A single-cell atlas of the peripheral immune response in patients with severe COVID-19

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Article

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A single-cell atlas of the peripheral immune response in patients with severe COVID-19

Aaron J. Wilk, Arjun Rustagi, Nancy Q. Zhao, Jonasel Roque, Giovanny J. Martínez-Colón, Julia L. McKechnie, Geoffrey T. Ivison, Thanmayi Ranganath, Rosemary Vergara, Taylor Hollis, Laura J. Simpson, Philip Grant, Aruna Subramanian, Angela J. Rogers ✉ & Catherine A. Blish ✉

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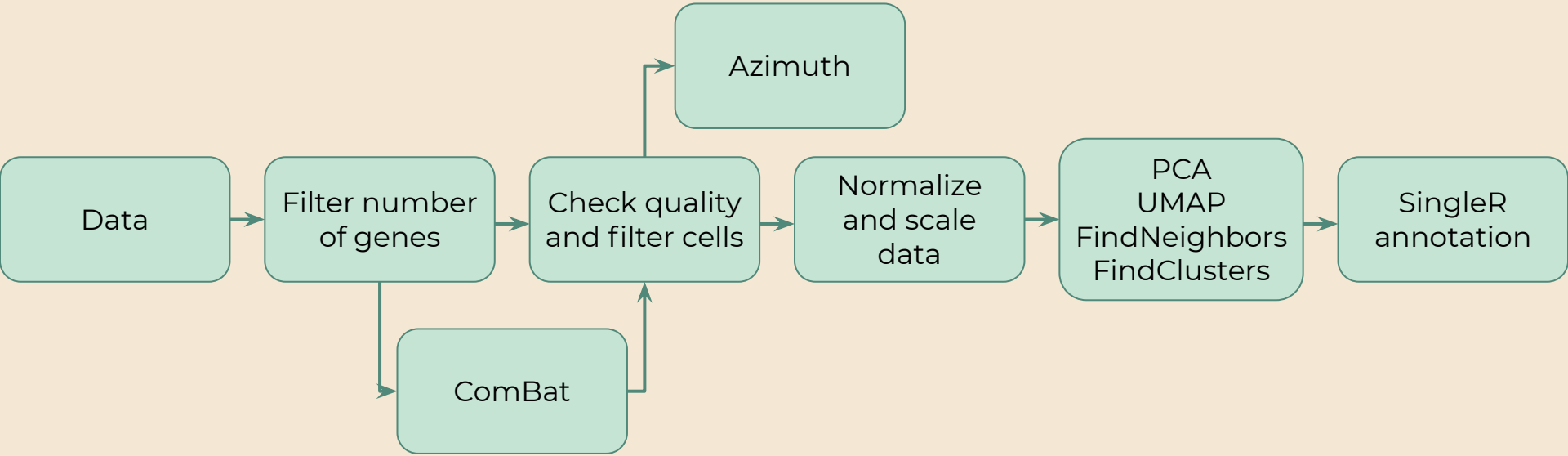
Workflow


Azimuth
Data
Filter number of genes
Check quality and filter cells
Normalize and scale data
PCA
UMAP
FindNeighbors
FindClusters
SingleR annotation
ComBat

Data

Cell type (coarse)	C1 A	C1 B	C4	C7	H4	H5
B	351	1020	1835	298	588	511
CD14 Monocyte	1561	1858	713	2095	166	444
CD16 Monocyte	29	48	29	289	202	403
CD4 T	326	627	384	111	451	781
CD8 T	563	904	432	102	624	257
DC	34	32	61	105	63	78
gd T	4	13	1	15	49	25
NK	354	387	104	130	2972	593
Total:	3222	4889	3559	3145	5115	3092

