

Immune profiles of COVID-19 patients by Single cell RNA Sequencing analysis

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Complement cascade and COVID-19

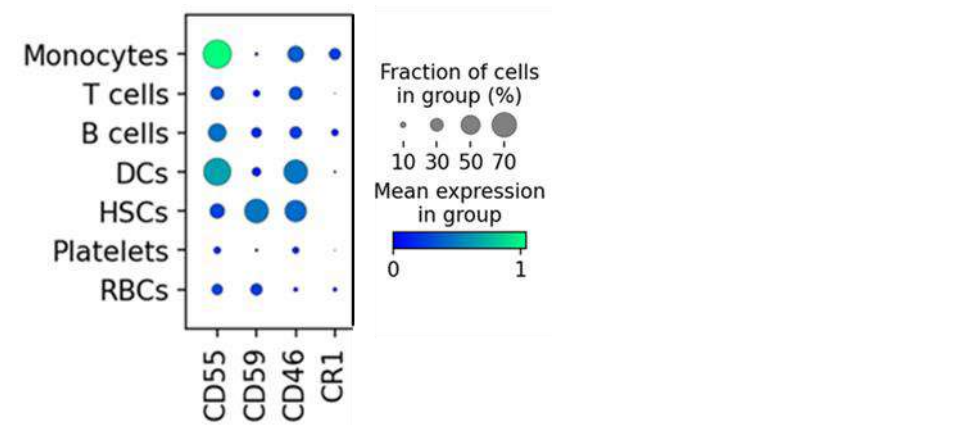
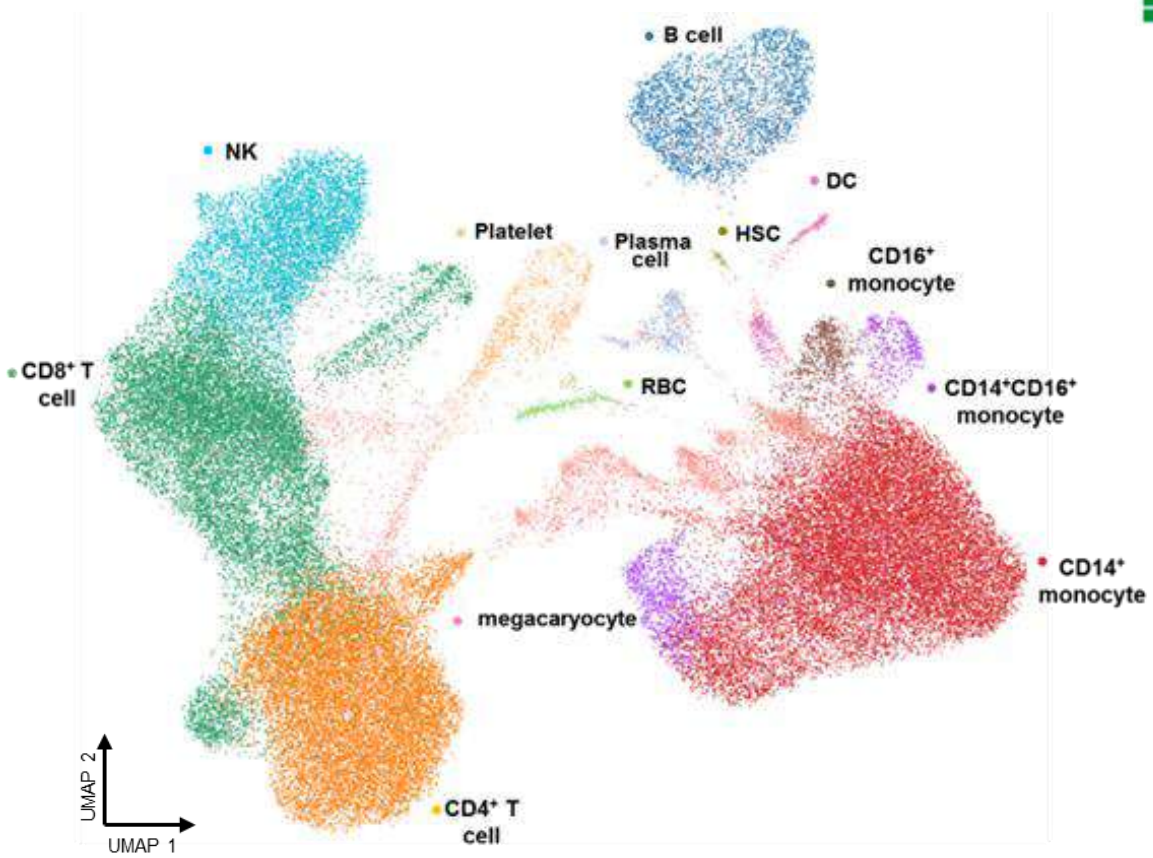
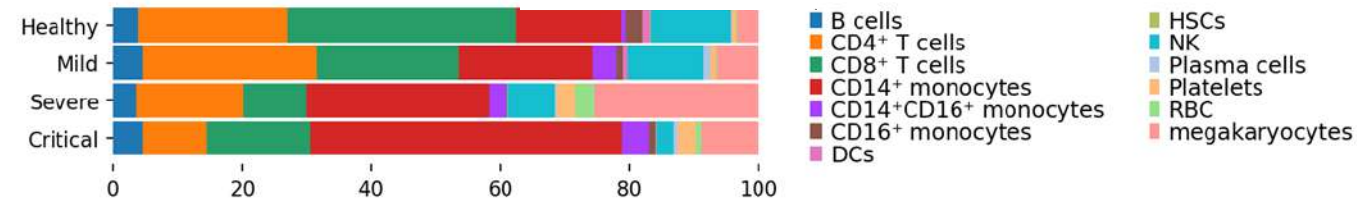
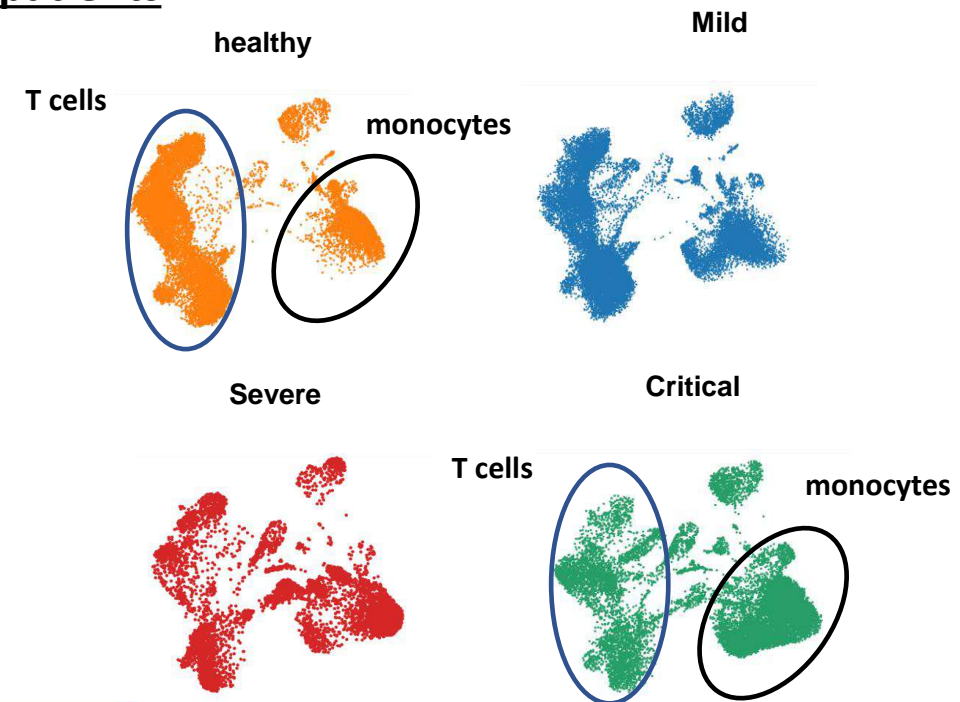
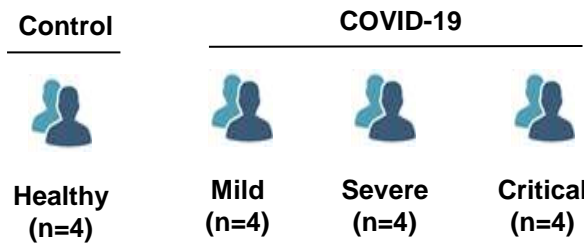
- Increased activation of complement cascade in COVID-19 severely and critically ill patients.
- Increase of serum levels of C3a and C5b-9. (Sinkovits G. et.al., Front. Immunol. 2021)
- Increased deposition of complement factors in tissue of critically ill COVID-19 patients. (Magro C. et.al., Trans. Res. 2020)

