

# Identification and Characterization of an Unconventional NK Subset in COVID-19 Andrew Platt<sup>1,2</sup>, Izabella Lach<sup>1</sup>, Jeffrey R. Strich<sup>1</sup>, Gustaf Wigerblad<sup>3</sup>, Ryan Curto<sup>4</sup>, Shreya Singireddy<sup>4</sup>, Jocelyn **NIH** Wu<sup>4</sup>, Katherine Raja<sup>4</sup>, Kapil K. Saharia<sup>5</sup>, Mariana Kaplan<sup>3</sup>, Daniel S. Chertow<sup>1,2</sup>

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### Introduction

The dysregulation of the **innate immune system** in **Coronavirus Disease 2019 (COVID-19)** results in a wide variability in illness severity and outcome<sup>3</sup>.

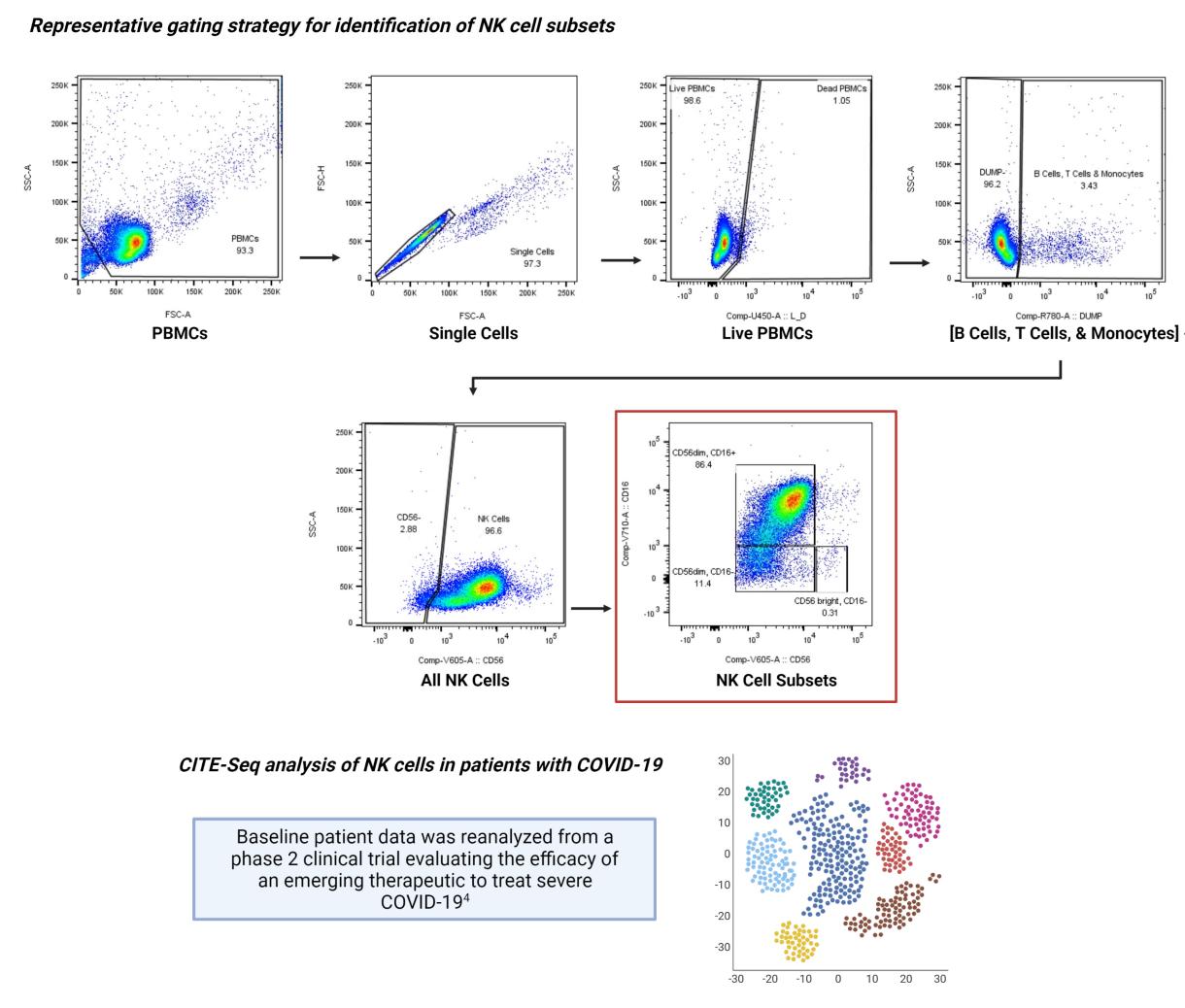
Natural Killer (NK) cells are a subset of innate immune cells that play a critical role in combating viral infection. In COVID-19, dysregulation in this cell type in has been correlated to greater disease severity<sup>2</sup>.

