Type I and III interferons synergize with TNF to promote virally-triggered

damage to the intestinal epithelium

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Abstract

Excessive cell death in the epithelium due to prolonged immune activation is associated

with intestinal diseases such as Crohn's disease. Mice with mutations in the Crohn's disease

susceptibility gene *Atg16l1* are susceptible to inflammation associated with intestinal epithelial

cell (IEC) death, including loss of antimicrobial Paneth cells triggered by infection with murine

norovirus (MNV). Here, we show that intestinal disease downstream of MNV depends on IFN-α/β

and IFN-λ signaling in IECs. In mouse organoids, IFNs synergize with TNF to induce RIPK1-

dependent cell death, amplified by ATG16L1 deficiency. We further show that human intestinal

organoids harboring the *ATG16L1* risk allele exhibit heightened sensitivity to TNF and IFN co-

stimulation and to serum from severe COVID-19 patients. Our findings reveal that virally triggered

cytokines including IFNs exacerbate epithelial vulnerability in genetically predisposed hosts.

Introduction

A single layer of epithelial cells in the intestine forms the first line of defense against

diverse microbial agents ranging from beneficial members of the microbiota to pathogens that

cause life-threatening disease (Ramanan & Cadwell, 2016). Intestinal epithelial cells (IECs)

include enterocytes that absorb nutrients, chemosensory tuft cells, mucus-secreting goblet cells,

and enteroendocrine cells that produce hormones. The small intestinal crypt also harbors Paneth

cells, IECs that secrete antimicrobial factors such as lysozyme and defensins. The proper

turnover of IECs maintains anatomical integrity and contributes to resolving infections, such as

through sloughing of damaged cells bound by adherent or invasive microbes (Churchill et al.,

2022). However, inflammatory or excessive cell death triggered by prolonged immune activation

is a hallmark of several intestinal diseases including inflammatory bowel diseases (IBDs) such as

Crohn's disease (CD) and ulcerative colitis (Patankar & Becker, 2020). The cell death modality,

timing, and cell type specificity are likely important variables that contribute to outcomes in

infectious and inflammatory diseases of the gut.

The etiology of IBDs is complex and associated with genetic and environmental factors

(Cadwell & Loke, 2025). Although sustaining remission continues to be a challenge in many

patients, the success of therapies that target cytokines and their signaling activities support a

disease model in which these soluble immune mediators disrupt the epithelial barrier in a

susceptible host. Consistent with this possibility, we demonstrated that mutations in the CD

susceptibility gene *ATG16L1* are associated with loss of function and viability of Paneth cells as

well as susceptibility to intestinal injury downstream of TNF (Cadwell et al., 2008; Cadwell et al.,

2010; Matsuzawa-Ishimoto et al., 2017; Matsuzawa-Ishimoto et al., 2022). ATG16L1 is necessary

for the cell biological process of autophagy in which cytosolic material, such as protein aggregates

and damaged organelles, is targeted to the lysosome for degradation and recycling (Matsuzawa-

Ishimoto et al., 2018). Multiple groups have independently demonstrated that ATG16L1 and other

autophagy genes have an epithelial-intrinsic role in promoting intestinal barrier function (Aden et

al., 2018; Asano et al., 2017; Benjamin et al., 2013; Conway et al., 2013; Foerster et al., 2023;

Jackson et al., 2020; Jung et al., 2019; Matsuzawa-Ishimoto et al., 2020; Matsuzawa-Ishimoto et

al., 2017; Patel et al., 2013; Pott et al., 2018; Tschurtschenthaler et al., 2017). Autophagy and

related processes may be particularly important in Paneth cells because of their longevity (2-3

months) and high secretory burden that make these cells susceptible to ER and mitochondrial

stress (Adolph et al., 2013; Bel et al., 2017; Burger et al., 2018; Cadwell et al., 2008; Matsuzawa-

Ishimoto et al., 2017).

We previously developed a model in which persistent infection with murine norovirus

(MNV) of *Atg16l1*-mutant mice, including mice with an IEC-specific deletion of *Atg16l1*

(*Atg16l1*$^{fl/fl}$;villin-cre, hereafter referred to as *Atg16l1*$^{\Delta IEC}$), are susceptible to chemical injury to the

gut by dextran sodium sulfate (DSS) and develop Paneth cell alterations similar to those observed

in patients with CD homozygous for the *ATG16L1 T300A* risk variant (Cadwell et al., 2010;

Matsuzawa-Ishimoto et al., 2017). Small intestinal organoids, a 3D cell culture model

differentiated from intestinal stem cells, generated from *Atg16l1*-mutant mice or patients with

ATG16L1^{T300A} undergo necroptosis (programmed necrosis) and loss of Paneth cells upon TNF

treatment (Aden et al., 2018; Matsuzawa-Ishimoto et al., 2017). Given that MNV can promote

beneficial immune development under certain settings and is otherwise tolerated (Abt et al., 2016;

Kernbauer et al., 2014; Neil et al., 2019), the virally-triggered intestinal damage observed in

Atg16l1$^{\Delta IEC}$ mice provides an opportunity to identify the immune factors that regulate IEC-viability

in response to environmental perturbations.

Type I Interferons (IFN-α/β) and type III interferons (IFN-λs) are best known for their

antiviral functions downstream of Janus kinases (JAK) and signal transducer and activator of

transcription proteins (STAT) upon receptor engagement. Although type I and III IFNs induce

similar interferon stimulated genes (ISGs), they have distinct activities mediated in part by

differential expression of their receptors. In the intestine, the type I IFN receptor (IFNAR) primarily

functions in immune cells and is downregulated in IECs in adult mice whereas the type III IFN

receptor (IFNLR) is highly produced in IECs and neutrophils (Ingle et al., 2018; Lin et al., 2016;

Mahlakoiv et al., 2015). In the context of MNV infection, IFN-α/β prevents extraintestinal

dissemination and IFN-λ restricts local replication and fecal shedding (Baldridge et al., 2017; Nice

et al., 2015; Nice et al., 2016; Rocha-Pereira et al., 2018; Thackray et al., 2012). Although

homeostatic IFN-λ produced by lymphocytes in response to commensal bacteria limits viral

replication during early infection (Van Winkle et al., 2022), the viral non-structural protein NS1

encoded by persistent strains mediates evasion of IFN-λ to establish prolonged infection of tuft

cells (Lee et al., 2017; Wilen et al., 2018). In addition to their antiviral role, IFNs impact intestinal

homeostasis. A recent study reported that mice lacking both IFNAR and IFNLR do not survive

even low levels of DSS exposure, which was associated with extensive destruction of the colonic

epithelium (McElrath et al., 2021). By contrast, IFN-λ levels are high in serum and small intestinal

tissue of patients with CD, and over-expression or administration of IFN-λ induces inflammatory

forms of epithelial cell death, necroptosis and pyroptosis (Gunther et al., 2019; Jena et al., 2024).