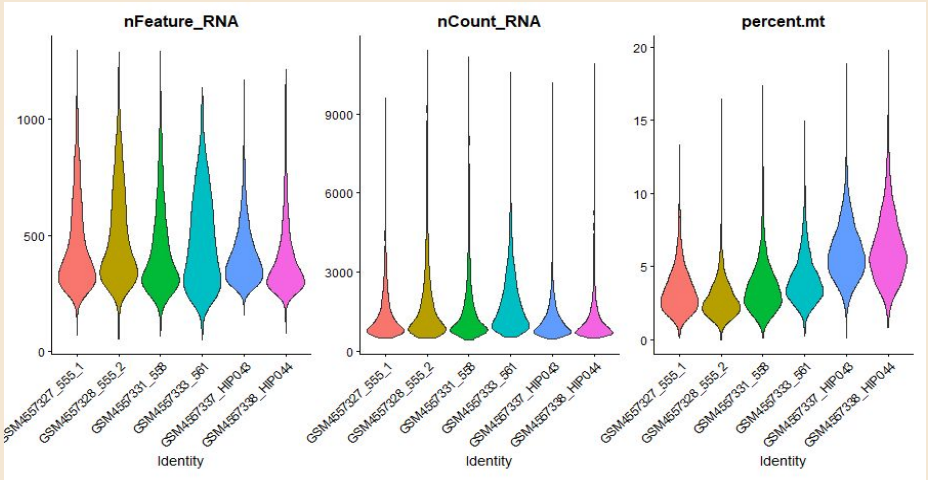
Number of genes:

- before filtering: 37 811
- after filtering: 2 140

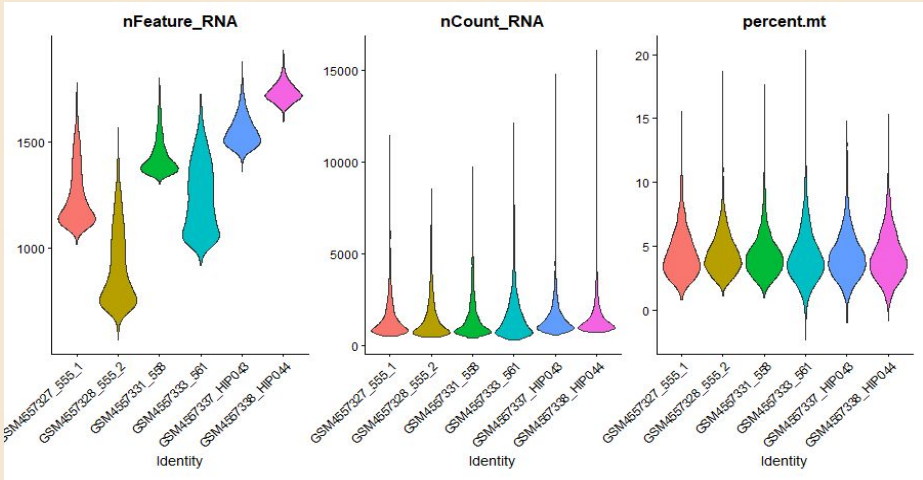
Number of cells: 25 886

Data quality

Original data

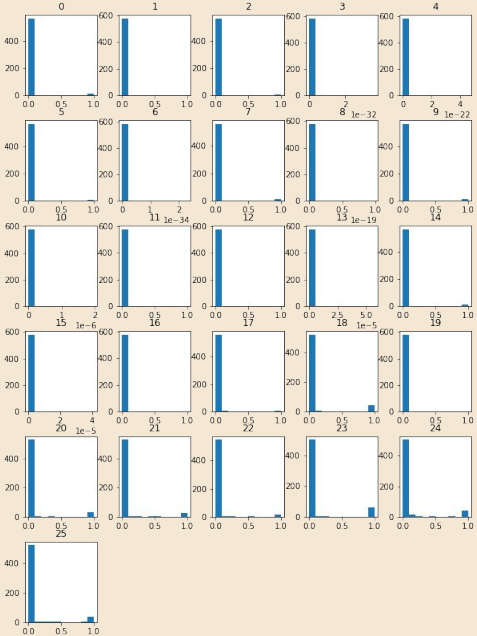


Data after ComBat



Cluster quality

Original data



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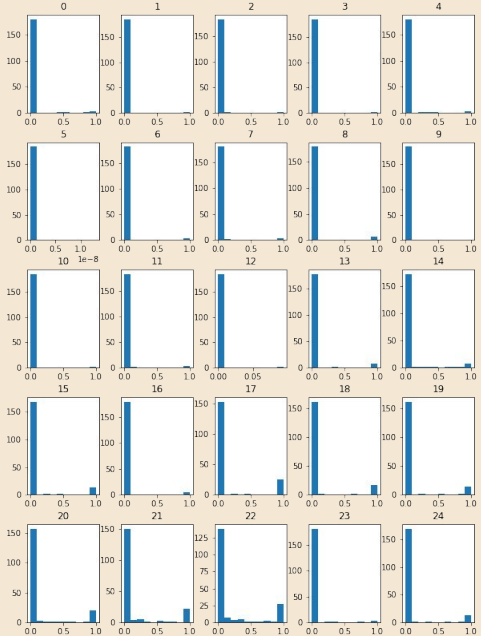
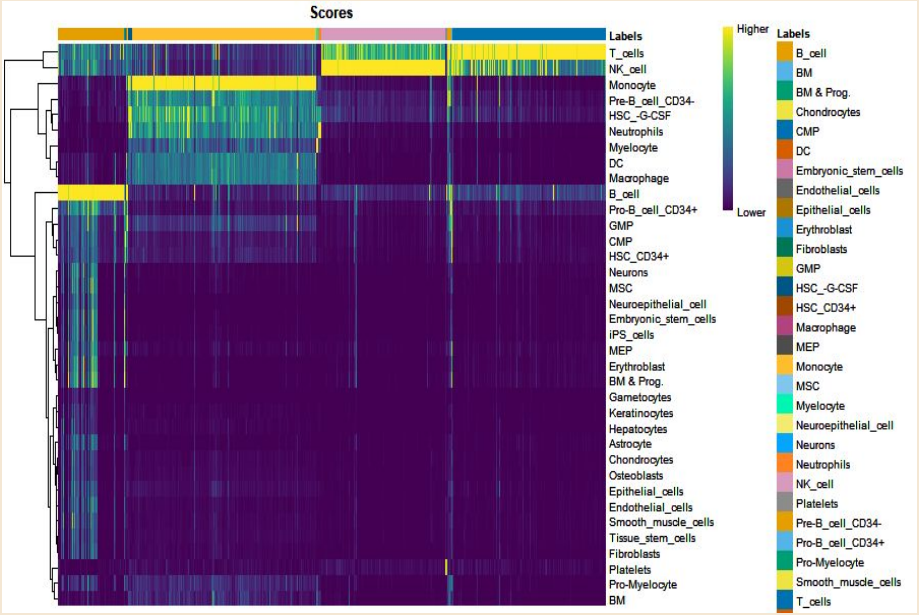


