

# Beneficial effects of the AT<sub>2</sub> receptor agonist buloxibutid (C21) against acute alveolar epithelial cell inflammation during anti-viral responses

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## Take-home message:

- The potent AT<sub>2</sub> receptor agonist, buloxibutid, reduces the proinflammatory pathogenetic response in a model of viral infection in primary human ATII cells.
- Crucially, buloxibutid treatment does not alter the protective alveolar antiviral responses.

Conflict of interest: JR is an employee of Vicore Pharma AB and holds shares and share options in the company. C-JD is a former employee of Vicore Pharma AB and holds shares and share options in the company. FC, JB, RR, LD, ML, JP, AA, MGJ and DD have nothing to declare.

## ABSTRACT

*Aim:* Activation of the angiotensin II type 2 receptor (AT<sub>2</sub> receptor; encoded by *AGTR2*) has been shown to be beneficial during tissue injury and repair. Therefore, we aimed to investigate the expression of AT<sub>2</sub> receptor in human alveolar type II (ATII) cells, a cell population responsible of lung repair and regeneration and the effect of the AT<sub>2</sub> receptor agonist buloxibutid (also known as C21), in an *in vitro* model of viral infection using primary ATII cells.

*Methods:* We described the expression of AT<sub>2</sub> receptor mRNA using publicly available lung single-cell RNA sequencing datasets. We evaluated the effects of buloxibutid on ATII cell biology at baseline and in response to treatment with double stranded RNA (polyinosinic:polycytidylic acid, a pathogen associated molecular pattern) using MTS cytotoxicity assay, transcriptomic analysis and ELISA.

*Results:* We found that buloxibutid was well tolerated by ATII cells under all conditions tested. RNA sequencing demonstrated that ATII cells responded to polyinosinic:polycytidylic acid with induction of a characteristic antiviral innate immune response. Gene set enrichment analysis revealed that buloxibutid caused a significant suppression of polyinosinic:polycytidylic acid-induced pro-inflammatory

responses whereas it was without effect on the expression of antiviral genes.

*Conclusions:* Our findings suggest that buloxibutid may have therapeutic potential for treatment of respiratory viral pneumonias by limiting excessive pro-inflammatory responses that have the potential to lead to a cytokine storm, while maintaining a protective antiviral response.

## INTRODUCTION

The renin-angiotensin system (RAS) is an important hormonal system that plays a crucial role not only in regulating blood pressure and fluid balance in the body but also in the pathophysiology of several diseases affecting the kidney, neuronal system, cardiocirculatory system and lung. The Angiotensin II (Ang-II) hormone is the principal mediator of the RAS acting via the angiotensin II type 1 receptor (AT<sub>1</sub> receptor), which is abundantly expressed in different tissues, and the angiotensin II type 2 receptor (AT<sub>2</sub> receptor), the expression of which has been shown to increase during tissue injury. Pharmacological activation of the AT<sub>2</sub> receptor has shown significant therapeutic benefit, as well as an ability to modulate immune and stem cell responses in order to promote tissue repair and regeneration (Fatima, Patel and Hussain 2021).

Circulating angiotensin I (Ang-I) is cleaved to generate angiotensin II (Ang-II) through the activity of angiotensin converting enzyme (ACE). Ang-II acts on AT<sub>1</sub> receptor or AT<sub>2</sub> receptor with opposing effects: AT<sub>1</sub> receptor promotes inflammation, fibrosis, alveolar-endothelial damage and increases microvascular permeability, while AT<sub>2</sub> receptor reduces inflammation, promotes alveolar-endothelial survival together with barrier integrity, and can reduce oedema and lung fibrosis (Wang et al. 2019). ACE is abundantly expressed in the

pulmonary capillary network and so, in some pathological conditions, Ang-II can cause excessive activation of AT<sub>1</sub> receptor to cause increased alveolar-capillary permeability, alveolar oedema, hypoxemia, sepsis and possibly death (Wang et al. 2019, Patel et al. 2020).

Since the availability of the non-peptide AT<sub>2</sub> receptor agonist buloxibutid, the anti-inflammatory effect of AT<sub>2</sub> receptor activation has been validated in different models of tissue injury and disease including brain injury, atherosclerosis, arthritis and kidney injury (Gao et al. 2022, Jabber, Mohammed and Hadi 2023, Sampson et al. 2016, Ismael and Ishrat 2022, Steckelings et al. 2022). In murine models of acute and chronic cigarette smoke-induced chronic obstructive pulmonary disease, activation of the AT<sub>2</sub> receptor by buloxibutid has been reported to exhibit anti-inflammatory effects resulting in the restoration of the lung function (Mei et al. 2020). However, little is known about the effects of buloxibutid in injury/repair of the human lung when homeostasis is perturbed by a viral infection. In cases of viral pneumonia, alveolar epithelial cells and vascular endothelial cells are damaged leading to the abnormal accumulation of fluid in the lung alveoli. This is accompanied by release of inflammatory cytokines from both immune and non-immune cells. If the inflammatory response is excessive, acute lung injury (ALI) or even acute respiratory distress syndrome (ARDS) can develop (Gao et al. 2020). The recent COVID-19 pandemic has

increased awareness of the potential deadly consequences of severe viral pneumonia caused by viruses like SARS-CoV-2, respiratory syncytial virus (RSV) as well as influenza and has highlighted the need for better control of virus-induced inflammation.

Considering the critical role of RAS homeostasis in lung injury and repair, we postulated that the AT<sub>2</sub> receptor agonist buloxibutid would control inflammatory responses in primary human ATII cells exposed to polyinosinic:polycytidylic acid (poly I:C), a synthetic double-stranded RNA which was used to mimic a viral infection.

## **RESULTS**

**Buloxibutid treatment did not show any significant cytotoxicity on primary human ATII cells.**

Buloxibutid is a potent agonist of AT<sub>2</sub> receptor and its activation has been reported to be beneficial in different lung conditions where ATII cells play a vital role in lung homeostasis (Mei et al. 2020, Menk et al. 2018, Sumners et al. 2019, Steckelings and Sumners 2020). Data mining of online published single cell-sequencing datasets (Habermann et al. 2020, Sikkema et al. 2023) of normal and pathological lung tissue identified that AT<sub>2</sub> receptor is mainly expressed in ATII cells (Fig.1A and Supp.

Fig.1) thus identifying these cells as a likely therapeutic target. In our dose response experiments, exposure of primary human ATII cells to buloxibutid in absence or presence of poly I:C did not affect cell morphology or cell density (Supp. Fig.2). Similarly, using an MTS cytotoxicity assay, we found no significant harmful effects of buloxibutid on primary human ATII cells in presence or absence of poly I:C (Fig.1B). Moreover, buloxibutid treatment did not affect AT<sub>2</sub> receptor gene (*AGTR2*) expression in ATII cells (Fig.1C). Our findings strongly suggest that buloxibutid is well tolerated by ATII cells and does not negatively regulate AT<sub>2</sub> receptor gene expression.

**Buloxibutid treatment inhibits inflammatory cytokine release in response to poly I:C without modulating antiviral genes.**

Polyinosinic:polycytidylic acid (poly I:C) is a synthetic analogue of double-stranded (ds)RNA that mimics viral infection by activating the RNA viral sensors, Toll-like receptor 3 (TLR3) and RNA helicases (Harris et al. 2013). Therefore, for initial experiments, we performed a dose-response study by treating ATII cells with different concentrations of buloxibutid in absence or presence of poly I:C. Consistent with the anti-inflammatory role of AT<sub>2</sub> receptor, we found that a small, non-significant suppressive effect of Buloxibutid on polyI:C-induced IL-6 gene

expression ( $p=0.99, 0.73, 0.27$  for 1000 nM buloxibutid vs control, 10nM, and 100 nM buloxibutid, respectively) was accompanied by a significant decrease in IL-6 protein release (Fig.2A). In contrast, the ability of double stranded RNA to induce *MX1* and *RSAD2*, interferon-inducible genes that inhibit the replication of a variety of viruses including HIV and influenza (Schoggins and Rice 2011), was not affected by buloxibutid treatment (Fig.2B). Our findings suggest a distinct anti-inflammatory role for buloxibutid during viral infection while maintaining antiviral gene expression.

