTIFICATION AND STATISTICAL ANALYSIS**

Student’s two-tailed t test, one- and two-way ANOVA and repeat measures two-way ANOVA with post-test analysis and log-rank test of groups were used to compare test groups, as indicated. Linear Regression was used for correlation analysis. For analysis of the human data, summary statistics were calculated using number (percentage) for binary and categorical data and mean (standard deviation) or median (interquartile range) for continuous data depending on the normality of the distribution. Logistic regression was performed to determine the association between Notch4 expression and mortality. Covariates including age, gender, and study site were selected based on a priori knowledge. In the case of highly correlated covariates, we chose the predictor that had the strongest univariate association between the potential predictor and outcome. In the final model, the outcome was death at any time after study enrollment, the predictors of interest were Notch4 expression and serum interleukin-6 levels, and covariates included age, gender, history of malignancy, and corticosteroid treatment. Analyses were performed in R version 3.6.1. Two-sided p values of < 0.05 were considered statistically significant.
Supplemental information

Notch4 signaling limits regulatory T-cell-mediated tissue repair and promotes severe lung inflammation in viral infections

Supplementary Materials

Notch4 signaling limits regulatory T cell mediated tissue repair and promotes severe lung inflammation in viral infections

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Supplementary Figure Legends.

Fig. S1. Expression of Notch1, Notch2 and Notch3 on circulating Treg cells of control and COVID-19 subjects. Related to Figure 1. A-C Flow cytometric analysis and graphical representation of Notch1 (A), Notch2 (B) and Notch3 (C) expression in Treg cells of control and COVID-19 subject groups. Each symbol represents one subject. Numbers in flow plots indicate percentages. Error bars indicate SEM. Statistical tests: One-way ANOVA with Dunnett’s post hoc analysis.
Fig. S2. Impact of Treg cell-specific deletion of different Notch, Hippo and Wnt pathway components on poly I:C-induced lung injury. Related to Figure 2. A, B, Weight index (A) and peak weight loss (B) of Foxp3<sup>YFP</sup><sub>Cre</sub>, Foxp3<sup>YFP</sup><sub>Cre</sub>Rbpj<sup>Δ/Δ</sup>, Foxp3<sup>YFP</sup><sub>Cre</sub>Notch1<sup>Δ/Δ</sup> Foxp3<sup>YFP</sup><sub>Cre</sub>Notch2<sup>Δ/Δ</sup> and Foxp3<sup>YFP</sup><sub>Cre</sub>Notch3<sup>Δ/Δ</sup> mice either sham-treated or treated with poly I:C, as indicated. C, AHR in the respective mouse groups in response to methacholine. D-F, Graphical representation of lung tissue neutrophils (D) and M1 (E) and M2 macrophages (F). G, H, Flow cytometric analysis (G) and graphical representation (H) of Yap and β-Catenin in lung tissue Treg cells of Foxp3<sup>YFP</sup><sub>Cre</sub> mice that were either sham-treated or treated with poly I:C. I, J, Weight index (I) and peak weight loss (J) of Foxp3<sup>YFP</sup><sub>Cre</sub>, Foxp3<sup>YFP</sup><sub>Cre</sub>Yap1<sup>Δ/Δ</sup>Wwtr1<sup>Δ/Δ</sup>, Foxp3<sup>YFP</sup><sub>Cre</sub>Ctnnb1<sup>Δ/Δ</sup> and Foxp3<sup>YFP</sup><sub>Cre</sub>Yap1<sup>Δ/Δ</sup>Wwtr1<sup>Δ/Δ</sup> Ctnnb1<sup>Δ/Δ</sup> mice