113   Although MNV can activate cell death proteins directly in infected IECs to promote its

reproduction and immune evasion (Aktepe et al., 2024; Bok et al., 2009; Deerain et al., 2024;

Robinson et al., 2019; Song et al., 2025; Wang et al., 2023), persistent strains display specific

tropism for tuft cells due to the restricted expression of the viral entry receptor *Cd300lf* (Graziano

et al., 2021; Orchard et al., 2016; Wilen et al., 2018). Thus, in the *Atg16l1* mutant setting, in which

cell death is observed in Paneth cells that do not express *Cd300lf*, extracellular factors mediate

IEC defects. MNV increases TNF and IFN-γ producing intra-epithelial lymphocytes and inhibits

protective γδ T cells upstream of Paneth cell death and DSS-induced disease (Cadwell et al.,

2010; Matsuzawa-Ishimoto et al., 2017; Matsuzawa-Ishimoto et al., 2022). Here, we identify a

critical cytotoxic role of type I and III IFNs in mediating these effects. We report that deletion of

IFNAR or IFNLR in IECs rescues intestinal defects in *Atg16l1* deficient mice and identify a role

for IFNs in potentiating TNF-induced cell death. Using organoids and serum from patients with

COVID, we provide evidence that the general epithelial cytotoxic effect of cytokines produced in

response to viral infections is conserved in humans. Thus, our results suggest that a component

of viral sequelae includes production of soluble immune mediators such as TNF and IFNs that

compromise the viability of IECs, which is especially detrimental in genetically susceptible hosts.

Results

Epithelial type I and III interferon signaling mediate intestinal damage downstream of viral

infection.

Atg16l1-mutant mice display spontaneous ISG expression in the gut dependent on the

microbiota (Marchiando et al., 2013; Martin et al., 2018). To determine whether ISG expression

is further increased in the presence of MNV, we examined the small intestine (ileum) and colon

of WT and *Atg16l1$^{\Delta IEC}$* mice 10 days post intragastric inoculation with MNV strain CR6. The levels

of three representative ISGs (*Mx2*, *Oasl2*, and *Zbp1*) in the ileum and colon were increased by

MNV infection, and for the ileum, highest in MNV-infected *Atg16l1$^{\Delta IEC}$* mice (Sup. Fig. 1A). IFN-λ

is primarily responsible for ISG expression in IECs (Odendall et al., 2014). To confirm that IFN-λ

is responsible for the ISG expression, we crossed *Ifnlr* floxed mice to *Atg16l1$^{\Delta IEC}$* mice to obtain

Atg16l1;Ifnlr$^{\Delta IEC}$ mice that are deficient in ATG16L1 and IFNLR in IECs. ISG expression in MNV-

infected *Atg16l1;Ifnlr$^{\Delta IEC}$* mice was not significantly different from uninfected Cre-negative

controls, hereafter referred to as wild-type (WT) (Sup. Fig. 1A).

To determine whether IFN-λ signaling contributes to virally triggered intestinal defects, we

examined the susceptibility of *Atg16l1;Ifnlr$^{\Delta IEC}$* mice to DSS following MNV infection. *Atg16l1$^{\Delta IEC}$*

mice showed increased lethality, weight loss, and disease score compared to WT mice upon MNV

+ DSS treatment (Fig. 1A-C), similar to our previous study (Matsuzawa-Ishimoto et al., 2017). In

contrast, these disease readouts were abrogated in MNV + DSS treated *Atg16l1;Ifnlr ^{ΔIEC}* mice

and were similar to *Ifnlr^{ΔIEC}* (*Ifnlr*$^{fl/fl}$villin-cre) and WT controls (Fig. 1A-C). We also generated

Atg16l1;Ifnar^{ΔIEC} (*Atg16l1*$^{fl/fl}$*Ifnar*$^{fl/fl}$villin-cre) mice for additional comparison and unexpectedly

found that disease was ameliorated. Consistent with a dominant antiviral role of IFNLR at the

epithelial barrier during MNV infection (Nice et al., 2015), *Atg16l1;Ifnlr^{ΔIEC}* mice, but not

Atg16l1;Ifnar^{ΔIEC} mice, displayed increased shedding of virus in stool compared to *Atg16l1^{ΔIEC}* or

WT mice (Fig. 1D). None of the mice examined displayed mortality or exacerbated disease in

response to DSS in the absence of MNV, except *Atg16l1;Ifnlr^{ΔIEC}* mice (Sup. Fig 1B). These

results indicate that IFNLR and IFNAR in IECs are necessary for the exacerbated intestinal injury

response in *Atg16l1;Ifnlr ^{ΔIEC}* mice infected with MNV and may have a different role in uninfected

Atg16l1 mutant mice.

We previously showed that Paneth cells are less frequent and structurally altered in the

ileum and the colons are shortened in MNV + DSS treated *Atg16l1^{ΔIEC}* mice (Matsuzawa-Ishimoto

et al., 2017). *Atg16l1^{ΔIEC}* mice displayed a lower number of Paneth cells compared to similarly-

treated WT mice, and the remaining Paneth cells showed diffuse lysozyme staining and/or

reduced number of lysozyme^{+} granules that are a characteristic of CD (Cadwell et al., 2010).

Deleting *Ifnlr* or *Ifnar* in *Atg16l1 ^{ΔIEC}* mice failed to fully restore Paneth cells to WT levels, although

we note that there was an increase in the number of Paneth cells in *Atg16l1;Ifnar^{ΔIEC}* mice

compared to *Atg16l1^{ΔIEC}* mice suggesting a partial restoration (Fig. 1E, F). To test potential

redundancy, we crossed *Atg16l1;Ifnlr^{ΔIEC}* mice with *Atg16l1;Ifnar^{ΔIEC}* mice to generate

Atg16l1;Ifnlr;Ifnar ^{ΔIEC} mice deficient in both receptors. However, *Atg16l1;Ifnlr;Ifnar ^{ΔIEC}* mice still

displayed reductions in Paneth cells and a high proportion showed abnormal lysozyme staining