**RNA-sequencing show a significant effect of buloxibutid treatment on inflammatory pathways without affecting antiviral responses.**

In order to further evaluate the anti-inflammatory role of buloxibutid in the context of a viral infection, we performed RNA-sequencing on A7II cells treated without and with buloxibutid in presence or absence of poly I:C. Bioinformatic analysis showed that gene expression profiles were largely dependent on presence or absence of poly I:C (Fig.3A), where the top differentially expressed genes were identified as being involved in cellular response to virus (Fig.3B).

Virus infection activates specific proinflammatory pathways that include the interferon system, JAK-STAT and NF- $\kappa$ B which in turn promote the expression of cytokines, chemokines and antiviral factors in order to preserve tissue homeostasis and block viral spreading (Nan, Wu and Zhang 2017, Pfeffer 2011). In order to understand how changes in the expression of individual genes might reflect broader changes within the cell, we performed gene set enrichment analysis, which highlights pathways enriched in differentially expressed genes in our RNA-seq results. This showed that, in the presence of polyI:C, buloxibutid significantly downregulated a range of inflammation-associated pathways (Fig.4A). Further interrogation of these pathways individually showed that the effect of buloxibutid was seen across multiple genes within each pathway, and cells were clearly defined by the presence or absence of buloxibutid (Fig.4B and Supp. Table2). Of note, some of the pro-inflammatory factors and chemokines down-regulated by buloxibutid (Fig.5A and Supp. Fig.3) are those that have been implicated as mediators of the cytokine storm, a hyperinflammatory state that is associated with severe uncontrolled respiratory viral infection in some individuals (Murdaca et al. 2021, Kirsch-Volders and Fenech 2021). In contrast key antiviral transcripts were not affected by buloxibutid treatment (Fig.5B). These findings demonstrate the potential of buloxibutid to act exclusively as an anti-inflammatory agent with

no effect on the antiviral cell response during a respiratory viral infection.

## **Discussion and conclusions**

Our work provides evidence of an anti-inflammatory effect of the AT<sub>2</sub> receptor agonist buloxibutid in our model of viral infection in primary human ATII cells. Buloxibutid was able to significantly attenuate inflammation pathways including markers of acute inflammation that are typical of the deleterious cytokine storm. Most importantly, the advantageous anti-inflammatory effect of buloxibutid did not alter the crucial alveolar antiviral responses that are required to control viral replication and spread and so limit further progression of virus-induced lung injury.

The global impact in human history of respiratory diseases like Spanish flu, SARS, MERS, influenza A H1N1 2009 and COVID-19 highlight the crucial role of proinflammatory pathogenetic mechanisms in the respiratory system known as “cytokine storm”. During a respiratory viral infection, a normal immune response to tackle virus spreading can progress in an uncontrolled immune response characterised by an hyperinflammatory status typical of the so called cytokine storm (Murdaca et al. 2021, Kirsch-Volders and Fenech 2021). As respiratory viruses develop various strategies to evade the anti-

viral immune response the rapidly growing infection triggers the uncontrolled production of typical mediators of the cytokine storm including cytokines such as IL-6, IL-8, IL-1 $\beta$  and GM-CSF, and chemokines such as CCL2, CCL-5, IP-10 and CCL3. This is due an exaggerated activation and expansion of immune cells leading to hypersecretion of deleterious amounts of proinflammatory cytokines resulting in acute lung damage, systemic inflammation, multiorgan dysfunction and possibly death (Murdaca et al. 2021, Kirsch-Volders and Fenech 2021). During the COVID19 pandemic, many people died due to the cytokine storm induced by SARS-CoV2 due to the limited availability of effective anti-inflammatory therapy for COVID-19. Corticosteroids such as dexamethasone were widely used after platform trials demonstrated a significant decrease in mortality among patients who were receiving either invasive mechanical ventilation or oxygen alone at randomization but not among those receiving no respiratory support (Group et al. 2021). While corticosteroids have a potent anti-inflammatory effect, they also suppress the antiviral response (Bahsoun et al. 2023). In fact recent studies have indicated increased mortality and delayed viral clearance when either high dose corticosteroids or early initiation of treatment was administered (Cron 2022, Bahsoun et al. 2023). In contrast to corticosteroids, buloxibutid is able to reduce inflammation while retaining the protective antiviral response. Moreover, buloxibutid has shown efficacy in COVID-

19 caused by the original Wild-Type SARS-CoV-2 variant that replicates primarily in ATII cells (Tornling et al. 2021, Szekely et al. 2021). In this study, treatment of hospitalised patients with moderately severe COVID-19 with buloxibutid for 7 days on top of standard of care (including glucocorticoids and remdesivir in the majority of the subjects) reduced the requirement for oxygen supplementation.

In view of the critical role of proinflammatory pathogenetic mechanisms involved in severe lung viral infections, there is a strong need to identify the most suitable immunomodulatory strategy that does not blunt the antiviral response. Our results suggest that buloxibutid could be a potential approach to dampen the pathogenetic cytokine storm while leaving the antiviral mechanism unaltered in order to suppress residual virus spread and limit further tissue damage. Most importantly, by acting upstream of the cytokine storm network, buloxibutid could help to prevent damage to alveolar epithelium and of the microvasculature, modulating the exaggerated infiltration of inflammatory cells and promoting epithelial repair (Fig.6). While this study provides important insights into the cellular responses of alveolar epithelial cells during viral mimic stimulation, certain limitations should be acknowledged. First, all experiments were conducted in vitro, which, while allowing for controlled mechanistic investigations, may not fully capture the complex interactions present in the in vivo lung environment, including cell

crosstalk, vascular influences, and effects of the tissue microenvironment. Second, although the use of primary cells is a strength of this study, the relatively small number of experimental replicates (n) and donors is a limitation. Third, although ATII cells are a key component of the distal lung and play a central role in respiratory viral infections, we did not assess responses in airway epithelial cells, which represent the initial site of viral entry and are crucial in early response to viral infection. Lastly, we used polyI:C as a surrogate for viral infection. While polyI:C is a well-established tool to study innate immune activation, it does not fully replicate the complexities of live viral infection, including viral replication and shedding. Future studies incorporating live virus models would be valuable to confirm the relevance of our findings.

## **METHODS**

### **Primary alveolar type II (ATII) isolation**

Human lung experiments were approved by the Southampton and South-West Hampshire and the Mid and South Buckinghamshire Local Research Ethics Committees, and all subjects gave written informed consent.