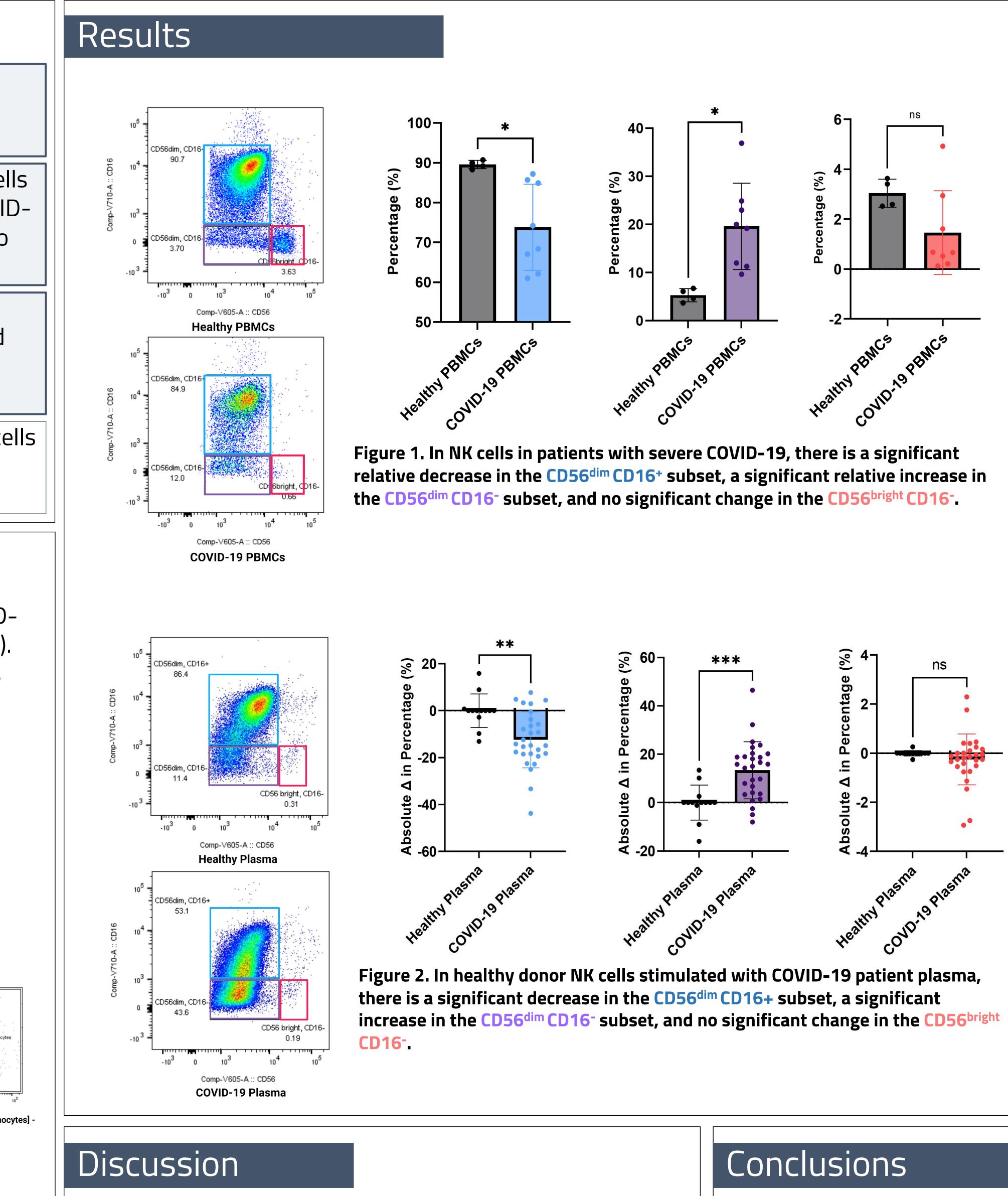
NK cells are divided into two main subsets based on their surface expression of **CD56** and **CD16**: CD56<sup>dim</sup> CD16<sup>+</sup> and CD56<sup>bright</sup>CD16<sup>-</sup>. A third unconventional subset, CD56<sup>dim</sup> CD16<sup>-</sup>, is expanded in patients with COVID-19<sup>1</sup>.

