Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

preclinical testing of novel systemic therapies to ultimately benefit penile cancer patients.

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[a]*Laboratory of Experimental Urology, Department of Development and Regeneration, KU Leuven, Department of Urology, University Hospitals Leuven, Leuven, Belgium*
[b]*Urology and Pediatric Urology, University Medical Center Mainz, Mainz, Germany*
[c]*Biomedical MRI/Molecular Small Animal Imaging Center, KU Leuven, Leuven, Belgium*
[d]*Nuclear Medicine & Molecular Imaging, Department of Imaging & Pathology, KU Leuven, Leuven, Belgium*
[e]*Department of Human Genetics, University Hospitals Leuven, Leuven, Belgium*
[f]*Trace, Department of Oncology, LKI, KU Leuven, Leuven, Belgium*
[g]*Laboratory of RNA Cancer Biology, Department of Oncology, LKI, KU Leuven, Leuven, Belgium*
[h]*Department of Pathology, University Hospitals Leuven, Leuven, Belgium*
[i]*NIHR Biomedical Research Centre, University College London Hospital, London, UK*
*Corresponding author. Department of Urology, University Hospitals Leuven. Herestraat 49, 3000, Leuven, Belgium.
[1]Anita Thomas and Joren Vanthoor contributed equally.

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Expression of ACE2, the SARS-CoV-2 Receptor, and TMPRSS2 in Prostate Epithelial Cells

Hanbing Song[a,b,c], *Bobak Seddighzadeh*[a,b,c], *Matthew R. Cooperberg*[d,e,f], *Franklin W. Huang*[a,b,c,f,*]

The SARS-CoV-2 virus has infected more than 1.8 million people across 213 countries and killed more than 110 000 [1]. Emerging reports across countries indicate higher COVID-19 mortality among men compared to women, but the underlying reasons remain unclear [2]. The extent to which this disparity is due to biological rather than behavioral or comorbidity sex differences is unknown. The SARS-CoV-2 receptor ACE2 and the entry-associated serine protease TMPRSS2 are expressed in lung and other tissues implicated in the clinical manifestations of COVID-19. However, less is known about the exact cell types expressing *ACE2* and *TMPRSS2* that serve as cells of entry and pathogenesis for SARS-CoV-2 [3].

Intriguingly, *TMPRSS2*, one of the most dysregulated genes in prostate cancer, is highly expressed in human prostate epithelial cells and is androgen-responsive [4]. Given high *TMPRSS2* expression in the prostate, we investigated whether *TMPRSS2* and *ACE2* are co-expressed in human prostate epithelial cells.[5] Using publicly available single-cell RNA sequencing data, we analyzed 24 519 epithelial cells from a normal human prostate data set [5]. In this data set (Supplementary material), 0.32% of all epithelial cells (78 of 24 519) expressed *ACE2* and 18.65% expressed *TMPRSS2* (4573 of 24 519). Overall, the prostate cell types co-expressing *ACE2* and *TMPRSS2* were hillock and club cells that were originally identified in lung. We identified 0.61% of club cells and 0.40% of hillock cells that were double-positive (Fig. 1; Supplementary Fig. 1).

We then investigated lung single-cell data sets (one non-human primate, one human, and one mouse) to determine whether lung club cells also co-express *ACE2* and *TMPRSS2* (Supplementary Table 1). Double-positive cells were found in 16.07% (18 of 112) of non-human primate lung secretory cells in data set 1, 0.33% (7 of 2113) of human lung club cells in data set 2, and 1.86% (48 of 2578) of mouse lung club cells in data set 3 (Supplementary Fig. 1).

To test for sex differences in the expression of these genes, we compared *TMPRSS2* and *ACE2* expression in lung epithelial cell types [6]. Overall, there was no significant difference in *TMPRSS2* expression between males and females in human lung, but higher *ACE2* expression in males (log 2 normalized expression level 0.02 vs 0.0065 in females; $p < 0.001$; Supplementary Fig. 2A). Examining the cell types expressing *ACE2* and *TMPRSS2*, we found that pneumocytes I/II in males