Primary ATII culture were established from macroscopically normal regions of surgically resected lung parenchyma tissue in

accord with the method described by Witherden et al. ,2001(Witherden and Tetley 2001). Briefly, the lung tissue was perfused with 0.9% sodium chloride solution and infused with 0.25% Trypsin solution (Sigma-Aldrich, Poole, UK) at 37 °C for 45 min. After trypsin digestion, the tissues were finely cut in the presence of newborn calf serum (NCS) (Life Technologies Limited, Paisley, UK) and DNase 250 µg/ml (Sigma-Aldrich, Poole, UK), then cells were filtered by sequential passage through a 400-µm metal mesh and 40- µm nylon filter. The cells were re-suspended in DCCM-1 medium (Biological Industries Ltd, Kibbutz Beit-Haemek, Israel) supplemented with 1% penicillin, 1% streptomycin, and 1% L-glutamine, and incubated at 37 °C in a humidified incubator for 2 h in tissue culture flasks to allow differential adherence and removal of contaminating cells. The ATII cells were re-suspended in fresh DCCM-1 supplemented with 10% NCS, 1% penicillin, 1% streptomycin and 1% L-glutamine (all supplements from Life Technologies Limited, Paisley, UK) and plated on collagen 1 (PureCol 5005-b, Advanced BioMatrix Inc, California, USA) coated 96-well plates at 60% density; after 48h purity was tested by staining for alkaline phosphatase.

### **Cell treatment and cytotoxicity assay**

Buloxibutid was dissolved in dimethylsulphoxide (DMSO) (Sigma-Aldrich, Gillingham, UK) at a final concentration of 0.1% and 0.1% DMSO was used as vehicle CTRL. Human primary ATII cells at passage 1 were cultured at a cell density of 70-80% on collagen 1 (PureCol 5005-b, Advanced BioMatrix Inc, California, USA) coated 96well plate and treated for 24h without or with buloxibutid in presence or absence of poly I:C HMW (InvivoGen Europe, Toulouse, France). After 24h treatment, any cytotoxic effect has been evaluated using an MTS assay *CellTiter 96® AQueous One Solution Cell Proliferation Assay* from Promega UK Ltd. in accord with the manufacture instruction. A vehicle control (DMSO) was run in each experiment.

### **Reverse transcription and quantitative PCR (RTqPCR)**

Human primary ATII cells were cultured at a cell density of 70-80% on collagen 1 coated 96 well plate and treated for 24h without or with buloxibutid in presence or absence of poly I:C (InvivoGen Europe, Toulouse, France). After the 24h treatment, RNA was isolated using Monarch® Total RNA Miniprep Kit (New England Biolabs Limited, Herts, UK). RNA was reversed to cDNA using precision nanoScript2 Reverse Transcription Kit from Primer Design, Southampton, UK or High-Capacity cDNA Reverse Transcription Kit from Life Technologies Limited, Paisley, UK.

Probe-based qPCR primers sets were obtained from Primer Design, Southampton, UK (*MX1 catalog no. DD-hu-600-MX1; RSAD2 catalog no. DD-hu-600-RSAD2; UBC/GAPDH catalog no. HK-PP-hu-d-UBC/GAPDH*) and SYBR green qPCR primers sets were obtained from Life Technologies Limited, Paisley, UK (*IL6: FW-CTGGCAACAATGAGTCTACCTT and RV-GCCACAGCGAGGTTGAAGAT; AGTR2: FW-ACTCACCTCTTCAGAACGAATTG and RV-CCATCTTTGGAAGGTTTCAGGTTG*). Changes in mRNA expression using the following primers were analysed by qPCR and normalized to the housekeeping genes ubiquitin C and glyceraldehyde-3-phosphate dehydrogenase (*UBC and GAPDH*). Data were analysed using the  $\Delta\Delta CT$  method.

### **ELISA and multiplex electrochemiluminescence immunoassay analysis**

Human Interleukin 6 (IL6) and Monocyte chemoattractant protein-1 (MCP1) were evaluated in culture media using a DuoSet ELISA (R&D, Abingdon, UK) in accordance with manufacturer's instructions. Human Interleukin 15 (IL15), Human Interleukin 1-beta (IL1 $\beta$ ), Macrophage Inflammatory Protein 1 Alpha (MIP1a) and tumor necrosis factor alpha (TNF $\alpha$ ) were evaluated in culture media using a multiplex electrochemiluminescence immunoassay (U-PLEX MSD, Rockville, Maryland, USA). Each sample was evaluated in

duplicates and the mean value used for subsequent analyses.  $p < 0.05$  was accepted as statistically significant. \*  $p < 0.05$ .

### **RNA sequencing and Bioinformatic Analyses**

Cells were harvested 24h after treatment and RNA was isolated using Monarch<sup>®</sup> Total RNA Miniprep Kit (New England Biolabs). RNA sequencing was performed by Novogene (UK) using an Illumina Novaseq 6000 sequencer after passing the quality control checks. RNA samples were enriched for mRNA using polyA enrichment using poly-T-oligo magnetic beads. After fragmentation, cDNA was synthesised using random hexamer primers. ~150bp paired end read sequencing was performed on an Illumina Novaseq 6000 sequencer. Kallisto running in paired-end mode was used to pseudoalign raw fastq data with human reference transcriptome hg38 (from human reference genome GRCh38), using RefSeq's transcripts to generate raw counts data. Raw counts were imported into R using the tximport package. Differential expression analysis was performed using edgeR, with Benjamini-Hochberg multiple test correction. Normalised counts per million reads (CPM) were calculated using EdgeR. Gene set enrichment analysis was performed using NCBI's GSEA software (<https://www.gsea-msigdb.org/gsea/index.jsp>), run in preranked mode, with genes ranked by  $-\log_{10}$  (adjusted P-value). Heatmaps were produced using pheatmap. Graphs were produced using ggplot2.

## **Statistics**

All the experiments were performed using 4 different donors (3 male and 1 female) . 'n' indicates the number of repeated experiments with different donors. ELISA and qPCR results are expressed as means of  $\pm$  SD. Differences between groups were assessed using Kolmogorov-Smirnov test, Mann-Whitney test, oneway-ANOVA or 2ways-ANOVA test with Dunnett's multiple comparisons test. All data were analysed using Prism (GraphPad, CA, USA).  $p < 0.05$  was accepted as statistically significant. \*  $p < 0.05$  and  $p\text{-value} < 0.01$  \*\*.

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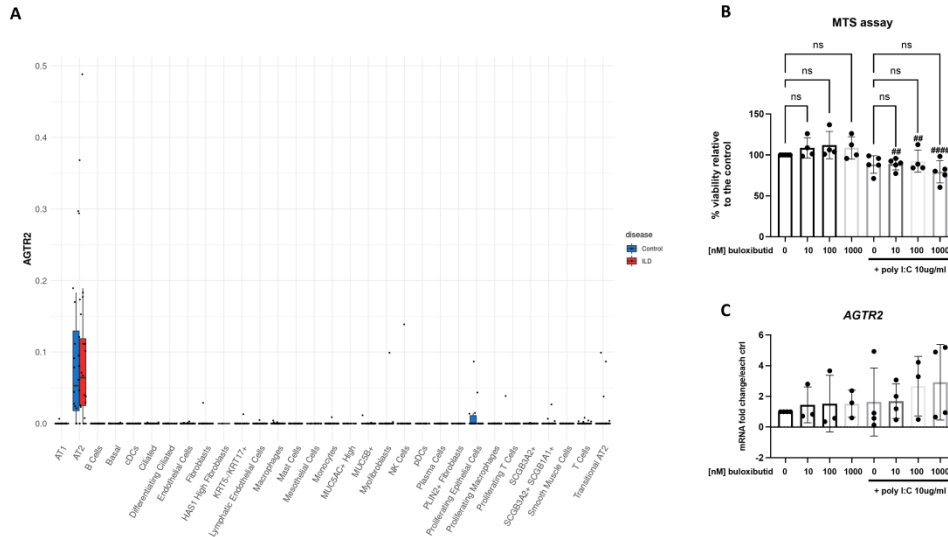


Fig.1: AT2 receptor gene (AGTR2) expression in lung cells and buloxibutid treatment (10–1000nM) of primary ATII cells in absence or presence of poly I:C. A) Banovich/Kropski dataset from the IPF atlas averaged per subject and braked by disease confirm the high expression of AT2 receptor in ATII cells in both control donors and ILD patients. B) MTS cell viability assay showed no significant effect of buloxibutid treatment on ATII cell viability (n=4/5). # – significance vs. equivalent buloxibutid-treated, poly-IC free culture. C) AT2 receptor gene expression is not modulated by buloxibutid compound treatment in absence or presence of poly I:C (n=3/4). Values are expressed as means of  $\pm$  SD, of n=3-5 independent experiments, each performed using cells from a different donor. Samples were generated by pooling lysates from 3 wells per condition keeping donors separate and analysed in technical duplicate. Analysis: 2ways-ANOVA (p-value <0.01## and <0.0001#### ).