(Fig. 1G). We cannot rule out the possibility that the above analyses would miss Paneth cells that

lose their granules, which can happen in the *Atg16l1* mutant setting (Cadwell et al., 2008). To

more broadly capture abnormalities, we stained sections for cell death using terminal

deoxynucleotidyl transferase–mediated dUTP nick-end labeling (TUNEL). TUNEL-positive cells

were rarely detected in the crypts of WT mice whereas a subset of crypts displayed multiple

TUNEL-positive cells in *Atg16l1* $^{\Delta IEC}$ mice (Fig. 1E, H, I). Rather than a decrease, the number of

TUNEL-positive cells displayed a non-significant increase in *Atg16l1;Ifnar*$^{\Delta IEC}$ mice compared with

Atg16l1 $^{\Delta IEC}$ mice. However, the *Atg16l1;Ifnlr* $^{\Delta IEC}$ mice were similar to WT controls and did not

display crypts with >2 TUNEL-positive cells. *Atg16l1;Ifnlr;Ifnar* $^{\Delta IEC}$ mice were similar to *Atg16l1*

$^{\Delta IEC}$ mice (Fig. 1E, H). *Atg16l1*$^{\Delta IEC}$ mice also exhibited a shorter colon than WT and *Atg16l1;Ifnlr*

$^{\Delta IEC}$ mice following MNV + DSS (Fig. 1I). These results indicate that IFNLR and IFNAR signaling

mediate some aspects of disease development in MNV-infected *Atg16l1*$^{\Delta IEC}$ mice including

lethality and IEC death but granule alterations in Paneth cells may be involve a more complex

role for IFNs.

IFNβ and IFNλ exacerbate TNF-mediated cell death of intestinal organoids.

We previously found that organoids generated from *Atg16l1*$^{\Delta IEC}$ mice (*Atg16l1*$^{-/-}$ organoids)

display a striking spontaneous ISG signature and that treatment with the JAK inhibitor ruxolitinib

prevents TNF-induced cell death of these *Atg16l1*$^{-/-}$ organoids (Matsuzawa-Ishimoto et al., 2020).

Although these results are consistent with a role for signaling downstream of cytokine receptors

that use the JAK/STAT pathway, it was unclear whether IFNs can cooperate with TNF to induce

loss of organoid viability. Because the majority of *Atg16l1*$^{-/-}$ organoids die within the first 2-3 days

of seeding when TNF is administered on day 0 (Matsuzawa-Ishimoto et al., 2017), we modified

our protocol to increase the dynamic range of the assay and assess the synergistic effect of TNF

and IFNs. We found that >50% of *Atg16l1*$^{-/-}$ organoids and ~80% of *Atg16L1*$^{+/+}$ organoids (derived

from *Atg16l1*$^{fl/fl}$ mice that were negative for Cre) remained viable 72 hours post-stimulation when

TNF was added 3 days after seeding (Fig. 2A, B). Treatment with IFN-β and IFN-λ2 led to similar

or slightly greater loss of viability as TNF for both *Atg16L1*$^{+/+}$ and *Atg16l1*$^{-/-}$ organoids (Fig. 2A, B).

In contrast, the combination of TNF and IFN led to substantial organoid death. After only 24 h,

Atg16l1$^{-/-}$ organoids with TNF + IFN-β or TNF + IFN-λ2 resulted in complete loss of viability (Fig.

2A, B). *Atg16L1*$^{+/+}$ organoids started to display loss of viability at 24 hours and were completely

dead by 48 hours post-treatment with TNF + IFN-β or TNF + IFN-λ2 (Fig. 2A, B). Titration of IFN-

β and IFN-λ2 in the presence of TNF showed dose responsiveness and that *Atg16l1*$^{-/-}$ organoids

are more sensitive to IFN since 10x less IFN induced same level of cell death in this genotype

compared with *Atg16L1*$^{+/+}$ organoids (Fig. 2C). Therefore, IFN-β and IFN-λ2 increase the toxicity

of TNF, and ATG16L1 deficiency further sensitizes organoids to the combination of these

cytokines.

IFN-β can induce TNF production (Aden et al., 2018), which may explain why IFN

treatment alone can induce some degree of cytotoxicity to organoids (Fig. 2B). We observed that

TNF expression and protein secretion were increased in *Atg16l1*$^{-/-}$ organoids but not *Atg16L1*$^{+/+}$

organoids treated with IFN-β (Fig. 2D and Sup. Fig. 2A). Antibody-mediated blockade of TNF

rescued viability of *Atg16l1*$^{-/-}$ organoids stimulated with TNF as expected and also greatly

improved viability of *Atg16l1*$^{-/-}$ organoids treated with IFN-β (Fig. 2E). Anti-TNF improved viability

of *Atg16l1*$^{-/-}$ organoids treated with TNF + IFN-λ2 but not IFN-λ2 alone (Sup. Fig. 2B). These

results indicate that IFN-β increases the production of TNF in *Atg16l1*$^{-/-}$ organoids, which

contributes to its toxicity.

We confirmed the specificity of IFN-β and IFN-λ2 for their cognate receptors. *Atg16l1*$^{-/-}$

Ifnar$^{-/-}$ organoids were resistant to TNF + IFN-β and *Atg16l1*$^{-/-}$*Ifnlr*$^{-/-}$ organoids were resistant to

TNF + IFN-λ2 (Fig. 2F). Also, IFN-β and IFN-λ2 did not induce representative ISGs in the absence

of their respective receptors (Sup. Fig. 2C). However, the spontaneous ISG expression observed

in untreated *Atg16l1*^{-/-} organoids was absent in *Atg16l1*^{-/-}*Ifnlr*^{-/-} but not *Atg16l1*^{-/-}*Ifnar*^{-/-} organoids

(Sup. Fig. 2C), suggesting a dominant role for IFNLR, possibly due to the overexpression of *Ifnl2*

in absence of IFNAR as previously described (Ardanuy et al., 2020). The necroptosis gene *Mlkl*

is also an ISG and displayed similar IFNAR and IFNLR dependent expression patterns (Sup. Fig.

2C). Given our prior finding that ATG16L1-deficient organoids display spontaneous ISG

expression (Matsuzawa-Ishimoto et al., 2020), we determined whether IFN receptor signaling

contributed to cell death induced by TNF alone. For these experiments, we added TNF to

organoids on day 0, a condition that allows us to examine toxicity of TNF treatment alone.

Although the effect of deleting IFNAR or IFNLR individually (*Atg16l1*^{-/-}*Ifnar*^{-/-} and *Atg16l1*^{-/-}*Ifnlr*^{-/-})

was modest, deleting both IFN receptors improved the viability of *Atg16l1*^{-/-} organoids (*Atg16l1*^{-/-}

Ifnar^{-/-}*Ifnlr*^{-/-}) (Fig. 2G). When these experiments using exogenous cytokines and receptor

deletions are taken together, they show that IFNs synergize with TNF to mediate cell death,

especially in the ATG16L1-deficient setting.