Complement regulatory
proteins (CRP)
CD55, CD46, CD59 control
complement activation

→ *Dysregulated expression of CRPs in COVID-19?*

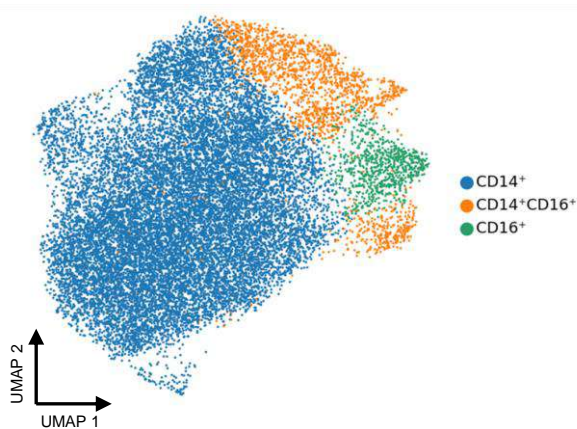
→ *What is the role of CRPs in COVID-19?*

PBMC immune profiles of COVID-19 patients

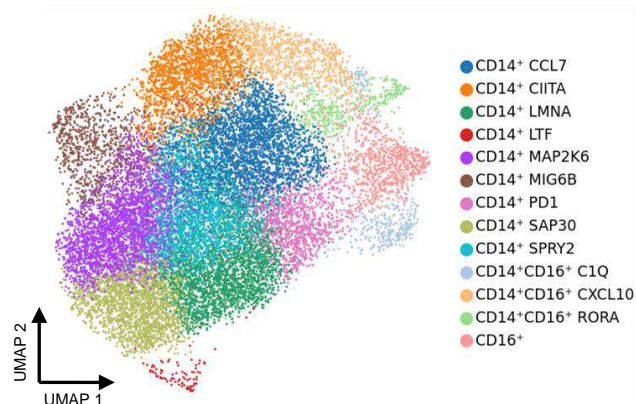


Subclustering analysis-Monocyte immune profiles of COVID-19 patients

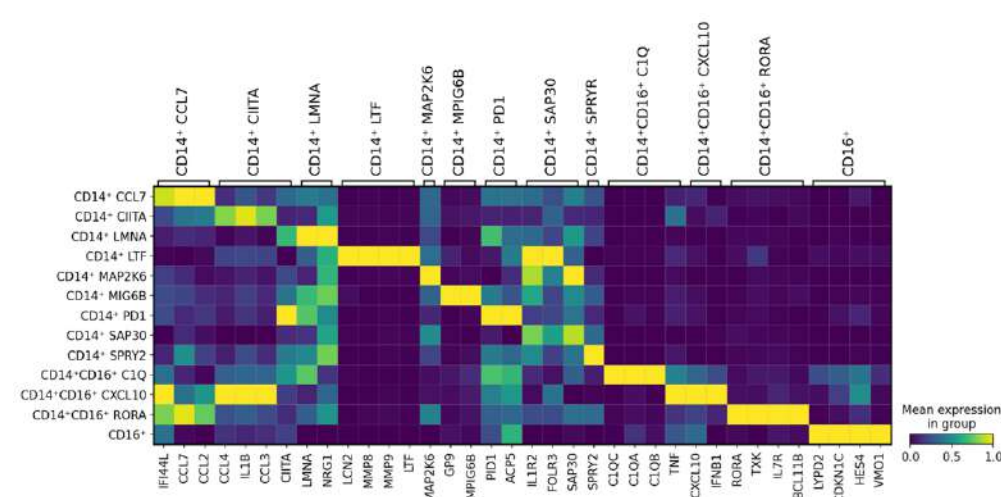