856x485mm (130 x 130 DPI)

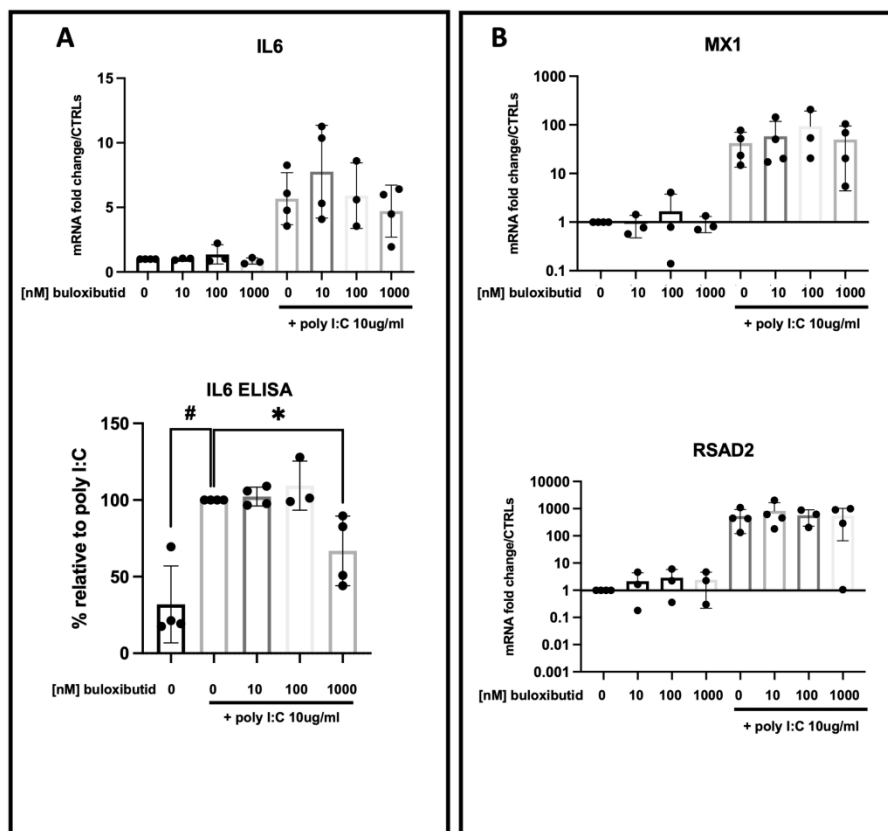


Fig.2: Expression of the inflammatory marker, IL6, and of anti-viral genes during buloxibutid treatment (10-1000nM) in absence or presence of poly I:C. A) Buloxibutid treatment shows a small, non-significant suppressive effect in IL6 gene expression induced by poly I:C, confirmed by a significant decrease in IL-6 protein release, measured by ELISA (bottom panel, Mann-Whitney p-value < 0.05 # ; oneway-ANOVA p-value < 0.05 \*). B) Buloxibutid treatment does not affect induction of the anti-viral genes, MX1 or RSAD2, by poly I:C. Values are expressed as means of  $\pm$  SD, of n=3-4 independent experiments, each performed using cells from a different donor. Samples were generated by pooling lysates or supernatants from 3 wells per condition keeping donors separate and analysed in technical duplicate. Analysis: 2ways-ANOVA (p-value < 0.05 \*).

209x180mm (300 x 300 DPI)

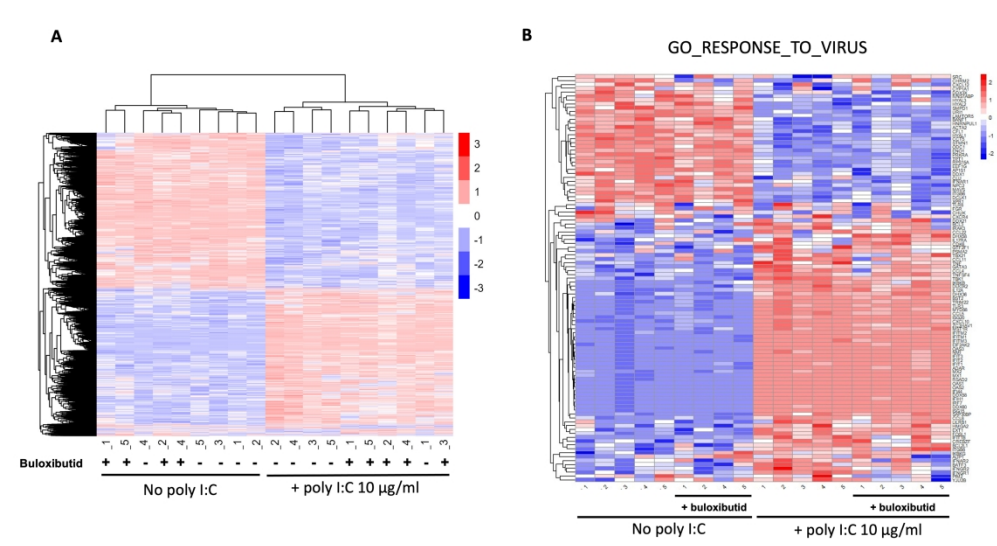


Fig.3: RNA sequencing of primary ATII cells treated with buloxibutid 1000nM in absence or presence of poly I:C. A) Heat map of all differentially expressed genes show a strong clustering mainly between conditions without or with poly I:C in absence or presence of buloxibutid 1000nM. B) Heatmap of GO\_RESPONSE\_TO\_VIRUS genes show top differentially expressed genes clustering between conditions without or with poly I:C. n=4-5 independent experiments, each performed using cells from a different donor. Samples were generated by pooling lysates from 3 wells per condition keeping donors separate.

337x182mm (300 x 300 DPI)