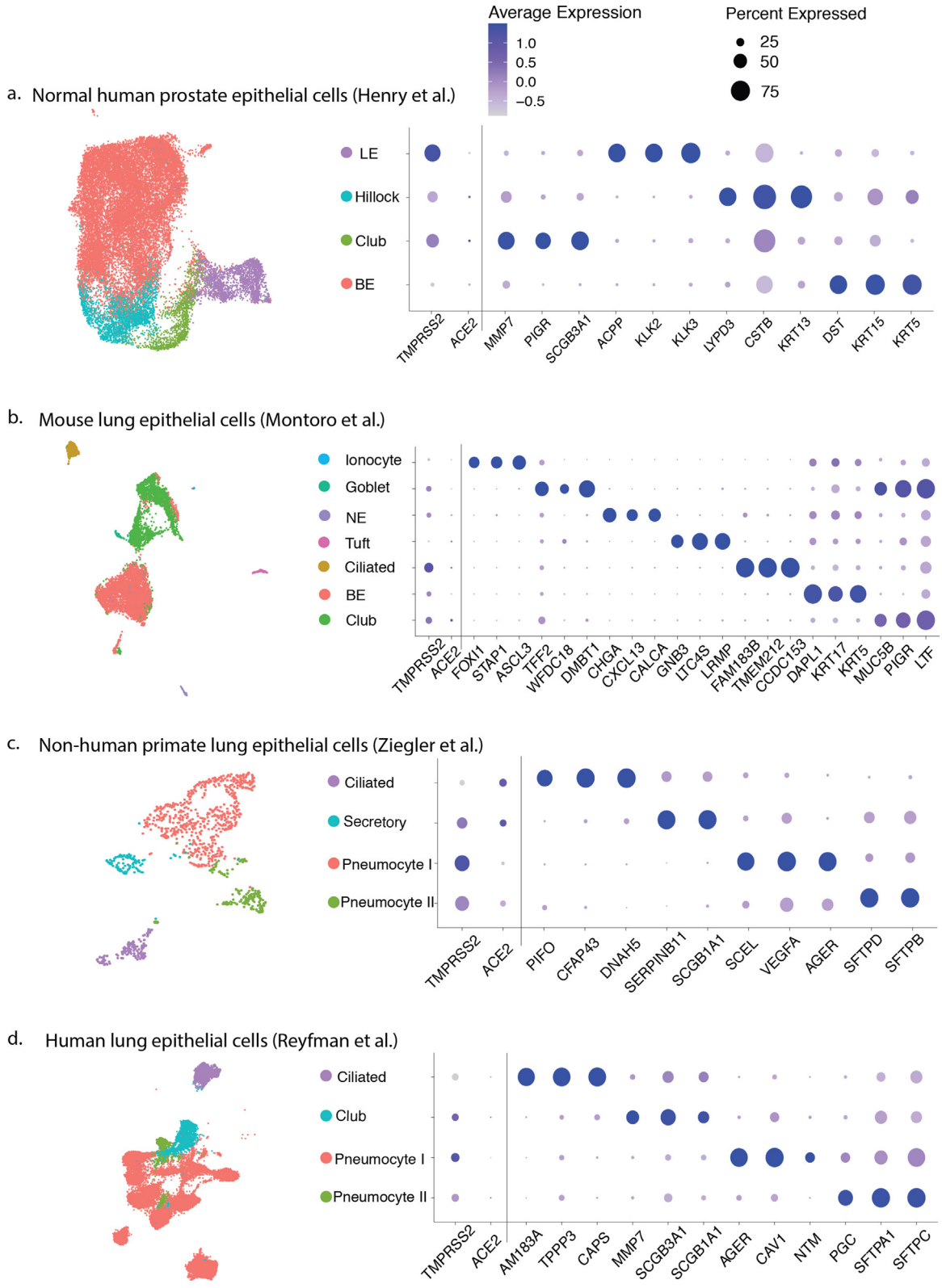

Fig. 1 – Cell type distribution and top differentially expressed gene marker expression of the four datasets used in the current study. (A) Normal human prostate epithelial cells. (B) Mouse lung epithelial cells. (C) Non-human primate lung epithelial cells. (D) Human lung epithelial cells. Each data set was reclustered and annotated by cell type, with distribution shown in the uniform manifold approximation and projection. For each data set, a dot plot was generated showing the percentage of expression (marker radius) and the average expression level (color gradient) for the most differentially expressed genes in each cell type, as well as *ACE2* and *TMPRSS2*. BE = basal epithelial; LE = luminal epithelial.

compared to females had a higher proportion of cells with expression (Supplementary Fig. 2C). However, we caution against the generalizability of these findings due to the confounding variables that may modulate *ACE2* or *TMPRSS2* expression such as smoking and age. It is not clear if *TMPRSS2* and *ACE2* expression is regulated by the same process, but their expression levels are positively correlated in lung cell lines (Supplementary Fig. 3).

In summary, we found a small percentage of prostate hillock and club cells that co-express *TMPRSS2* and *ACE2*. Whether differences in *TMPRSS2* and *ACE2* expression mediate SARS-CoV-2 pathogenesis and whether androgen signaling can affect COVID-19 disease remain to be studied; sex differences in *TMPRSS2* expression alone may not drive the higher burden of SARS-CoV-2 disease among men. Further research into *TMPRSS2* expression and its modulation within the lung and other relevant cell types that may impact *ACE2* and SARS-CoV-2 pathogenesis is needed.

Conflicts of interest: The authors have nothing to disclose.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.eururo.2020.04.065.

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[a]*Division of Hematology/Oncology, Department of Medicine, Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA, USA*
[b]*Bakar Computational Health Sciences Institute, University of California, San Francisco, San Francisco, CA, USA*
[c]*Institute for Human Genetics, University of California, San Francisco, San Francisco, CA, USA*
[d]*Department of Urology, Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA, USA*
[e]*Department of Epidemiology and Biostatistics, Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA, USA*
[f]*San Francisco Veterans Affairs Health Care System, San Francisco, CA, USA*

*Corresponding author. Division of Hematology/Oncology, University of California, San Francisco, 513 Parnassus Avenue, San Francisco, CA 94143-0570, USA. Tel. +1 415 5020696, Fax: +1 415 4760659.
E-mail address: franklin.huang@ucsf.edu (F.W. Huang).

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Severe Acute Respiratory Syndrome Coronavirus 2 Infection in Renal Failure Patients: A Potential Covert Source of Infection

Yu Xiao [a], Kaiyu Qian [a,b], Yongwen Luo [a], Song Chen [a], Mengxin Lu [a], Gang Wang [b], Lingao Ju [b], Xinghuan Wang [a,b,]*

COVID-19, a highly infective disease caused by a newly identified coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; previously 2019-nCoV), is spreading around the world [1]. Increasing evidence has confirmed the human-to-human transmission. A special group of COVID-19 patients is comorbid with chronic kidney disease (CKD) [2]. In patients with CKD, innate and adaptive immune function impairment would result in increased