Heatmap cell type

Original data



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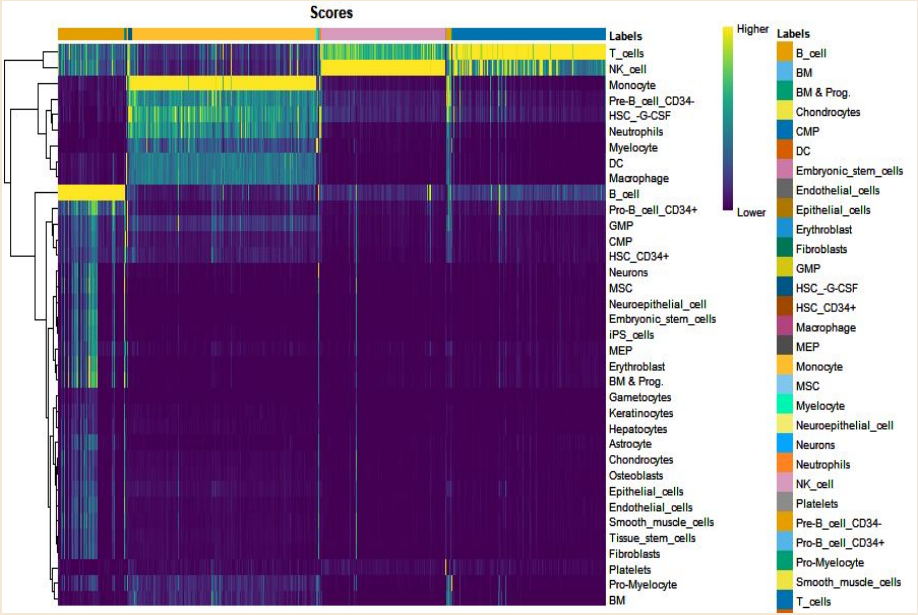
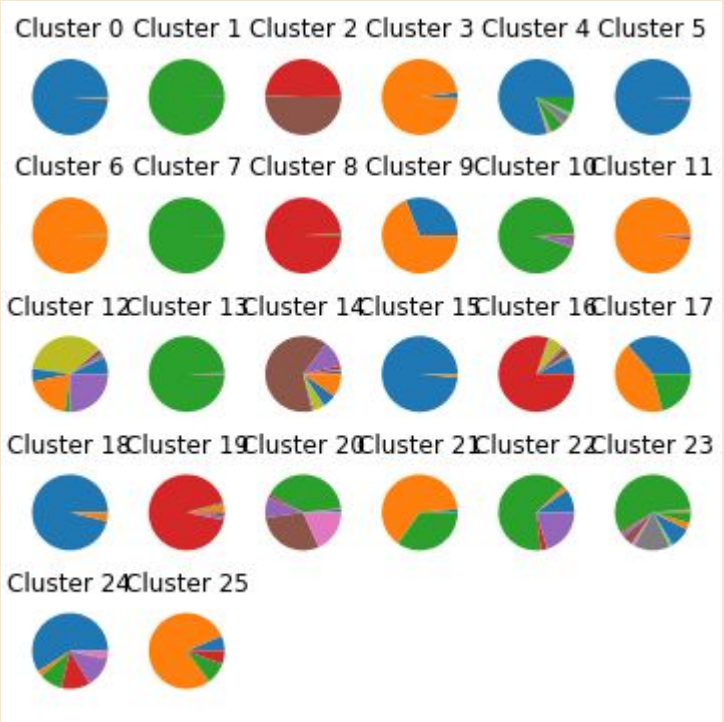