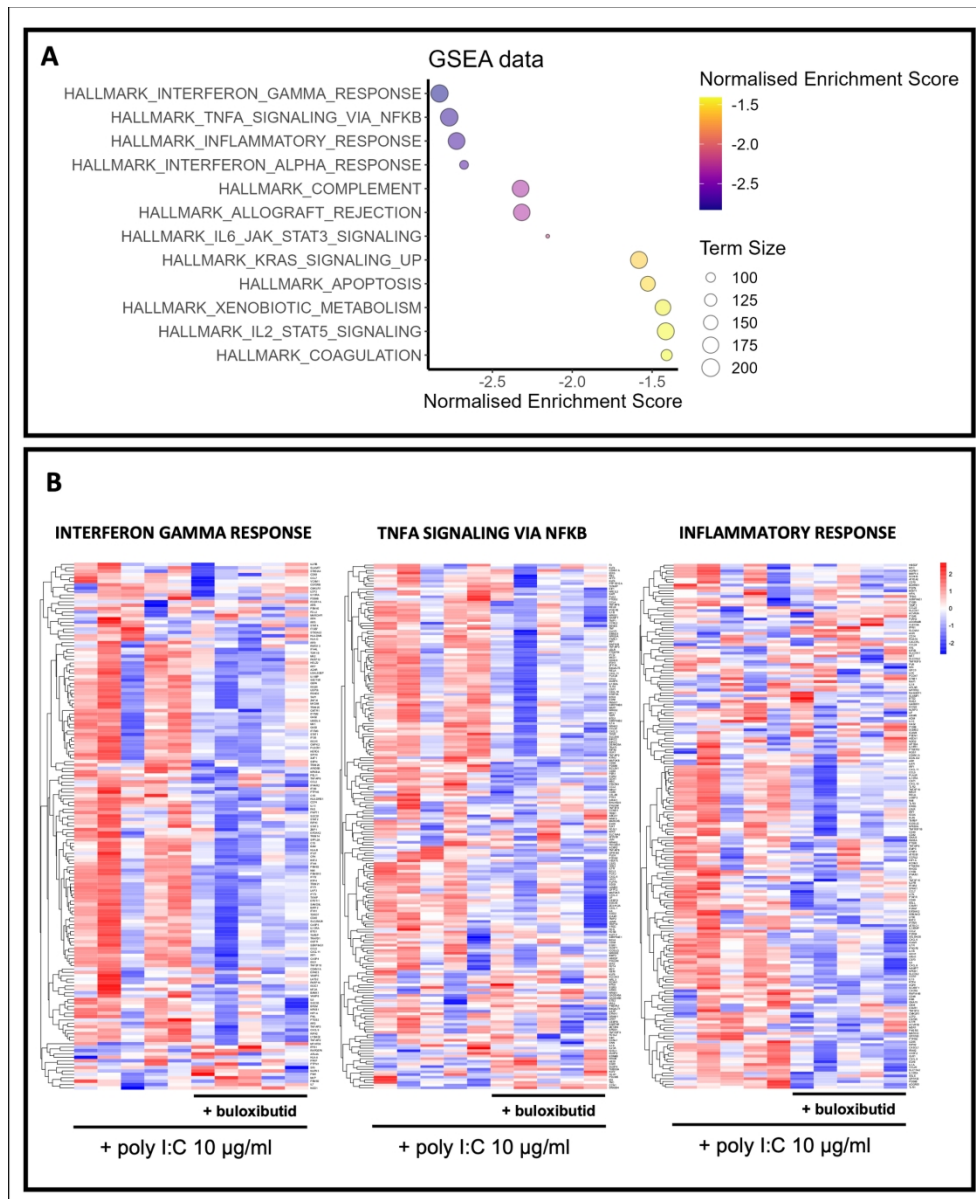


Fig.4: Gene set enrichment analysis (GSEA) of RNA sequencing datasets. A) GSEA analysis shows that mainly inflammation related pathways are significantly downregulated by buloxibutid 1000nM in presence of poly I:C compared to poly I:C alone ( $p$ -value  $< 0.05$ ). B) Heat maps showing downregulation of the top 3 pathways of GSEA analysis by buloxibutid 1000nM in presence of poly I:C compared to poly I:C alone.  $n=5$  independent experiments, each performed using cells from a different donor. Samples were generated by pooling lysates from 3 wells per condition keeping donors separate.

185x226mm (300 x 300 DPI)

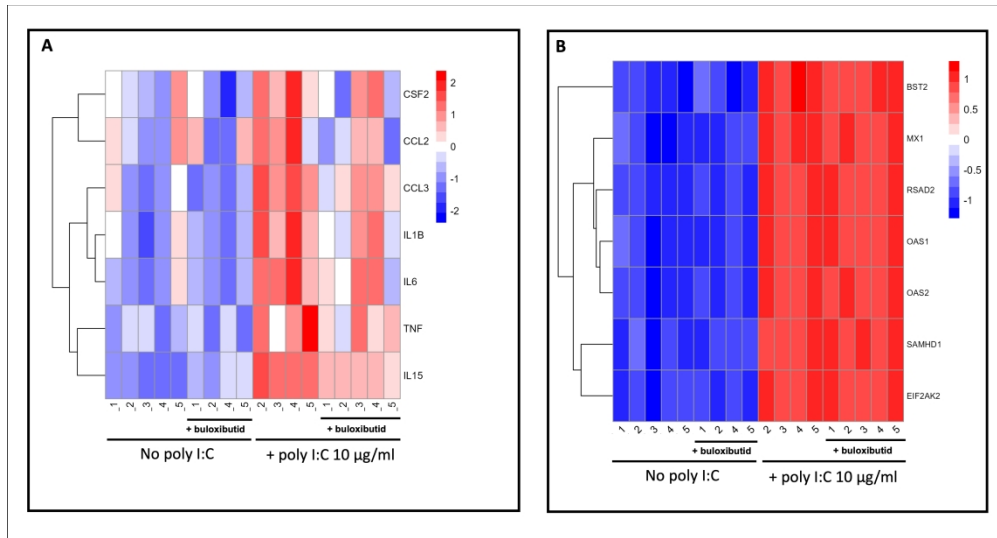


Fig.5: Mediators of the cytokine storm and antiviral transcripts during buloxibutid treatment. A) The Heatmap generated from RNA-sequencing shows that transcripts of the mediators of the cytokine storm are increased by poly I:C and down regulated by buloxibutid 1000nM treatment in presence of poly I:C. B) Antiviral genes induced by poly I:C treatment mimicked viral infection are not affected by buloxibutid compound 1000nM treatment. n=5 independent experiments, each performed using cells from a different donor. Samples were generated by pooling lysates from 3 wells per condition keeping donors separate.

336x179mm (330 x 330 DPI)