Classical/Non-classical/Intermediate



Subclustering analysis



Marker genes



→ Mapping of CD14⁺, CD16⁺ and CD14⁺CD16⁺ monocytes

→ 13 clusters in total

Healthy



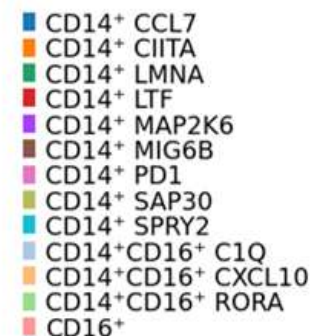
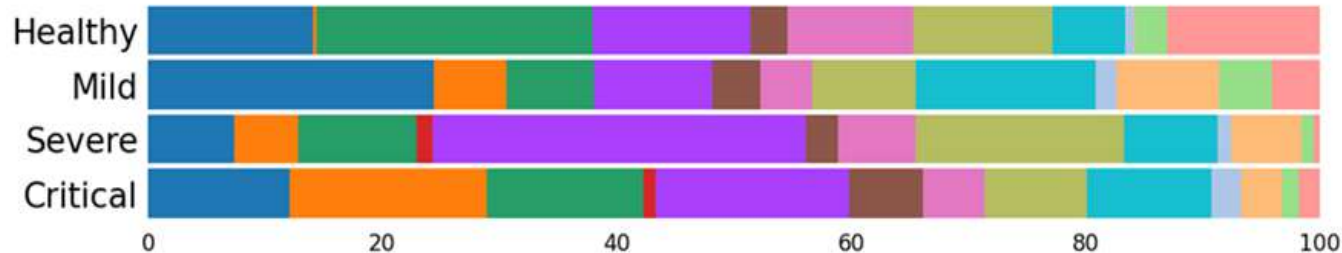
Mild



Severe



Critical



clusters



Fraction of cells in group (%)

• ○ ● ●

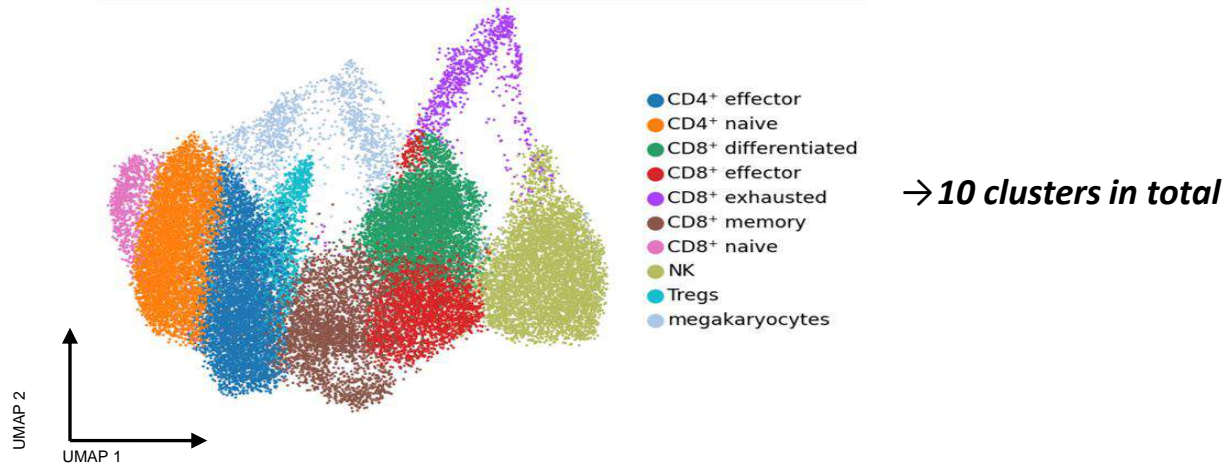
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Mean expression in group