Clusters annotations

Original data



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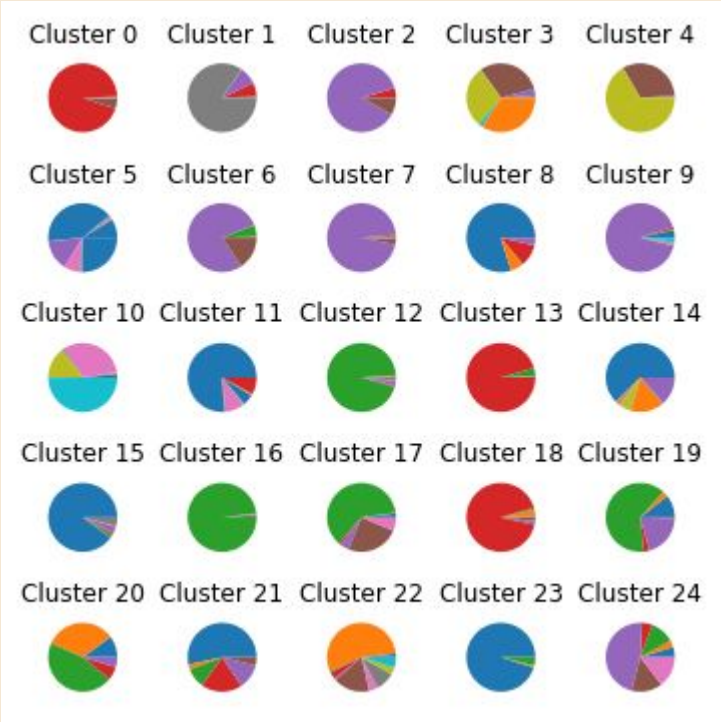
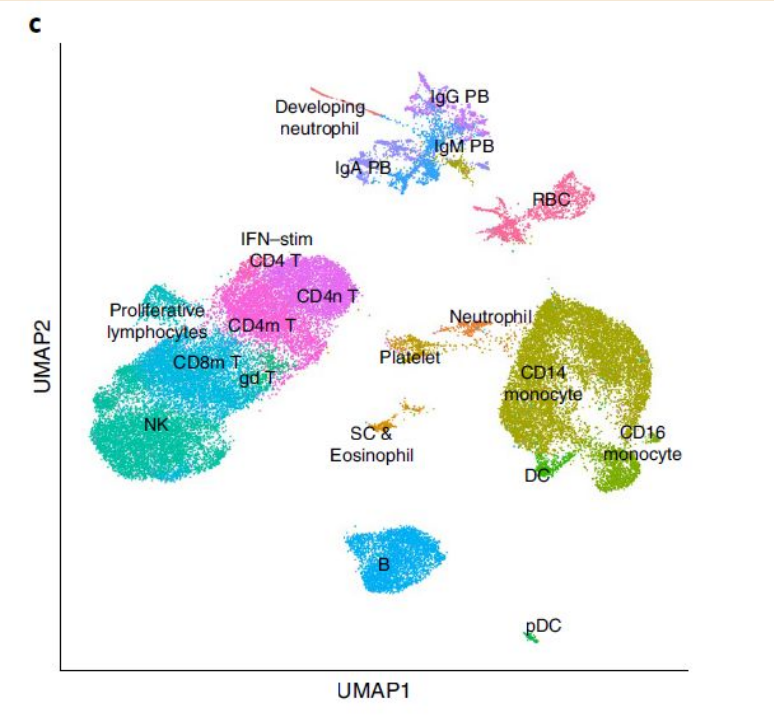
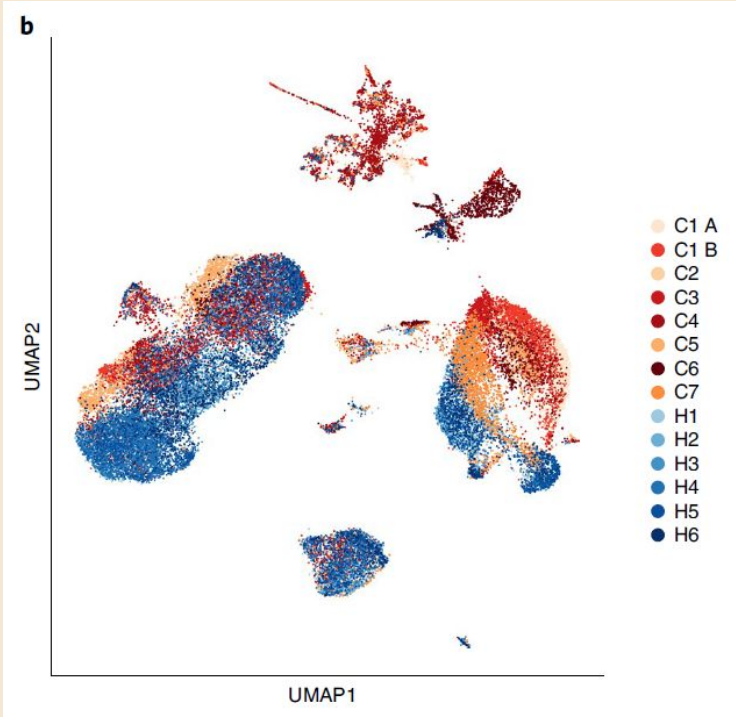