Exacerbation of TNF-induced toxicity in organoids by IFNs is partially dependent on necroptosis

signaling.

TNF receptor engagement in IECs leads to activation of receptor-interacting

serine/threonine protein kinase 1 (RIPK1) to mediate either apoptosis or necroptosis in IECs

(Dannappel et al., 2014; Kattah et al., 2018); RIPK1 mediates apoptosis through caspases, and

when apoptosis or caspases are inhibited, necroptosis occurs through forming a complex with

RIPK3 to phosphorylate the pore forming molecule MLKL that disrupts cell membrane integrity.

We and others have shown that TNF-induced cell death in *Atg16l1* deficient intestinal organoids

and macrophages is dependent on RIPK1, RIPK3, and MLKL (Aden et al., 2018; Lim et al., 2019;

Matsuzawa-Ishimoto et al., 2017). To investigate how the combination of TNF and IFN reduced

viability, we treated organoids with ruxolitinib as a control, a pan-caspase inhibitor (QVD), and a

RIPK1-inhibitor (Nec1s). Ruxolitinib and Nec1s improved viability of both WT and *Atg16l1*-

deficient organoids treated with TNF + IFN-λ2 and TNF + IFN-β (Fig. 3A, B, Sup. Fig. 3A). By

contrast, QVD did not improve the viability of TNF + IFN stimulated organoids.

We first examined protein levels of cell death mediators at an early time point of cytokine

treatment before *Atg16l1*$^{-/-}$ organoids displayed signs of cytotoxicity. Even at 2 h post-stimulation,

phosphorylated RIPK3 (pRIPK) and cleaved caspases, especially caspase-3, were visible in TNF

or TNF + IFN stimulated *Atg16l1*$^{-/-}$ organoids and not WT organoids (Fig. 3C-F, Sup. Fig. 3B).

This result is consistent with the delayed onset of cell death in WT organoids. MLKL and cleaved

caspase-3 were detected in WT organoids treated with IFN-λ2 for 24 h, with or without TNF;

pMLKL was faintly visible when both cytokines were present (Fig. 3C, D, G, H, Sup. Fig. 3B).

Although our earlier observation implicated necroptosis because RIPK1 inhibition and not

caspase inhibition protected organoids, we noted the prominent cleavage of caspase-3.

Therefore, we tested whether cell death induced by TNF and IFN treatment were dependent on

MLKL. *Mlkl*$^{-/-}$ organoids displayed increased viability when treated with TNF + IFN-λ2 or TNF +

IFN-β at 24 h, but this protection was less consistent at 48 h (Fig. 3I, H). These results indicate

that necroptosis contributes to the loss of viability induced by TNF + IFN treatment of organoids.

Virally-triggered intestinal disease in Atg16l1 mutant mice is RIPK3-dependent.

Paneth cell abnormalities and mortality are ameliorated by RIPK1 inhibition in MNV + DSS

treated *Atg16l1*^{ΔIEC} mice (Matsuzawa-Ishimoto et al., 2017). As a kinase, RIPK3 may also be a

targetable molecule. We found that *Atg16l1*^{ΔIEC}*;Ripk3*$^{-/-}$ mice showed substantially reduced

lethality and weight loss compared to *Atg16l1*^{ΔIEC} mice following MNV + DSS treatment and was

similar to WT and *Ripk3*$^{-/-}$ control mice (Fig. 4A). Although not a complete reversal, disease score

and colon length of *Atg16l1*^{ΔIEC}*;Ripk3*$^{-/-}$ mice were not significantly different from WT and *Ripk3*$^{-/-}$

mice (Fig. 4A, B), indicating a general improvement in disease outcomes. In contrast to deletion

of IFNLR and IFNAR, Paneth cell numbers and lysozyme staining were restored in

Atg16l1ᐃIEC;Ripk3-/- mice (Fig. 4C-E). These results show that RIPK3 is necessary for

susceptibility of *Atg16l1ᐃIEC* mice to MNV.

Human organoids are susceptible to cell death induced by antiviral factors.

The combination of TNF and IFNs is toxic to colonic organoids derived from humans,

although the concentration of cytokines necessary for cell death is high (Jang et al., 2024). Based

on our data with mouse organoids, we hypothesized that human small intestinal organoids will be

sensitive to TNF + IFN treatment, especially in the presence of the *ATG16L1* risk allele. To test

this hypothesis, we utilized organoids that we previously generated from endoscopic biopsy

specimens that were genotyped for the *ATG16L1T300A* variant (Sup Table 1) (Matsuzawa-Ishimoto

et al., 2020). As in the mouse model, the combination of TNF + IFN-λ2 induced cell death in

human organoids, which was exacerbated in those derived from individuals homozygous for

ATG16L1T300A (Fig. 5A-C).

TNF and IFNs are produced in response to most viral infections. We previously showed

that SARS-CoV-2 infected mice display a reduction in Paneth cell numbers and abnormal

lysozyme staining, reminiscent of *Atg16l1* mutant mice infected with MNV (Bernard-Raichon et

al., 2022). We did not detect replication competent SARS-CoV-2 particles in the gut of these mice,

raising the possibility that circulating antiviral cytokines can mediate long-range cytotoxic effects

on IECs in situations in which they reach high levels, such as observed in severe COVID (Araujo

et al., 2025; Ghaffarpour et al., 2025). Indeed, gastrointestinal symptoms are common in patients

with COVID-19 and many hospitalized patients display blood stream infections (BSI) caused by

microbes originating from the gut, suggesting intestinal barrier defects (Bernard-Raichon et al.,

2022). To test whether soluble immune mediators associated with severe COVID-19 are cytotoxic

to human IECs, we incubated the above organoids with serum samples pooled from hospitalized

patients during the height of the pandemic when individuals were screened for SARS-CoV-2

infection. These samples were compared with serum from healthy volunteers and hospitalized

individuals who were COVID-negative but BSI-positive. Compared with serum from healthy

volunteers, addition of serum from patients with severe COVID led to increased loss of viability,

which was worse in organoids homozygous for $ATG16L1^{T300A}$ (Fig. 5D-F). Serum from BSI-

positive control also worsened organoid death but not as severely as the COVID-positive samples

(Fig. 5 D-F). Therefore, circulating factors associated with severe COVID-19 display cytotoxicity

to IECs, and the *ATG16L1* risk variant further sensitizes cells to this activity.