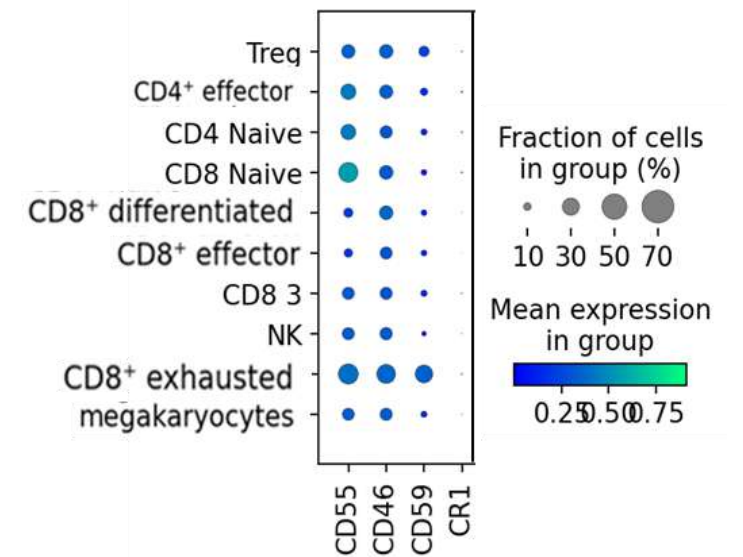
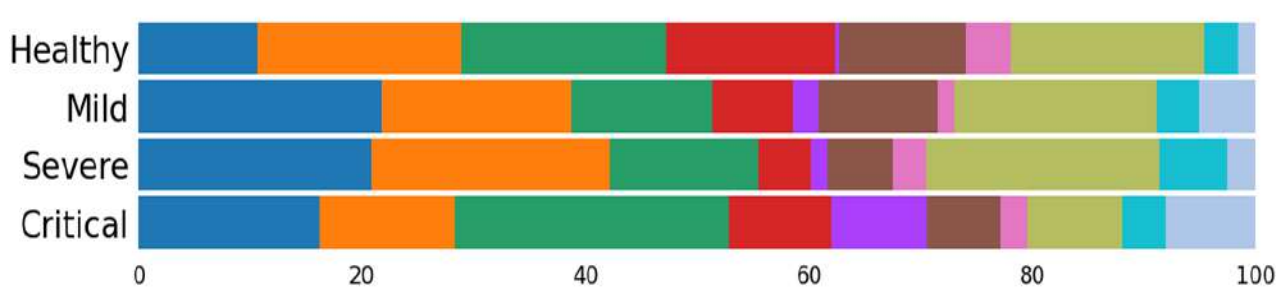
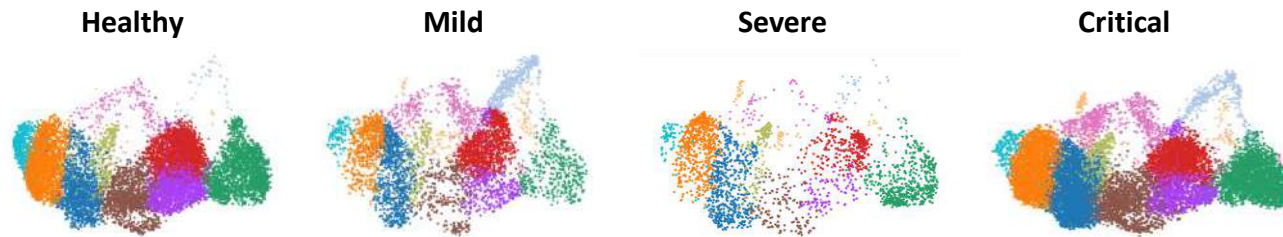
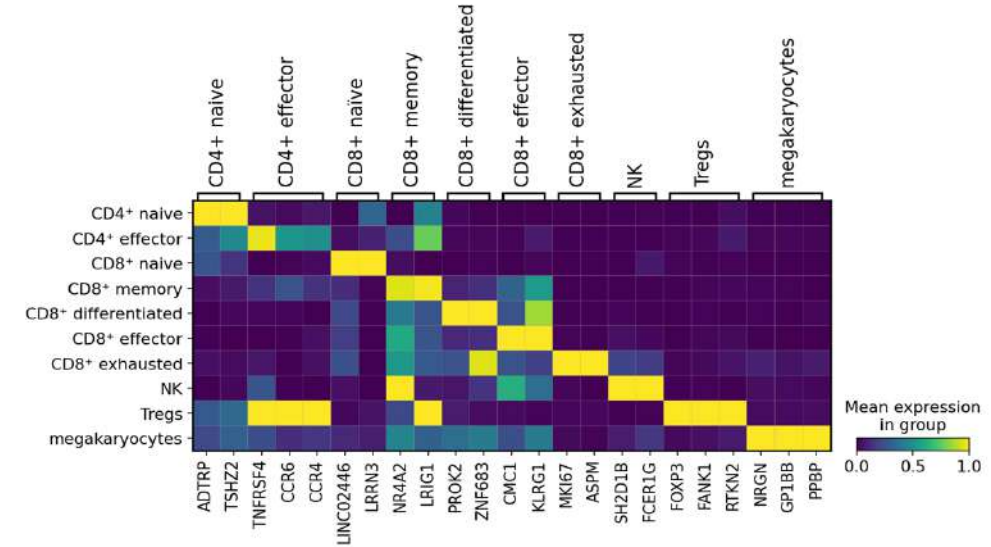
0.5 1.0