**OUR GOALS:** Characterize phenotypic changes in the NK cells of patients with severe COVID-19 and describe the functionality of the expanded atypical NK cell subset.

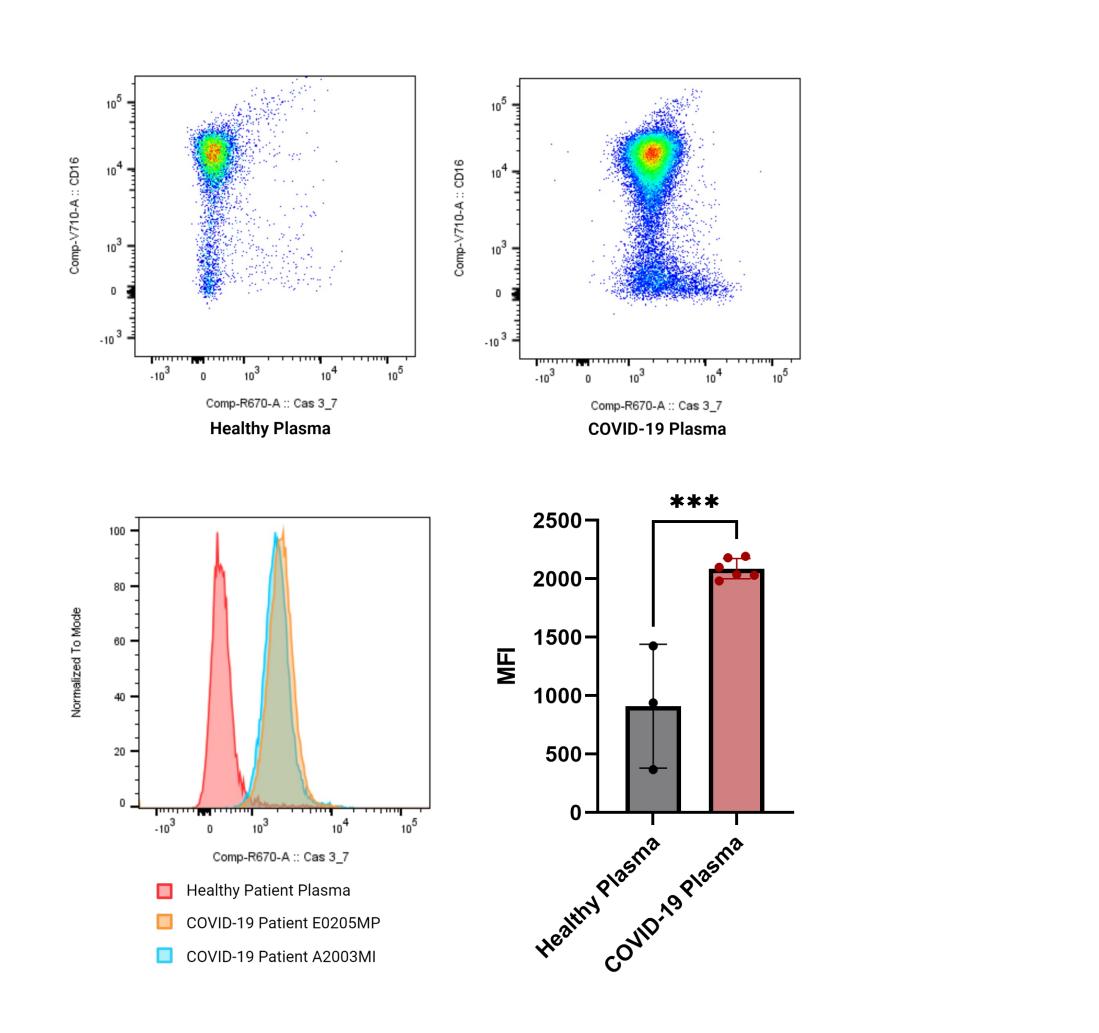
### Methods

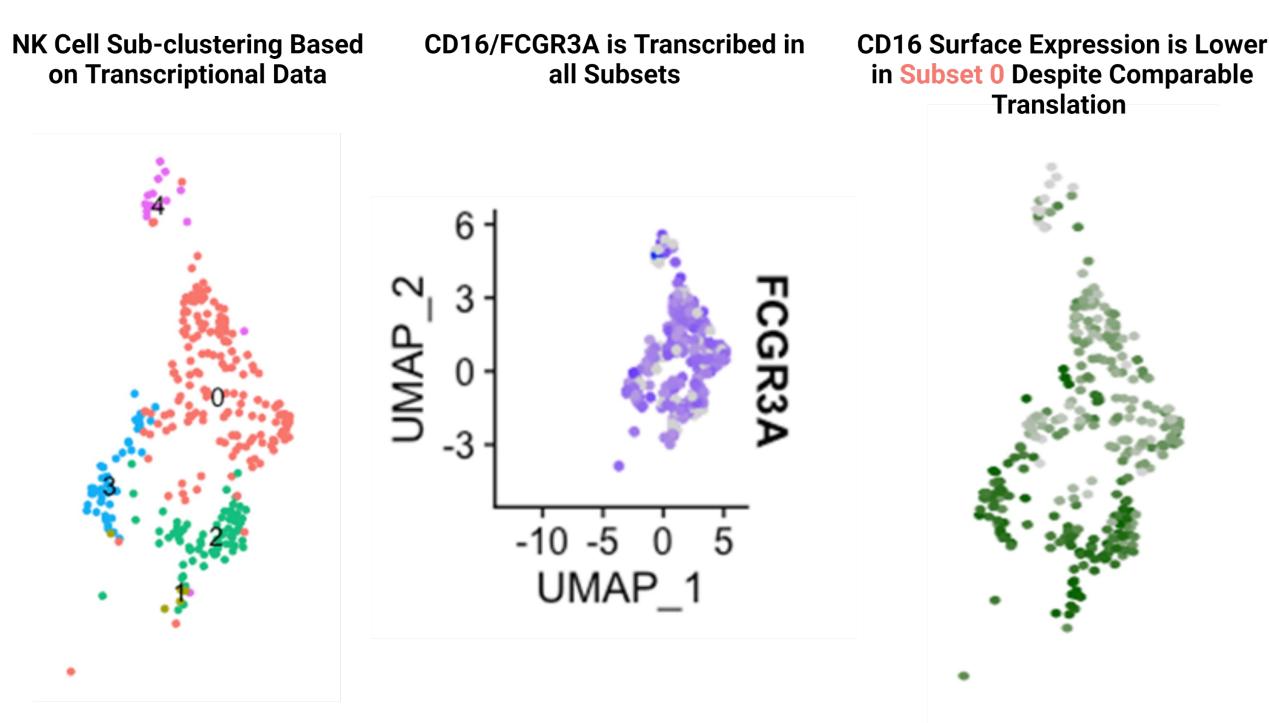
- PBMCs and plasma collected from patients with COVID-19 on Extra-Corporeal Membrane Oxygenation (ECMO).
- Healthy donor NK cells stimulated with 10% healthy vs COVID-19 plasma *ex vivo*.
  - Cells analyzed by flow cytometry.
- CITE-Seq single cell RNA sequencing data used from previously published dataset of hospitalized patients.





- The CD56<sup>dim</sup> CD16<sup>-</sup> subset is expanded in patients severe COVID-19.
  - The phenotype is seen across multiple different patient cohorts using several approaches.
  - This phenotype can be replicated *in vitro*.
- Given the findings of loss of CD16 and increased Caspase-3/7 activation, this suggests a common pathway through phosphatidylserine.





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- A more robust characterization of the **CD56**<sup>dim</sup> **CD16**<sup>-</sup> subset by RNA sequencing is needed. Functional assays will be required to
- define the role of these NK cells
- The kinetics of CD56<sup>dim</sup> CD16<sup>-</sup> cells and their role in mild disease remains open.







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Figure 3. NK cells stimulated with COVID-19 patient plasma have a significantly higher level of Caspase-3/7 activity.

Figure 4. In patients with COVID-19, a subset of NK cells lose surface expression of CD16 despite expression of CD16 at the transcriptional level.

## References

- 1. Leem, G. et al. Abnormality in the NK-cell population is prolonged in severe COVID-19 patients. J Allergy Clin *Immunol.* 2021. **148**(4): 996-1006.
- Paludan SR. et al. Innate immunological pathways in COVID-19 pathogenesis. *Sci Immunol*. 2022. **7**(67): eabm5505.
- Schultze, J. and Aschenbrenner, A. COVID-19 and the human innate immune system. *Cell*. 2021. **184**(7):11671-1692.
- 4. Strich J et al. Fostamatnib for the Treatment of Hospitalized Adults With Coronavirus Disease 2019: A Randomized Trial. 2021. *Clinical Infectious Diseases.* Ciab732.