Discussion

Our study demonstrates that type I and III IFNs are central mediators of intestinal epithelial

damage following viral infection in the context of ATG16L1 deficiency. Antiviral IFNs and ISG

expression have been observed in IBD patients but their contribution to the pathology is

incompletely understood (Gunther et al., 2019; Mavragani et al., 2020; Ostvik et al., 2020;

Veyssiere et al., 2025). We show that IFN signaling in IECs drives epithelial cell death and disease

exacerbation in MNV-infected $Atg16l1^{\Delta IEC}$ mice, while organoid models reveal a synergistic

cytotoxicity between IFNs and TNF associated with necroptosis signaling. Notably, deletion of

IFN receptors rescued overall survival but had partial effects on Paneth cells. This may reflect a

confounding role for IFNs in controlling the virus, or alternatively, redundancy with other cytokines

such as IFN-γ, which is known to be upregulated during MNV infection and can also trigger Paneth

cell dysfunction (Farin et al., 2014; Matsuzawa-Ishimoto et al., 2022; Tomov et al., 2017). IFN-γ

and type I/III IFNs display redundancy in a model of chronic murine astrovirus infection (Herrmann

et al., 2025). Also, the role of IFNAR was unexpected given the dominance of IFNLR signaling in

IECs and may reflect selective functions in a subset of IECs or specifically in the *Atg16l1* mutant

setting. Future studies should explore whether each IFN has a distinct IEC target and timing of

activity that controls their cytotoxic effects.

These findings strengthen the link between infectious agents such as noroviruses and CD

(Axelrad et al., 2023; Axelrad et al., 2019; Cadwell & Loke, 2025). Although noroviruses are

associated with CD in some patients, they most often cause self-resolving gastroenteritis and are

detected in many asymptomatic individuals, suggesting that as in our mouse model, the

consequences of their presence depend on host factors and may be immune mediated (Bernard-

Raichon & Cadwell, 2023; Lindesmith et al., 2008). A recent study showed that Epstein-Bar virus

(EBV) infection precedes CD (Nandy et al., 2025). Thus, triggers of intestinal inflammation are

unlikely to be exclusive to noroviruses but there may be some specificity. Although many types of

gut microbes including commensal bacteria evoke TNF and IFNs, our finding that serum from

patients with severe COVID-19 displays higher toxicity to organoids compared with serum from

patients with non-viral BSIs raises the possibility that certain types of infections are more likely to

trigger responses that cause IEC death. These observations also raise the intriguing possibility

that viral sequelae and chronic diseases like IBD share underlying mechanisms that include IEC

death. However, we acknowledge that our experimental system does not allow for such

comparisons, and that IBD is much more complex with a prolonged disease development and

cycles of healing and recurrence.

Therapeutically targeting signaling molecules upstream of cell death may offer a strategy

to protect the epithelium in at-risk individuals. Although RIPK3 deletion ameliorated disease in

Atg16l1$^{\Delta IEC}$ mice *in vivo*, RIPK1 inhibition may provide broader protection by blocking multiple

death pathways. Crosstalk between necroptosis, apoptosis, and pyroptosis and their co-

occurance (Araujo et al., 2021; Malireddi & Kanneganti, 2025; Newton et al., 2014) may be

especially relevant to organoids that harbor multiple IEC types. Our time course experiments

show that necroptosis inhibition delays but does not completely prevent loss of viability in

organoids. The partial rescue of viability is reminiscent of findings showing that deleting *Tnfaip3*

and *Tnip1* (genes that are also linked to IBD and autoimmunity) sensitizes to TNF toxicity in the

presence of microbial and viral ligands (Rusu et al., 2022; Su et al., 2019). Interventions that can

be personalized to restore function of a cell type that is specifically affected in a given susceptible

host, such as Paneth cells in the ATG161 deficient background, may be ideal. In this sense, our

observation that RIPK3 deletion better restores Paneth cells compared with IFN receptor deletion

supports targeting nodes at the intersection of multiple cytokine signaling pathways. Indeed,

clinically used JAK inhibitors effectively protect patient-derived colonic organoids from cytokine

cocktails (Jang et al., 2024).

In summary, this work positions IFNs as key players in virally triggered intestinal pathology

associated with TNF toxicity, particularly in the setting of ATG16L1 deficiency. It underscores the

need to consider synergistic cytokine responses in the management of CD and other barrier-

associated disorders.

Materials and Methods

Mice

Age- and gender-matched 8–12-week-old mice on the C57BL/6J (B6) background were used.

Atg16l1$^{f/f}$;VillinCre (*Atg16l1$^{\Delta IEC}$*) mice were provided by S. Virgin (Washington University School

of Medicine, St. Louis, MO) and crossed to *Ifnar1$^{f/f}$* (Jax, 028256) and *Ifnlr1$^{f/f}$* mice (provided by S.

Virgin) to obtain *Atg16l1;Ifnar$^{\Delta IEC}$* and *Atg16l1;Ifnlr1$^{\Delta IEC}$* mice, respectively. To generate littermate

VillinCre-negative and *Atg16l1$^{\Delta IEC}$* controls, mice were bred heterozygous for either the *Ifnar^{f}* or

Ifnlr^f genes and crossed VillinCre-positive with VillinCre-negative. Ifnar1$^{\Delta IEC}$ and *Ifnlr*$^{\Delta IEC}$ mice were

bred separately by crossing VillinCre-positive with VillinCre-negative mice. *Atg16l1;Ifnlr;Ifnar*$^{\Delta IEC}$

mice were obtained by crossing *Atg16l1;Ifnar1*$^{\Delta IEC}$ and *Atg16l1;Ifnlr*$^{\Delta IEC}$ mice. WT mice are a pool

of VillinCre-negative mice from different crosses. *Rip3*$^{-/-}$ mice were provided by G. Miller (NYU

School of Medicine, New York, NY). *Mlkl*$^{-/-}$ mice were provided by J. Murphy (WEHI, Parkville,

Australia). All animal studies were performed according to approved protocols by the New York

University School of Medicine Institutional Animal Care and Use Committees.