either sham-treated or treated with Poly I:C, as indicated. K, AHR in the respective mouse groups in response to methacholine. L-N, Graphical representation of lung tissue neutrophils (L) and M1 (M) and M2 (N) macrophages. Each symbol represents one mouse (n=5 per group). Numbers in flow plots indicate percentages. Error bars indicate SEM. Statistical tests: Two-way ANOVA with Sidak’s post hoc analysis (A,C,I,K); One-way ANOVA with Dunnett’s post hoc analysis (B,D,E,F,J,L,M,N). **P<0.01, ***P<0.001, ****P<0.0001.
Fig. S3. Treg cell-specific deletion of *Il6ra* partially protects against Poly I:C-induced lung injury. Related to Figure 2. **A**, BAL concentrations of IFNγ, TNFα, IL-12p70, IL-1β, IFNβ, IL-10, IL-1α, MCP-1, IL-27, GM-CSF, IL-17, OSM, LIF and CXCL5 in PBS or Poly I:C-treated Foxp3<sup>YFP<sup>Cre</sup> and Foxp3<sup>YFP<sup>Cre</sup>Notch4<sup>Δ/Δ</sup> mice, the former also co-treated with either isotype control or anti-Notch4 mAb. **B**, Weight index (A) and peak weight loss of Foxp3<sup>YFP<sup>Cre</sup> and Foxp3<sup>YFP<sup>Cre</sup>Il6ra<sup>Δ/Δ</sup> mice either sham-treated or treated with Poly I:C, as indicated. **C**, AHR in response to methacholine. **D, E, F, G, H**, Flow cytometric analysis (D) and graphical representation (E) of Notch4 expression in lung tissue Treg cells of Foxp3<sup>YFP<sup>Cre</sup> and Foxp3<sup>YFP<sup>Cre</sup>Il6ra<sup>Δ/Δ</sup> mice that were either sham-treated or treated with Poly I:C. **F-H**, Flow cytometric analysis and graphical representation of lung tissue neutrophils (F) and M1 (G) and M2 macrophages (H). Each symbol represents one mouse (n=5 per group). Numbers in flow plots indicate percentages. Error bars indicate SEM. Statistical tests: Two-way ANOVA with Sidak’s post hoc analysis (**A, C**); One-way ANOVA with Dunnett’s post hoc analysis (**B, E, F, G, H**); **P<0.01, ****P<0.0001.
Fig. S4. Protective effect of Notch4 inhibition in influenza A H1N1 virus infection. Related to Figure 3. A, Flow cytometric analysis (A) and graphical representation of lung neutrophils in the indicated mouse groups. B, Flow cytometric analysis and graphical representation of lung M2 macrophages in the indicated mouse groups. C, Flow cytometric analysis and graphical representation and graphical representation of lung M1 macrophages in the indicated mouse groups. D, BAL concentrations of IFNγ, TNFα, IL-12p70, IL-1β, IFNβ, IL-10, IL-1α, MCP-1, IL-27, GM-CSF, IL-17, OSM, LIF and CXCL5 in PBS or H1N1-infected Foxp3^YFP^Cre and Foxp3^YFP^Cre Notch4^Δ/Δ^ mice, the former also co-treated with either isotype control or anti-Notch4 mAb. Each symbol represents one mouse (n=5 per group). Numbers in flow plots indicate percentages. Error bars indicate SEM. Statistical tests: One-way ANOVA with Dunnett’s post hoc analysis (A-D). **P<0.01, ***P<0.001, ****P<0.0001.