Subclustering analysis T cell immune profiles of COVID-19 patients

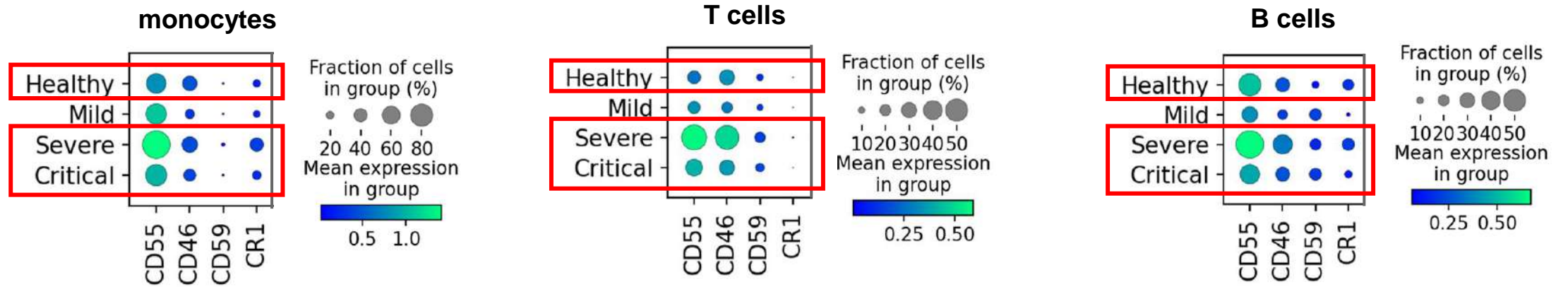
Subclustering analysis



Marker genes

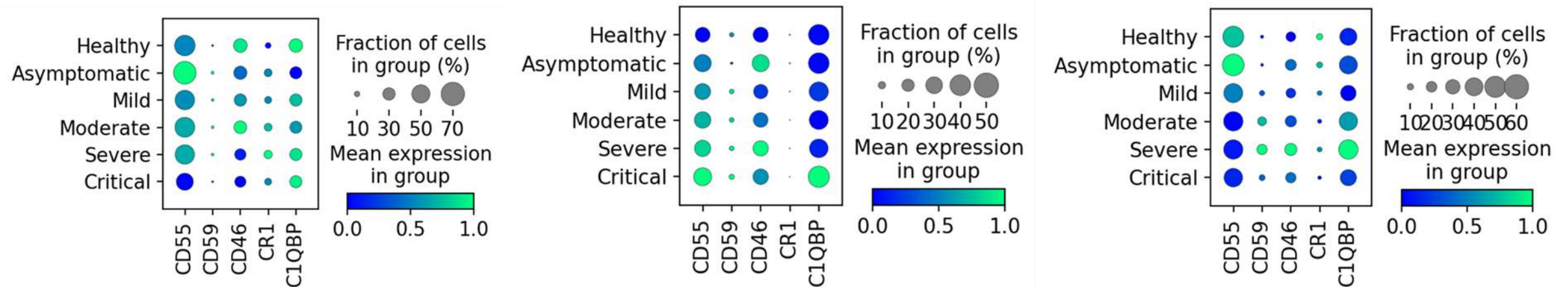


CRP expression in COVID-19 patients by SC RNA Seq analysis



- ↑ CD55 expression in severe and critical COVID-19 in monocytes, T cells and B-cells compared to healthy controls
- ↑ CD46 expression in severe and critical COVID-19 in T cells and B-cells

Validation in large COVID-19 sample database



Conclusions

- *Trend of reduced expression of CRPs in critically ill COVID-19 patients.*
- *Dysregulated expression of CRPs in critically ill COVID-19 patients.*
- *Effect on immune responses of critically ill COVID-19 patients.*

Acknowledgements

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