UMAP from the article





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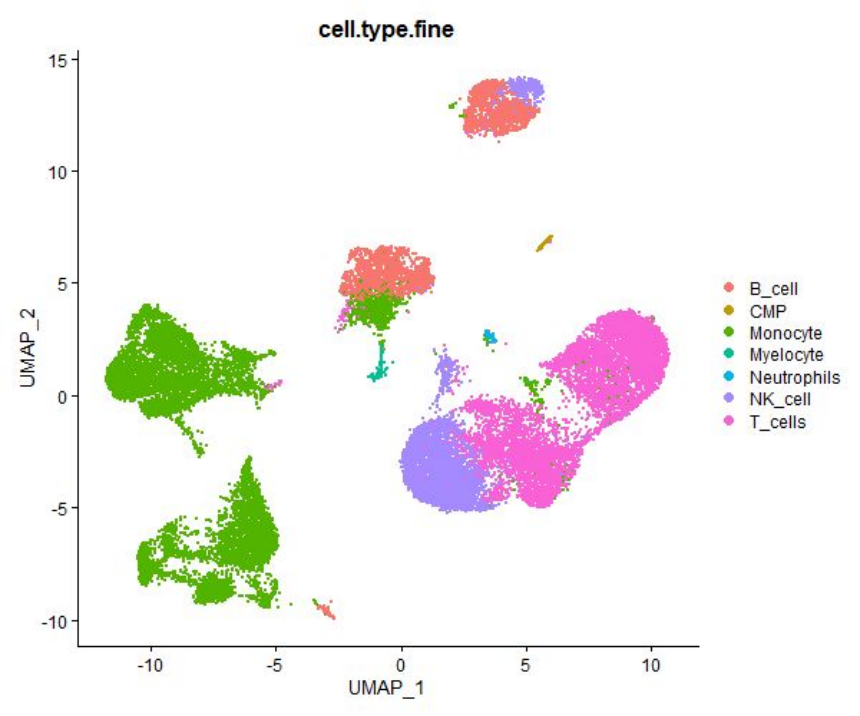