MNV-triggered disease model

MNV.CR6 stock was prepared as previously described (Strong et al., 2012). In brief, supernatant

from 293T cells transfected with a plasmid containing the viral genome was applied to RAW264.7

cells to amplify virus production, and virions were concentrated by ultracentrifugation and

resuspended in endotoxin-free PBS. Concentration of stock was determined by plaque assay as

previously described with few modifications (Gonzalez-Hernandez et al., 2012). Diluted stock was

incubated on confluent RAW264.7 cells for 1h after what cells were overlayed with 10g/L

methylcellulose media (Sigma-Aldrich). Cells were incubated at 37°C for 72 h and stained with

1g/L crystal violet solution. Mice were infected orally with 3×10^6 PFUs resuspended in PBS. Viral

burden in stool at day 10 post infection was determined by plaque assay as for the stock. On day

10 post-infection, mice were administered 5% DSS (TdB Consultancy) in their drinking water for

6 d after which it was replaced by regular drinking water. *Ripk3*$^{-/-}$ mice showed increased lethality

when given 5% DSS. When these mice were used, 3% DSS was used instead of 5% as indicated

in the figure legend. Clinical disease score and mouse weight were assessed daily. Disease score

was quantified on the basis of five parameters as described previously, including diarrhea (0–2),

hunched posture (0–2), fur ruffling (0 or 1), mobility (0–2), and blood stool (0 or 1), in which 8 was

the maximum score for the pathology (Matsuzawa-Ishimoto et al., 2017). For survival

experiments, mice were euthanized if they reached the humane end point. In other experiments,

mice were sacrificed before receiving DSS or after receiving 5 days of DSS for analysis (which

occurred before clinical disease signs).

Intestinal organoid culture

Murine small intestinal crypts were isolated and cultured as described previously using ENR

media composed of DMEM/F-12 (ThermoFisher) in the presence of 100IU Penicillin and 100

µg/ml Streptomycin (Corning), 125 µg/ml Gentamicin (ThermoFisher), 2 mML-Glutamine

(Corgning), 20 ng/ml mEGF (PeproTech), 100 ng/ml mNoggin (R&D systems), and 500 ng/ml

mR-Spondin 1 (R&D systems) (Matsuzawa-Ishimoto et al., 2017). Human organoids were

generated during previous studies and frozen (Jang et al., 2022; Matsuzawa-Ishimoto et al.,

2020). For this study, they were thawn and cultured in Human IntestiCult Organoid Growth

Medium (Stemcell Technologies). For viability assays, crypts were embedded at 50 crypts /10 µl

Matrigel (Stemcell Technologies) and cultured in triplicate for 3 days in 96-well culture plates. The

assay was performed in ENR medium for mouse organoids and in differentiation medium for

human organoids. Differentiation medium was composed of DMEM/F-12 containing 100ng/mL

rhIGF-1 (Biolegend), 50ng/mL hFGF-basic (PeproTech), 1µg/mL rhR-Spondin 1 (R&D systems),

100ng/mL rmWnt-3A (R&D systems), 100ng/mL rmNoggin (R&D systems), 10mM Nicotinamide

(Millipore), 10 nM [Leu15]- Gastrin 1 human (Sigma-Aldrich), 500nM A 83-01 (TOCRIS), 1X B-27

supplement (ThermoFisher) as in (Fujii et al., 2018; Matsuzawa-Ishimoto et al., 2022). Murine

organoids were treated with 20 ng/ml mTNFα (Peprotech) and indicated concentrations of mIFNβ

(PBL assay science) and mIFNλ2 (Peprotech). In some experiments, organoids were pre-treated

with 100nM Ruxolitinib, 10µM Q-VD-OPh (Millipore Sigma), 10 µM Nec-1s (Biovision), 20 µg/ml

anti-TNFα antibody (XT3.11, BioXcell) and 20 µg/ml Rat IgG1 isotype control (HRPN, BioXcell).

Human organoids were treated with 50 ng/mL hTNFα (Peprotech), 100 ng/mL hIFNλ2 (R&D

systems). In another experiment, half of the DMEM/F-12 in the differentiation medium was

replaced by human serum (growth factors were maintained at same concentrations). Serum from

healthy donors from the United States was purchased from SeraCare. The serum from patients

with BSI and SARS-CoV-2 infection was collected at the NYU Langone hospital in 2020 and also

used for a previous study (Table S3) (Lubkin et al., 2024). This experiment was performed in a

BSL2+ cell culture room to confine infectious agents. Percent viable organoids was determined

based on morphology by daily quantification as before (Matsuzawa-Ishimoto et al., 2017). Dead

organoids were also marked by staining with 100 µg/ml PI (Sigma-Aldrich) and 100 µg/ml Hoechst

33342 (Invitrogen) to confirm phenotypes.

Quantitative qPCR

RNA was extracted from organoids and intestinal tissue using the RNeasy mini kit (Qiagen). DNA

was removed using the RNA-free DNase set (Qiagen). cDNA was synthesized using the High-

Capacity cDNA reverse transcription kit (Thermo Fisher) according to the manufacturer's protocol.

Quantitative PCR was performed on a Roche 480 II LightCycler using SYBR Green I Master mix

(Roche). Gene expression was normalized to either *Gapdh* (organoids) or *β-actin* (tissue). All

primers are listed in Table S2.

Immunoblotting

600 small intestinal organoids were seeded in 24 well plates and cultured for 3 days in ENR

before cytokine stimulation with 20 ng/ml mTNFα in the presence of either 100 U/ml IFNβ or 1

ng/ml IFNλ2 for 2-24h. Organoids were incubated in lysis buffer (20 mM Tris-HCl, pH 7.4, 150

mM NaCl, 1% Triton X-100, 10% glycerol) containing Halt protease and phosphatase inhibitor

cocktail (Thermo Fisher Scientific) and run on a 4%–12% Bis-Tris Plus Gel (Invitrogen) as before

(Matsuzawa-Ishimoto et al., 2022). The following antibodies were used for immunoblotting

studies: anti–β-actin (AC-15; Sigma-Aldrich), anti–Phospho-MLKL (Ser345) and anti-MLKL (Cell

Signaling), anti-RIP3 (phospho S232; Abcam), anti-RIP3 (AHP1797; AbD Serotec), and anti-

Atg16L (Sigma-Aldrich). Secondary antibodies IRDye 680RD goat anti–rabbit IgG (925-68071)

and IRDye 800CW goat anti–mouse IgG (925-32210) were purchased from LI-COR.

Histology and Immunohistochemistry

Quantification of all microscopy data were performed blind. Intestinal sections were prepared and

stained as previously described (Matsuzawa-Ishimoto et al., 2022). TUNEL staining was

performed using the In situ Cell Death Detection POD kit (Roche Diagnostics) on the Discovery

XT according to the manufacturer's protocol. Lysozyme staining was performed using anti-

lysozyme (ab108508, Abcam) and DAPI immunostaining. All slides were analyzed using a Zeiss

AxioObserver.Z1 with Axiocam 503 Mono operated with Zen Blue software. Images were

processed and quantified using QuPath (for HE and TUNEL staining) or ImageJ (for anti-lysozyme

staining). At least 100 villi or crypts per mouse were quantified. Abnormal Paneth cells were

defined as Paneth cells showing disordered, depleted and/or diffuse lysozyme staining as in

(Bernard-Raichon et al., 2022; Matsuzawa-Ishimoto et al., 2022) and adapted from (Cadwell et

al., 2010).