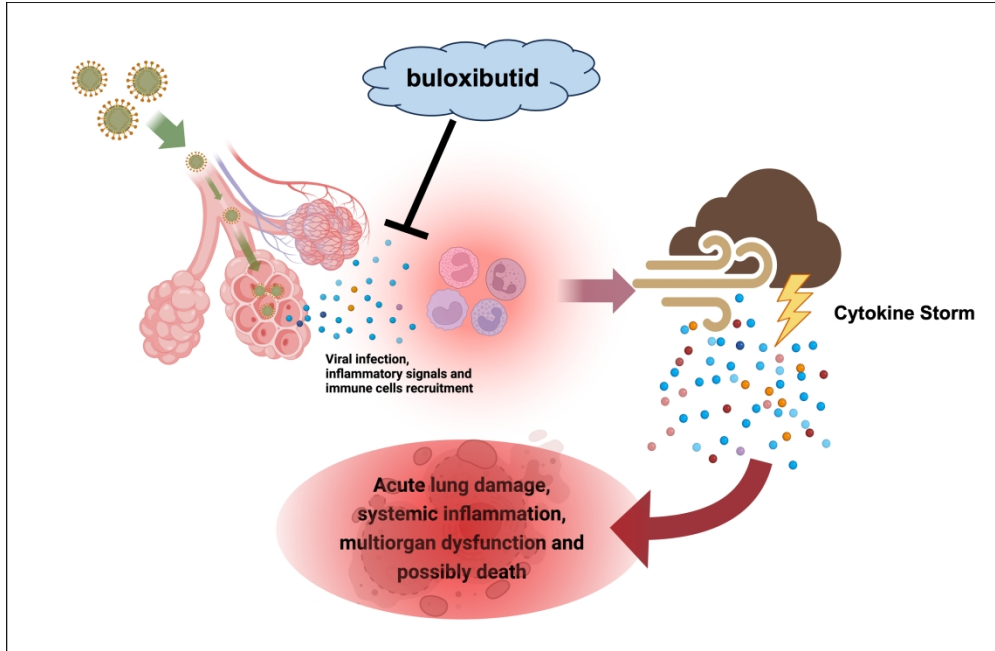
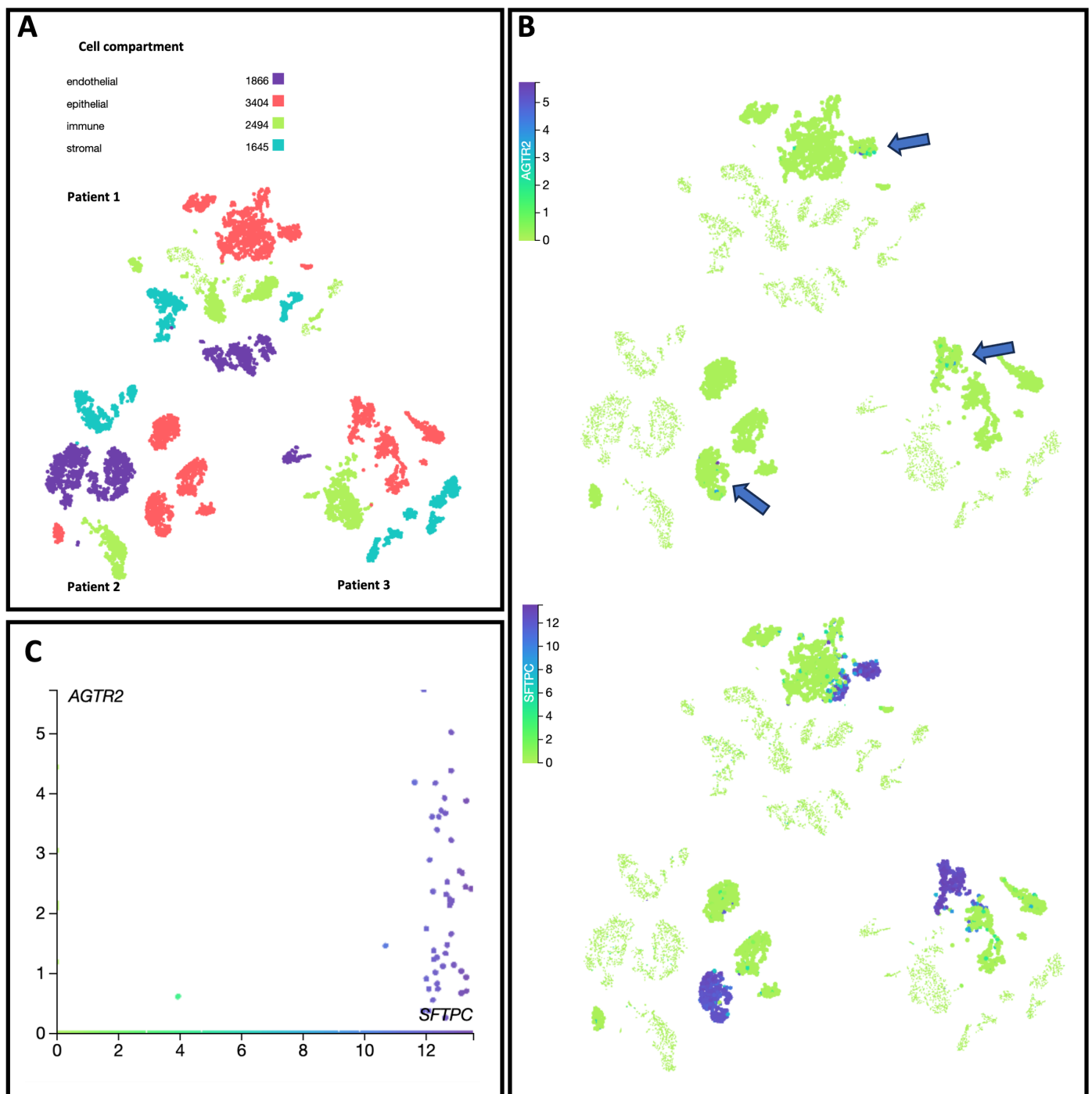
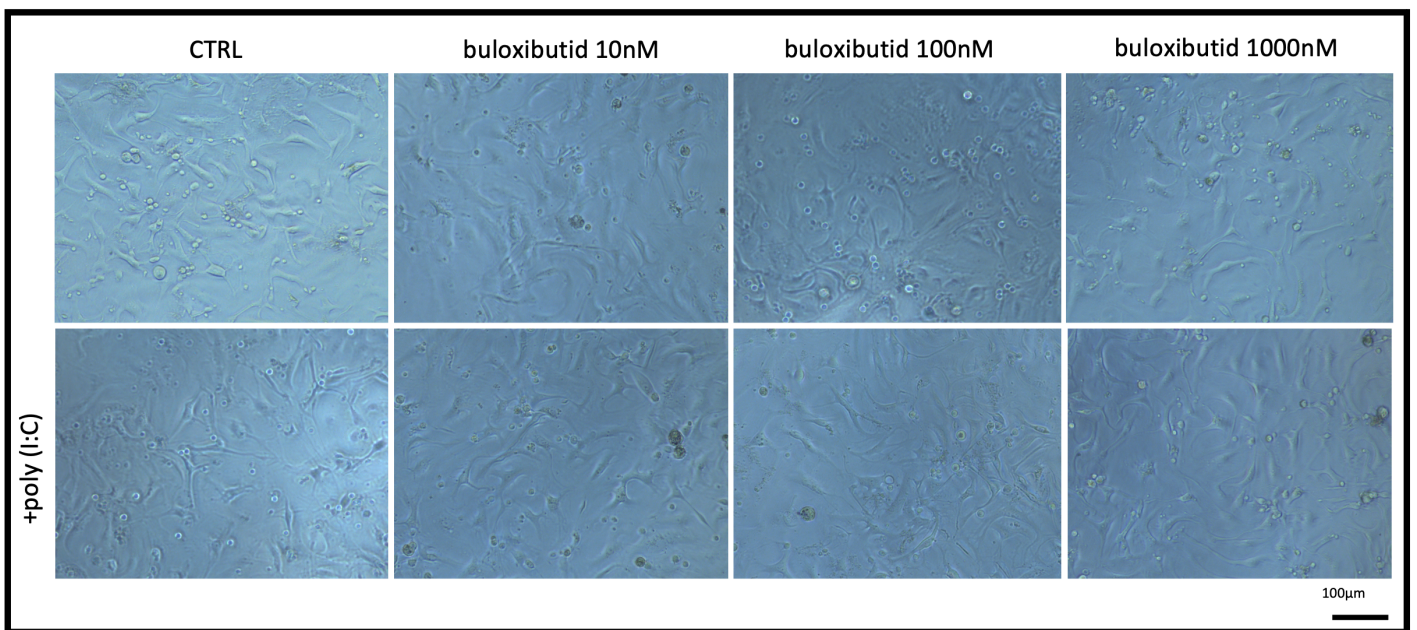


Fig.6: Graphical representation of role of buloxibutid in viral infection and inflammation. buloxibutid treatment during virus infection may help to reduce the cytokine storm by acting mainly on the alveolar cell mitigating the immune cell response.