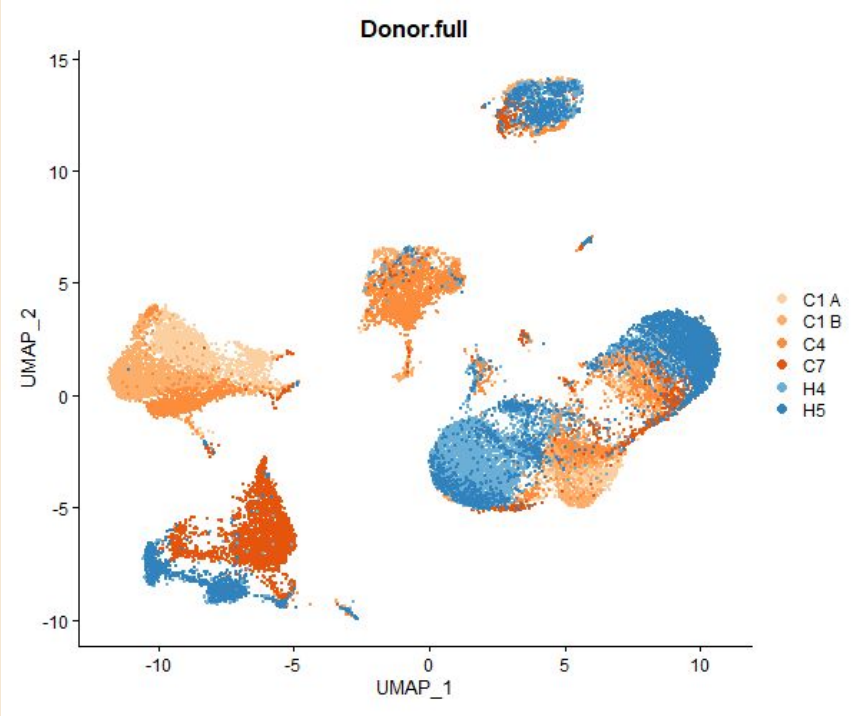

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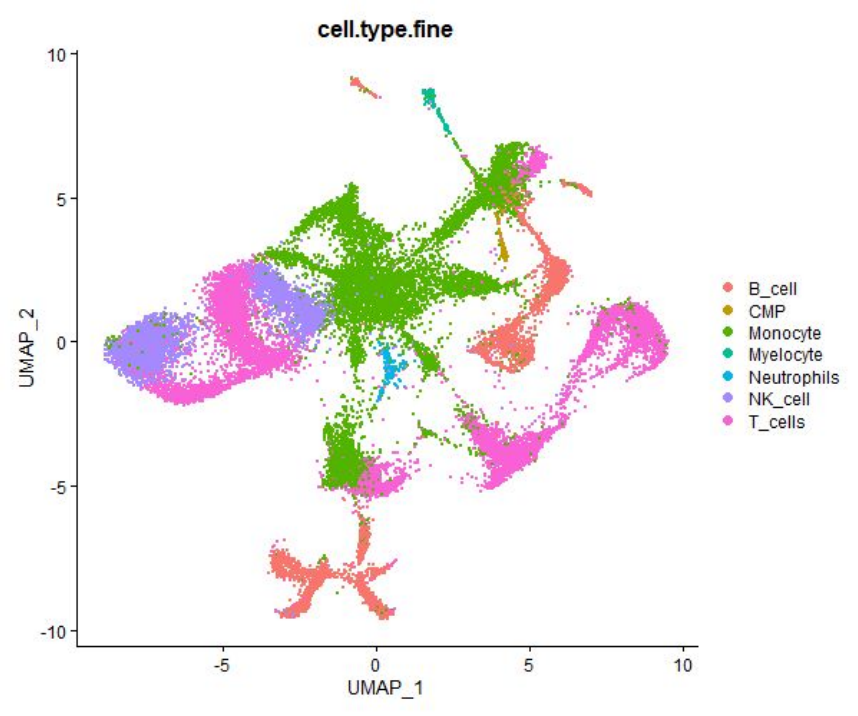
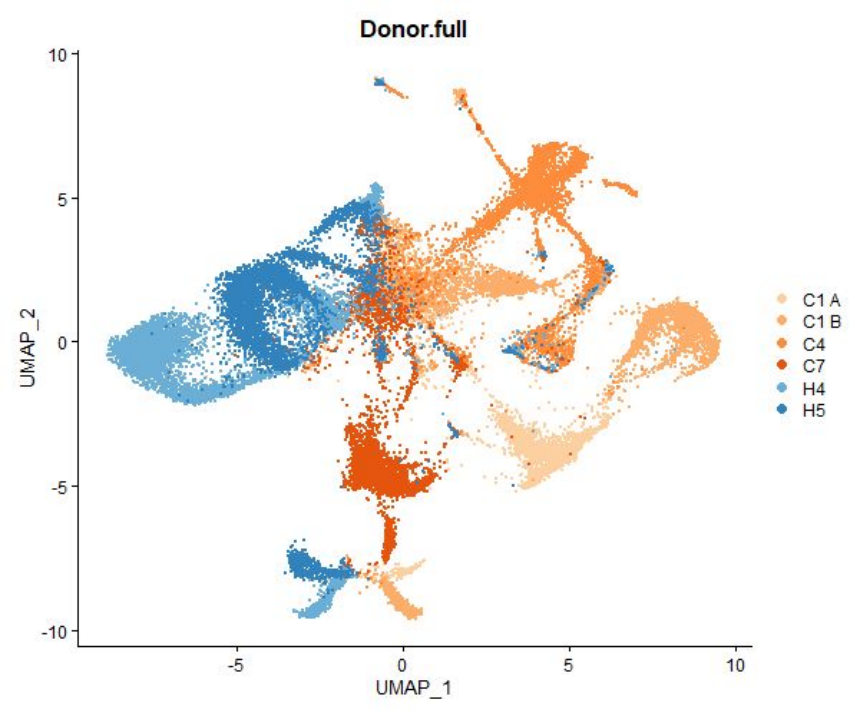
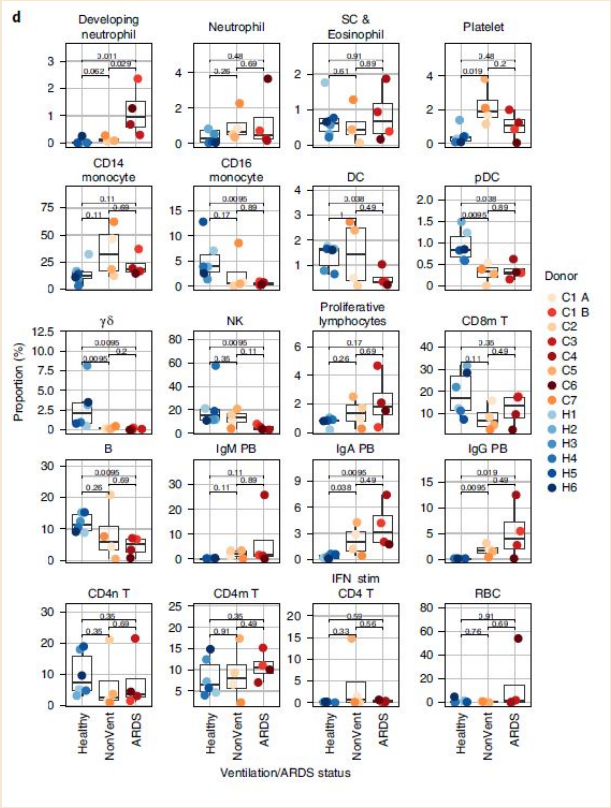