Statistical analysis

GraphPad Prism version 10 was used for statistical analysis unless otherwise specified. <u>*In-vivo*</u>

<u>model</u>: Survival data were analyzed by Kaplan-Meier with Log-rank test followed by Holm Sidak's

multiple comparison test (Figure 1A). For other parameters measured on mice in Figure 1 and 4,

ordinary or lognormal ordinary (PFU, Figure 1D) one-way ANOVA and Turkey's multiple

comparison was used when data followed a normal distribution or a Kruskal-Wallis test followed

by Dunn's multiple comparison test when they did not (disease score, Figure 1B). For histological

measurements, the effect of mouse genotype was determined on R using individual

measurements (e.g. length of 50 villus per mouse) while adjusting for batch effect caused by

individual mouse and experiments. ANOVA type III followed by Tukey's multiple comparison

Generalized Linear Mixed Model (GLMM) was used for Paneth cell counts. A beta-binomial

analysis followed by Tukey's multiple comparison was used for Paneth cell abnormality. Negative

Binomial GLMM was used to compare the number of TUNEL+ cells per crypt.

Murine organoids: In Figure 2 and 3, in each experiment, organoids derived from a single mouse

per genotype were stimulated with different cytokines and inhibitors (experiments were then

repeated in independent experiments using organoids derived from different mice). Ordinary one-

way ANOVA were used to compare the effect of the treatment within a genotype, two-way ANOVA

were used when comparing the effect of the treatment and of the genotypes, followed by Sidak's

multiple comparison test. Comparison of area under the curve was performed to compare time-

course curves.

Human organoids: In Figure 5A-C, several experiments were performed to study the response of

each organoid donor to cytokine stimulation. The average of viability observed for each

stimulation in technical triplicates obtained from 2-5 experiments were calculated for each donor.

In Figure 5D-F, given the limited quantity of plasma available, the experiment was performed only

once on organoids from 3 donors per group (with technical triplicates). In both cases, an ANOVA

followed by Sidak's multiple comparison test was used to compare the effect of the stimulation on

organoid viability depending on the genotype.

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Declaration of interests

K.C. has received research funding from Pfizer, Takeda, Pacific Biosciences, Genentech and

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applications filed by New York University, which are currently under commercial license to

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Author contributions

LBR, JAN, YMI and KC designed the study. LBR, JAN and YMI performed most of the experiments with assistance from KK, TH, and DM and BMM. YMI and JA provided the human organoids lines. AL, AD and VJT provided the human serum samples. LBR, JAN and KC drafted the manuscript. All authors contributed to refinement of the study protocol and approved the final manuscript.

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Figure legends

Figure 1: *Epithelial type I and III interferon signaling mediate intestinal damage*

downstream of viral infection. **(A)** Survival of wildtype (WT; villin-cre⁻ littermate controls),

Atg16l1$^{\Delta IEC}$, *Atg16l1;Ifnlr$^{\Delta IEC}$*, *Ifnlr$^{\Delta IEC}$*, *Atg16l1;Ifnar$^{\Delta IEC}$*, and *Ifnar$^{\Delta IEC}$* mice receiving 5% DSS in

drinking water for 6 days starting 10 days post inoculation (dpi) with MNV. **(B-C)** Cumulative

disease score (B) and weight loss (C) at day 6 post DSS from mice in (A). **(D)** Plaque forming

units (PFUs) of MNV per gram of stool from mice in (A) at 10 dpi. **(E-F)** Representative images of

ileal crypts stained for lysozyme (red) and DAPI (blue) (top) or for deoxynucleotidyl transferase–

mediated dUTP nick-end labeling (TUNEL) (bottom) of WT, *Atg16l1^{ΔIEC}*, *Atg16l1;Ifnar^{ΔIEC}*,

Atg16l1;Ifnlr^{ΔIEC}, and *Atg16l1;Ifnlr;Ifnar^{ΔIEC}* mice infected with MNV on day 5 post DSS treatment

as in (A) (scale bars 20μm). **(F)** Violin plots depicting the repartition of the number of Paneth cells

observed in individual crypts, overlayed with symbols representing the average number of Paneth

cells per crypt observed in each mouse based on the lysozyme staining shown in (E). **(G)** Average

proportion of abnormal Paneth cells per crypt observed in each mouse as determined on the basis

of whether each Paneth cell displayed a typical staining pattern with distinguishable granules

(normal, orange arrow) or depleted and/or diffuse lysozyme staining (abnormal, white arrow) as

indicated in (E). **(H)** Proportion of crypts with 1, 2 or 3-5 TUNEL+ cells per mouse of each

genotype. Orange arrowheads indicate TUNEL⁺ cells in (E). At least 50 villi and crypts were

quantified per mouse. **(I)** Measurement of colon length from mice in (E-H). Each symbol

represents individual mice (or the mean in A) with bars representing mean ± SEM from at least

two independent experiments. Comparison between all genotypes was performed, not significant

comparisons are not indicated, *p≤0.05, **p≤0.01, ***p≤0.001, ****p≤0.0001, See also Figure S1.

Figure 2: IFNβ and IFNλ2 exacerbate TNF-mediated cell death of intestinal organoids. (A)

Representative images of small intestinal organoids derived from WT (*Atg16l1^{+/+}*)

and *Atg16l1^{ΔIEC}* mice (*Atg16l1^{-/-}*) cultivated in ENR medium for 3 days and stimulated for another

24h ± 20 ng/ml TNF, ± 100 U/ml IFNβ and ± 1ng/ml IFNλ2, then stained with Hoechst (blue) for

nuclei and propidium iodide (PI) (red) for cell death. Scale bars represent 1000 μm. **(B)** Viability

of *Atg16l1^{+/+}* and *Atg16l1^{-/-}* organoids stimulated with indicated cytokines over time as determined

by PI staining and organoid morphology. **(C)** Viability of organoids 48h post stimulation with 20

ng/ml TNF and 1 (low), 10 (med), 100 (high) U/ml IFNβ (left panel) or 0.01 (low), 0.1 (med), 1