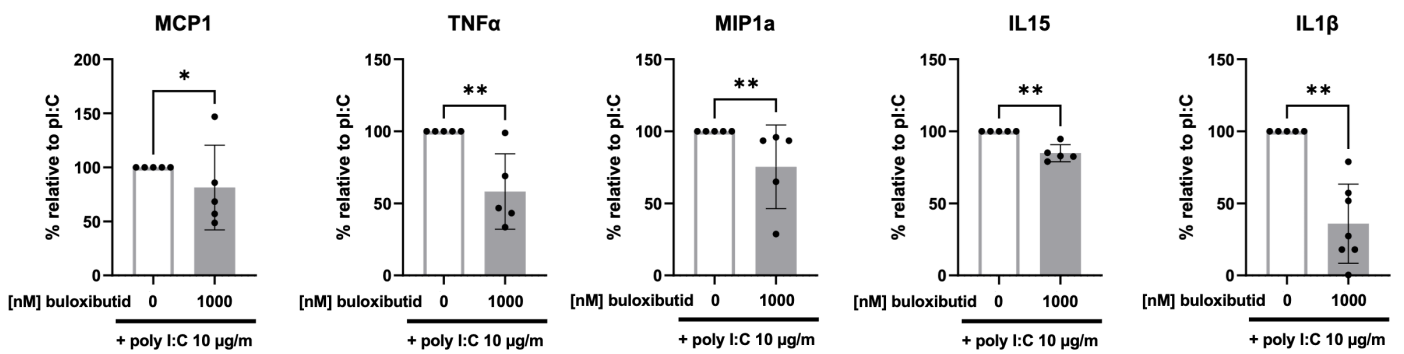
256x166mm (330 x 330 DPI)



**Supp. Fig.1:** AGTR2 transcript is highly expressed in ATII cells in the lung. A) Krasnow human lung cell atlas from single-cell RNA sequencing cell compartment. B-C) AGTR2 is mainly expressed in the epithelial compartment and strongly correlates with SFTPC expression that is a specific marker of ATII cells.



**Supp. Fig.2:** Buloxibutid (10-1000nM) treatment of primary ATII cells in absence or presence of poly I:C. shows no effects on ATII cell morphology and density.



**Supp. Fig.3:** ATII cell protein release of the mediators of the cytokine storm is significantly down regulated by buloxibutid 1000nM treatment in presence of poly I:C treatment. Values are expressed as means of  $\pm$  SD. Kolmogorov-Smirnov test (p-value < 0.05 \* and p-value < 0.01 \*\* ).

## GO\_RESPONSE\_TO\_VIRUS

GENE SYMBOL	NCBI GENE ID	name
SRC	6714	SRC proto-oncogene, non-receptor tyrosine kinase
CHRM2	1129	cholinergic receptor muscarinic 2
CXCL12	6387	C-X-C motif chemokine ligand 12
CYP1A1	1543	cytochrome P450 family 1 subfamily A member 1
DDX3X	1654	DEAD-box helicase 3 X-linked
IVNS1ABP	10625	influenza virus NS1A binding protein
HYAL3	6677	sperm adhesion molecule 1
HYAL2	8692	hyaluronidase 2
SMPD1	6609	sphingomyelin phosphodiesterase 1
URI1	8725	URI1 prefoldin like chaperone
LAMTOR5	10542	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5
BANF1	8815	barrier to autointegration nuclear assembly factor 1
HNRNPUL1	11100	heterogeneous nuclear ribonucleoprotein U like 1
ACTA2	59	actin alpha 2, smooth muscle
CFL1	6944	vacuolar protein sorting 72 homolog
HYAL1	6677	sperm adhesion molecule 1
CCT5	22948	chaperonin containing TCP1 subunit 5
STMN1	3925	stathmin 1
ODC1	89874	solute carrier family 25 member 21
ENO1	2023	enolase 1
PRKRA	8575	protein activator of interferon induced protein kinase EIF2AK2
TPT1	7178	tumor protein, translationally-controlled 1
RPS15A	6210	ribosomal protein S15a
EEF1G	1937	eukaryotic translation elongation factor 1 gamma
AP1S1	1174	adaptor related protein complex 1 subunit sigma 1
DDX1	1653	DEAD-box helicase 1
CLU	1191	clusterin
IFNAR1	3454	interferon alpha and beta receptor subunit 1
NPC2	10577	NPC intracellular cholesterol transporter 2
MAVS	57506	mitochondrial antiviral signaling protein
ITGB6	3694	integrin subunit beta 6
DCLK1	9201	doublecortin like kinase 1
XPR1	9213	xenotropic and polytropic retrovirus receptor 1
TLR8	51311	toll like receptor 8
FGR	2268	FGR proto-oncogene, Src family tyrosine kinase
CHUK	1147	component of inhibitor of nuclear factor kappa B kinase complex
CXCR4	7852	C-X-C motif chemokine receptor 4
DDX21	54606	DEAD-box helicase 56
BCL3	602	BCL3 transcription coactivator
IRAK3	11213	interleukin 1 receptor associated kinase 3
CCL22	6367	C-C motif chemokine ligand 22
DHX58	79132	DExH-box helicase 58
IL17RA	23765	interleukin 17 receptor A
CDK6	1021	cyclin dependent kinase 6
GTF2F1	2962	general transcription factor IIF subunit 1
PSMA2	5683	proteasome 20S subunit alpha 2
TBX21	30009	T-box transcription factor 21
CCL11	6356	C-C motif chemokine ligand 11
TNF	7124	tumor necrosis factor
GATA3	2625	GATA binding protein 3
CCL4	6351	C-C motif chemokine ligand 4
TNFSF4	7292	TNF superfamily member 4
TBK1	29110	TANK binding kinase 1
IKKB	3551	inhibitor of nuclear factor kappa B kinase subunit beta
DUOX2	50506	dual oxidase 2
IL12A	3592	interleukin 12A
DHX36	170506	DEAH-box helicase 36
BST2	684	bone marrow stromal cell antigen 2
TRIM22	10346	tripartite motif containing 22
TLR3	7098	toll like receptor 3
MYD88	4615	MYD88 innate immune signal transduction adaptor
CCL5	6352	C-C motif chemokine ligand 5
ISG20	3669	interferon stimulated exonuclease gene 20
CXCL10	3627	C-X-C motif chemokine ligand 10
ZC3HAV1	56829	zinc finger CCCH-type containing, antiviral 1
MST1R	4486	macrophage stimulating 1 receptor
IFITM2	10581	interferon induced transmembrane protein 2
IFITM1	8519	interferon induced transmembrane protein 1
IFITM3	10410	interferon induced transmembrane protein 3
EIF2AK2	5610	eukaryotic translation initiation factor 2 alpha kinase 2
OAS3	4940	2'-5'-oligoadenylate synthetase 3
NMI	4641	myosin IC
IFIT3	3437	interferon induced protein with tetratricopeptide repeats 3
IFIT2	3433	interferon induced protein with tetratricopeptide repeats 2
IFIT1	3434	interferon induced protein with tetratricopeptide repeats 1
ADAR	103	adenosine deaminase RNA specific
MX2	4600	MX dynamin like GTPase 2
MX1	4599	MX dynamin like GTPase 1
RSAD2	91543	radical S-adenosyl methionine domain containing 2
OAS1	4938	2'-5'-oligoadenylate synthetase 1
OSA2	57492	AT-rich interaction domain 1B
IFI44	10561	interferon induced protein 44
DDX58	23586	RNA sensor RIG-I
IFIH1	64135	IFIH1 interferon induced with helicase C domain 1
IRF7	3665	interferon regulatory factor 7
DDX60	55601	DExD/H-box helicase 60
ISG15	9636	ISG15 ubiquitin like modifier
SAP30BP	29115	SAP30 binding protein
CCL8	6355	C-C motif chemokine ligand 8
LILRB1	10859	leukocyte immunoglobulin like receptor B1
HMGA2	8091	high mobility group AT-hook 2
EXT1	2131	exostosin glycosyltransferase 1
FOSL1	8061	FOS like 1, AP-1 transcription factor subunit
IFIT1B	439996	interferon induced protein with tetratricopeptide repeats 1B
CREBZF	58487	CREB/ATF bZIP transcription factor
BCL2L1	598	BCL2 like 1
ITGB8	3696	integrin subunit beta 8
IKBK	8517	inhibitor of nuclear factor kappa B kinase regulatory subunit gamma
AUP1	550	AUP1 lipid droplet regulating VLDL assembly factor
IFNAR2	3455	interferon alpha and beta receptor subunit 2
BATF3	55509	basic leucine zipper ATF-like transcription factor 3
IFNGR2	3460	interferon gamma receptor 2
IFNGR1	3459	interferon gamma receptor 1
PIM2	11040	protein kinase Pim-2
YJU2B	81576	YJU2 splicing factor homolog B