**Fig. S5. Characterization of lung T cell infiltrates in H1N1 infected mice.** Related to Figure 3. **A,B,** Graphical representation of CD8\(^+\) T cell frequencies (A) and IFN\(_\gamma\)^+CD8\(^+\) T cell frequencies and numbers (B) in the lungs of Foxp3\(^{YFP}Cre\) and Foxp3\(^{YFP}Cre\) Notch4\(^{\Delta\Delta}\) mice that were either sham-treated or infected with H1N1 virus, in the case of the Foxp3\(^{YFP}Cre\) mice either alone or together with an anti-Notch4 mAb, as indicated. **C,D,** Graphical representation of CD4\(^+\) T cell frequencies (C) and IFN\(_\gamma\)^+CD4\(^+\) Teff cell frequencies and numbers (D) in the lungs. **E,** Graphical representation of IFN\(_\gamma\)^+ Macrophage frequencies and numbers. **F,** Graphical representation of IFN\(_\gamma\)^+ILC1 frequencies and numbers. **G,** Graphical representation of IL-17^CD8^+ T cell frequencies and numbers in the lungs. **H,** Graphical representation of IL-17^CD4^+ T cell frequencies and numbers in the lungs. Each symbol represents one mouse (n=5 per group). Error bars indicate SEM. Statistical tests: One-way ANOVA with Dunnett's post hoc analysis (**A-H**). *P<0.05, **P<0.001, ****P<0.0001.
Fig. S6. Validation of neutralizing anti-human Notch4 mAbs and amphiregulin<sub>91-140</sub> blocking peptide. Related to Figures 4 and 7. **A.** Reactivity of different Notch4 mAbs to Notch1, Notch2, Notch3 and Notch4 as measured by ELISA. **B, Left,** Flow cytometric analysis Jagged1-Notch4<sub>GFP</sub> interaction in Jurkat cells that were either sham transfected (control) or transfected with a construct encoding Notch4<sub>GFP</sub> then incubated with Jagged1 in the absence or presence of the indicated mAb. **B right,** Flow cytometric analysis and graphical representation of Jagged1-PE staining of Jurkat cells that were transfected with a construct encoding Notch4<sub>GFP</sub> in the absence of presence of the indicated mAb. **C,** Flow cytometric analysis and graphical representation of EGFR phosphorylation at tyrosine 1068 (pEGFR) in HEK293 cells treated with mouse amphiregulin in the presence increased concentrations of amphiregulin<sub>91-140</sub> blocking peptide (bp) or a neutralizing anti-amphiregulin mAb, as indicated. **D,** Weight index and peak weight loss of Foxp3<sup>YFPCre</sup> and Foxp3<sup>YFPCreNotch4<sup>Δ/Δ</sup></sup> mice treated with Poly I:C, either alone or together with anti-amphiregulin neutralizing mAb. **E,** Frequencies of neutrophils and M1 and M2 macrophages in lung tissues. **F,** Serum tetramethylrhodamine isothiocyanate (TRITC) dextran, measured as relative fluorescent units (RFU), in Poly I:C + anti-Amphiregulin mAb-treated Foxp3<sup>YFPCre</sup> or Foxp3<sup>YFPCreNotch4<sup>Δ/Δ</sup></sup> mice at 1-hour post intra-tracheal instillation. **G,** Frequencies of neutrophils and M1 and M2 macrophages in lung tissues from Foxp3<sup>YFPCre</sup> mice either sham treated or treated with Poly I:C, either alone or together with amphiregulin bp. **H,** frequencies of M1 and M2 macrophages in co-cultures of Poly I:C-treated lung macrophages incubated either alone, with amphiregulin, Treg cells from Poly I:C-treated Foxp3<sup>YFPCre</sup> mice or the combination thereof. Each symbol represents one mouse (n=5-10 per group). Numbers in flow plots indicate percentages.
Error bars indicate SEM. Statistical tests: One-way ANOVA with Dunnett’s post hoc analysis (D-F); two-way ANOVA with Sidak’s post hoc analysis (D); Student’s two tailed t-test (G). **P<0.01, ****P<0.0001).
Table S1. Demographics of COVID-19 patients stratified by disease severity and predictors of mortality. Related to Figure 1
Table S1. Demographics of COVID-19 patients stratified by disease severity and predictors of mortality.