(high) ng/ml IFNλ2 (right panel). **(D)** Quantification of TNF in culture supernatants by ELISA from

indicated organoids stimulated or not with 100 U/ml IFNβ for 48h. **(E)** Viability of *Atg16l1*$^{+/+}$ (left)

or *Atg16l1*$^{-/-}$ (right) organoids treated with 20 µg/ml anti-TNFα antibody or isotype control for at

least 30min before stimulation with cytokines. **(F)** Viability of *Atg16l1*$^{+/+}$, *Atg16l1*$^{-/-}$, *Atg16l1*$^{-/-}$*Ifnar*$^{-}$

$^{/-}$ (derived from *Atg16l1;Ifnar*^{ΔIEC} mice), and *Atg16l1*$^{-/-}$*Ifnlr*$^{-/-}$ organoids (derived from

Atg16l1;Ifnlr^{ΔIEC} mice) stimulated on day 3 for 48h. **(G)** Viability of organoids from the indicated

genotype stimulated 2h post seeding with 20 ng/ml TNF for 24 and 48h. For each condition, at

least 20 organoids were seeded in 3 different wells (technical triplicate), which was repeated in at

least 3 independent experiments with organoids derived from different mice each repeat. Each

symbol represents the average of one technical triplicate (or the mean for each stimulation in B)

with bars representing mean ± SEM. ns = not significant, *p≤0.05, **p≤0.01, ****p≤0.0001. See

also Figure S2.

Figure 3: TNF and IFNλ synergize to promote RIPK1-dependent cell death in small

intestinal organoids. (A) Representative images of Hoechst (blue) and PI (red) staining of small

intestinal organoids from WT (*Atg16l1*$^{+/+}$) and *Atg16l1*^{ΔIEC} mice (*Atg16l1*$^{-/-}$) cultivated in ENR

medium for 3 days and stimulated with ± 20 ng/ml TNF, ± 1ng/ml IFNλ2 for 48h. Organoids were

pre-treated with vehicle control, 100nM Ruxolitinib, 10µM Q-VD-OPh, or 10 µM Nec-1s for at least

30min before TNF+IFNλ2 stimulation. Scale bars represent 1000µm. **(B)** Quantification of

organoid viability from (A) at 24 and 48h post-stimulation. For each condition, at least 20

organoids were seeded in 3 different wells (technical triplicate), which was repeated in 3

independent experiments with organoids derived from different mice). **(C-E)** Representative

western blot of indicated proteins (C) and quantification of phosphorylated RIPK3 (pRIPK3) (D)

and cleaved caspase-3 normalized to β-actin and unstimulated control (E) in lysates from

Atg16l1$^{+/+}$ and *Atg16l1*$^{-/-}$ organoids stimulated for 2h with 20 ng/ml TNF alone or combined with

1ng/ml IFNλ2. C and FL designate cleaved and full length, respectively. **(F-G)** Representative

western blot of indicated proteins (F) and quantification of MLKL normalized to β-actin and

unstimulated control (G) in lysates from *Atg16l1$^{+/+}$* organoids stimulated for 24h with 20 ng/ml TNF

alone, 1ng/ml IFNλ2 alone or the combination of both. **(H-I)** Viability of organoids derived from

WT and *Mlkl$^{-/-}$* mice treated at day 3 with the indicated combinations of TNF, IFNλ2, and IFNβ for

24h (H) or 48h (I). Each symbol represents the average of one technical triplicate (B, I-J) or protein

expression observed from a pool of different wells in an independent experiment (F-H) with bars

representing mean ± SEM. ns = not significant, *p≤0.05, **p≤0.01, ****p≤0.0001. See also Figure

S2 and S3.

Figure 4: *Virally-triggered intestinal disease in Atg16l1 mutant mice is RIPK3-dependent.*

(A) Survival over time, cumulative disease score, and weight loss in *Atg16L1$^{f/f}$*, *Atg16L1^{ΔIEC}*,

Atg16L1$^{f/f}$;Ripk3$^{-/-}$, and *Atg16L1^{ΔIEC};Ripk3$^{-/-}$* mice infected for 10 days with MNV before receiving

3% DSS in their drinking water for 6 days. **(B)** Colon length on day 5 post DSS treatment of

indicated mice infected with MNV as in (A). **(C)** Representative images of H&E staining (top, scale

bar 100μm) and immunofluorescence of ileal crypts from mice in (B) stained for lysozyme (red)

and DAPI (blue) (bottom, scale bar 20μm). **(D)** Number of Paneth cells observed in each crypt in

mice from each genotype. **(E)** Average proportion of abnormal Paneth cells per crypt observed in

each mouse as determined on the basis of whether each Paneth cell displayed a typical staining

pattern with distinguishable granules (normal, orange arrow) or depleted and/or diffuse staining

(abnormal, white arrow). At least 50 crypts were quantified per mouse. Each symbol represents

individual mice with bars representing mean ± SEM from at least two independent experiments

(except for Paneth cell abnormality, n=1). ns = not significant, *p≤0.05, **p≤0.01, ***p≤0.001,

****p≤0.0001.

Figure 5: Intestinal organoids derived from *ATG16L1T300A* homozygous individuals exhibit heightened susceptibility to inflammatory factors. Organoids derived from human small intestine biopsies were expanded in IntestiCult medium for several days before seeding in differentiation medium to assess their viability. **(A-B)** Representative images at 24h post-stimulation with ± 50 ng/mL hTNFα, ± 100 ng/mL hIFNλ2 (A) and viability over time (B) of organoids from controls (n = 6 donors homozygous or heterozygous for the non-risk allele) and *ATG16L1^{T300A}* homozygous individuals (n=3 donors). **(C)** Bar graph representation of data from (B) comparing non-risk control and *ATG16L1^{T300A}* homozygous organoids. **(D-E)** Representative pictures at 48h (D) and viability over time (E) of non-risk (n=3) and *ATG16L1T300A* homozygous (n=3) organoids post incubation with pooled serum from healthy donors, patients with a blood stream infection (BSI+ SARS-CoV-2-) or patients with a BSI and infected with SARS-CoV-2 (BSI+ SARS-CoV-2+). **(F)** Bar graph representation of data from (E) comparing non-risk control and *ATG16L1^{T300A}* homozygous organoids. For each condition, at least 20 organoids were seeded in 3 different wells (technical triplicate). Each symbol represents the average viability per donor across experiments (calculated from technical triplicates) with bars representing mean ± SEM for each group. For (A-C) at least two independent experiments were performed for each organoid donor. For (D-E), one experiment was performed for each organoid donor due to the limited quantity of serum available. ns = not significant, *p≤0.05, **p≤0.01, ****p≤0.0001.

Figure 1

Figure 2

Figure 3

Figure 4

Figure 5