Supp. Table 1: Gene table of GO\_RESPONSE\_TO\_VIRUS top differentially expressed genes

INTERFERON GAMMA RESPONSE

TNFA SIGNALING VIA NFkB

INFLAMMATORY RESPONSE

NAME	SYMBOL	RANK IN GENE LIST	RAK METRIC SCORE	RUNNING ES	CORE ENRICHMENT	NAME	SYMBOL	RANK IN GENE LIST	RAK METRIC SCORE	RUNNING ES	CORE ENRICHMENT	NAME	SYMBOL	RANK IN GENE LIST	RAK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
row_0	DHOSL	5	2.81493563	0.02203946No		row_0	DUPE1	1	0.00048426No			row_0	IL12NB2	658	1.1206257	0.00000000	
row_1	FPF1	540	1.07126583	0.02064844No		row_1	DNABL4	297	1.93018583	0.0141885No		row_1	FPF1	609	0.7211885	0.07922877	
row_2	FCGR1A	182	0.9823405	-0.01132126No		row_2	NR4A1	799	1.00028283	-0.0201536No		row_2	CELC1A	1368	0.78808456	0.00464438No	
row_3	NCFB9	143	0.86883156	-0.0300477No		row_3	HES1	1322	0.86619687	0.01000000No		row_3	CELC4A	1744	0.7444000	0.00464438No	
row_4	NCOI1	270	0.53778799	0.01000000No		row_4	LRG1	1322	0.86619687	0.01000000No		row_4	CELC4	1765	0.65413609	0.00464438No	
row_5	RARGF6	270	0.50971091	-0.10664564No		row_5	HES1	1322	0.86619687	0.01000000No		row_5	CELC4	1765	0.65413609	0.00464438No	
row_6	ANKA4	2708	0.50682457	-0.1036751No		row_6	CCND1	1470	0.71831287	0.02527483No		row_6	SCAI1	2483	0.54804425	-0.09794590No	
row_7	PM1	2708	0.46588158	-0.14600251No		row_7	CCND1	1470	0.71831287	0.02527483No		row_7	SCAI1	2483	0.54804425	-0.09794590No	
row_8	L1	3726	0.37651031	-0.1562878No		row_8	GAD68B	1575	0.73635815	-0.00939754No		row_8	SCAI1	2483	0.54804425	-0.09794590No	
row_9	KLK1	721	0.25561071	-0.15000000No		row_9	SCZ3A3	2117	0.61419099	-0.0477393No		row_9	ITGB8	3084	0.62213037	-0.12036490No	
row_10	METTL7B	4868	0.24742386	-0.2197093No		row_10	GAD68B	3036	0.45096113	-0.0481071No		row_10	ITGB8	3084	0.62213037	-0.12036490No	
row_11	UPP1	4917	0.24219707	-0.22061577No		row_11	ITGB8	3036	0.45096113	-0.0481071No		row_11	ITGB8	3084	0.62213037	-0.12036490No	
row_12	PPP1	4917	0.24219707	-0.22061577No		row_12	ITGB8	3036	0.45096113	-0.0481071No		row_12	ITGB8	3084	0.62213037	-0.12036490No	
row_13	FGI2	6715	0.19757349	-0.32488544No		row_13	ITGB8	3036	0.45096113	-0.0481071No		row_13	ITGB8	3084	0.62213037	-0.12036490No	
row_14	MVP	6748	0.10778154	-0.32928183No		row_14	ITGB8	3036	0.45096113	-0.0481071No		row_14	ITGB8	3084	0.62213037	-0.12036490No	
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row_16	MHF2D	7376	0.0699889	-0.3618028No		row_16	ITGB8	3036	0.45096113	-0.0481071No		row_16	ITGB8	3084	0.62213037	-0.12036490No	
row_17	GZMA	7657	0.05387748	-0.3793124No		row_17	ITGB8	3036	0.45096113	-0.0481071No		row_17	ITGB8	3084	0.62213037	-0.12036490No	
row_18	STGAL5	8138	0.02461516	-0.46251156No		row_18	ITGB8	3036	0.45096113	-0.0481071No		row_18	ITGB8	3084	0.62213037	-0.12036490No	
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row_35	SCZ1A1	11575	-0.17854898	-0.5923244No		row_35	ITGB8	3036	0.45096113	-0.0481071No		row_35	ITGB8	3084	0.62213037	-0.12036490No	
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row_40	PSMB7	12262	-0.22828134	-0.6190392No		row_40	ITGB8	3036	0.45096113	-0.0481071No		row_40	ITGB8	3084	0.62213037	-0.12036490No	
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row_46	IT2	12497	-0.25470754	-0.6271506No		row_46	ITGB8	3036	0.45096113	-0.0481071No		row_46	ITGB8	3084	0.62213037	-0.12036490No	
row_47	AP0F4	12497	-0.25523128	-0.6271506No		row_47	ITGB8	3036	0.45096113	-0.0481071No		row_47	ITGB8	3084	0.62213037	-0.12036490No	
row_48	AR05B	12666	-0.26931148	-0.6329186No		row_48	ITGB8	3036	0.45096113	-0.0481071No		row_48	ITGB8	3084	0.62213037	-0.12036490No	
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row_50	EPST11	12788	-0.28207179	-0.63553323No		row_50	ITGB8	3036	0.45096113	-0.0481071No		row_50	ITGB8	3084	0.62213037	-0.12036490No	
row_51	XMT1	12830	-0.28663786	-0.6370144No		row_51	ITGB8	3036	0.45096113	-0.0481071No		row_51	ITGB8	3084	0.62213037	-0.12036490No	
row_52	KAP2	12830	-0.29399878	-0.6372923No		row_52	ITGB8	3036	0.45096113	-0.0481071No		row_52	ITGB8	3084	0.62213037	-0.12036490No	
row_53	IT2D	12830	-0.29289022	-0.63657743No		row_53	ITGB8	3036	0.45096113	-0.0481071No		row_53	ITGB8	3084	0.62213037	-0.12036490No	
row_54	RSAD2	13304	-0.33494304	-0.63871044No		row_54	ITGB8	3036	0.45096113	-0.0481071No		row_54	ITGB8	3084	0.62213037	-0.12036490No	
row_55	MTA2	13304	-0.31838016	-0.6427242No		row_55	ITGB8	3036	0.45096113	-0.0481071No		row_55	ITGB8	3084	0.62213037	-0.12036490No	
row_56	HLA-A	13304	-0.32882166	-0.64661525No		row_56	ITGB8	3036	0.45096113	-0.0481071No		row_56	ITGB8	3084	0.62213037	-0.12036490No	
row_57	HLA-G	13320	-0.33078903	-0.64518151No		row_57	ITGB8	3036	0.45096113	-0.0481071No		row_57	ITGB8	3084	0.62213037	-0.12036490No	
row_58	CSF2RB	13320	-0.33011623	-0.64518151No													