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<th></th>
<th>Overall</th>
<th>Mild</th>
<th>Moderate</th>
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<td>118</td>
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<td>Site, n (%)</td>
<td></td>
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<td>Boston</td>
<td>38 (32.2)</td>
<td>2 (10.0)</td>
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<td>Genoa</td>
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<td>Istanbul</td>
<td>36 (30.5)</td>
<td>18 (90.0)</td>
<td>12 (21.1)</td>
<td>6 (14.6)</td>
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<tr>
<td>Age, mean (SD)</td>
<td>63.12 (18.97)</td>
<td>42.60 (15.22)</td>
<td>65.21 (17.39)</td>
<td>70.22 (15.83)</td>
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<td>Male, n (%)</td>
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<td>25 (43.9)</td>
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<td>Any medical problems, n (%)</td>
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<tr>
<td>Hypertension</td>
<td>55 (46.6)</td>
<td>4 (20.0)</td>
<td>24 (42.1)</td>
<td>27 (65.9)</td>
<td>0.002</td>
</tr>
<tr>
<td>Hyperlipidemia</td>
<td>12 (10.2)</td>
<td>0 (0.0)</td>
<td>6 (10.5)</td>
<td>6 (14.6)</td>
<td>0.205</td>
</tr>
<tr>
<td>Endocrine disease</td>
<td>38 (32.5)</td>
<td>2 (10.0)</td>
<td>19 (33.3)</td>
<td>17 (42.5)</td>
<td>0.04</td>
</tr>
<tr>
<td>Diabetes</td>
<td>26 (22.0)</td>
<td>1 (5.0)</td>
<td>14 (24.6)</td>
<td>11 (26.8)</td>
<td>0.126</td>
</tr>
<tr>
<td>COVID-19 treatments</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Remdesivir</td>
<td>26 (22.0)</td>
<td>0 (0.0)</td>
<td>8 (14.0)</td>
<td>18 (43.9)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Hydroxychloroquine</td>
<td>54 (45.8)</td>
<td>15 (75.0)</td>
<td>24 (42.1)</td>
<td>15 (36.6)</td>
<td>0.014</td>
</tr>
<tr>
<td>Glucocorticoids</td>
<td>67 (56.8)</td>
<td>0 (0.0)</td>
<td>35 (61.4)</td>
<td>32 (78.0)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Anti-IL-6</td>
<td>9 (7.6)</td>
<td>0 (0.0)</td>
<td>2 (3.5)</td>
<td>7 (17.1)</td>
<td>0.016</td>
</tr>
<tr>
<td>Supportive care</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Supplemental oxygen</td>
<td>89 (75.4)</td>
<td>9 (45.0)</td>
<td>50 (87.7)</td>
<td>30 (73.2)</td>
<td>0.001</td>
</tr>
<tr>
<td>High flow oxygen</td>
<td>23 (19.5)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>23 (56.1)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Noninvasive ventilation</td>
<td>8 (6.8)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>8 (19.5)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Mechanical ventilation</td>
<td>20 (16.9)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>20 (48.8)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>ECMO</td>
<td>2 (1.7)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>2 (4.9)</td>
<td>0.148</td>
</tr>
<tr>
<td>Dead</td>
<td>19 (16.1)</td>
<td>0 (0.0)</td>
<td>5 (8.8)</td>
<td>14 (34.1)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>30-day, n (%)</td>
<td>8 (6.8)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>8 (19.5)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>90-day, n (%)</td>
<td>18 (15.3)</td>
<td>0 (0.0)</td>
<td>4 (7.0)</td>
<td>14 (34.1)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Biomarkers, mean (SD)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Notch4, %</td>
<td>15.00 (14.48)</td>
<td>4.67 (5.57)</td>
<td>10.82 (10.93)</td>
<td>25.84 (15.24)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>IL-6, pg/mL</td>
<td>89.10 (209.25)</td>
<td>124.22 (172.49)</td>
<td>43.15 (38.47)</td>
<td>137.70 (326.22)</td>
<td>0.071</td>
</tr>
<tr>
<td></td>
<td>Crude OR</td>
<td>95% CI</td>
<td>p-value</td>
<td>Adjusted OR</td>
<td>95% CI</td>
</tr>
<tr>
<td>-------------------------</td>
<td>----------</td>
<td>-----------------</td>
<td>---------</td>
<td>-------------</td>
<td>-----------------</td>
</tr>
<tr>
<td>Age, years</td>
<td>1.086</td>
<td>(1.044, 1.140)</td>
<td>&lt;0.001</td>
<td>1.094</td>
<td>(1.036, 1.177)</td>
</tr>
<tr>
<td>Male gender</td>
<td>1.613</td>
<td>(0.598, 4.654)</td>
<td>0.354</td>
<td>3.713</td>
<td>(0.942, 17.922)</td>
</tr>
<tr>
<td>History malignancy</td>
<td>5.954</td>
<td>(2.028, 17.718)</td>
<td>0.001</td>
<td>3.717</td>
<td>(0.950, 15.565)</td>
</tr>
<tr>
<td>Steroid treatment</td>
<td>5.020</td>
<td>(1.552, 22.55)</td>
<td>0.015</td>
<td>5.730</td>
<td>(1.177, 45.520)</td>
</tr>
<tr>
<td>Notch4, %</td>
<td>1.052</td>
<td>(1.020, 1.088)</td>
<td>0.002</td>
<td>1.046</td>
<td>(1.008, 1.090)</td>
</tr>
<tr>
<td>Interleukin-6, pg/mL</td>
<td>0.999</td>
<td>(0.992, 1.001)</td>
<td>0.553</td>
<td>1.000</td>
<td>(0.993, 1.004)</td>
</tr>
</tbody>
</table>

Disease severity classification. Mild = did not require hospitalization. Moderate = hospitalized but required only supplemental oxygen. Severe = hospitalized and required high flow oxygen, non-invasive ventilation, or mechanical ventilation.

Abbreviations: BMI = body mass index; ICU = intensive care unit; Anti-IL-6 = anti-interleukin-6 monoclonal antibody therapy; ECMO = extracorporeal membrane oxygenation; IL-6 = interleukin-6, OR = Odds Ratio. 95% CI = 95% confidence interval.