Cell proportions from article

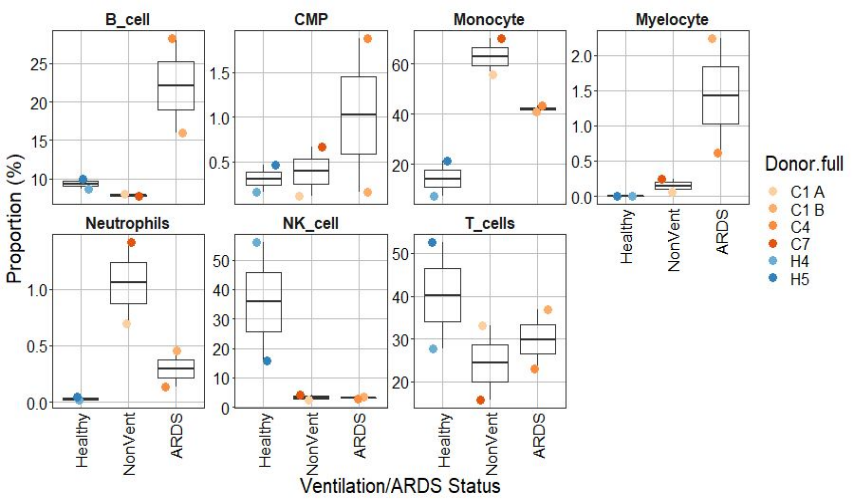


COVID-19-driven changes in the cell type proportions:

- **γδ** T cells
- plasmacytoid dendritic cells (pDCs)
- conventional dendritic cells (DCs)
- CD16+ monocytes
- NK cells

Cell proportions

Original data



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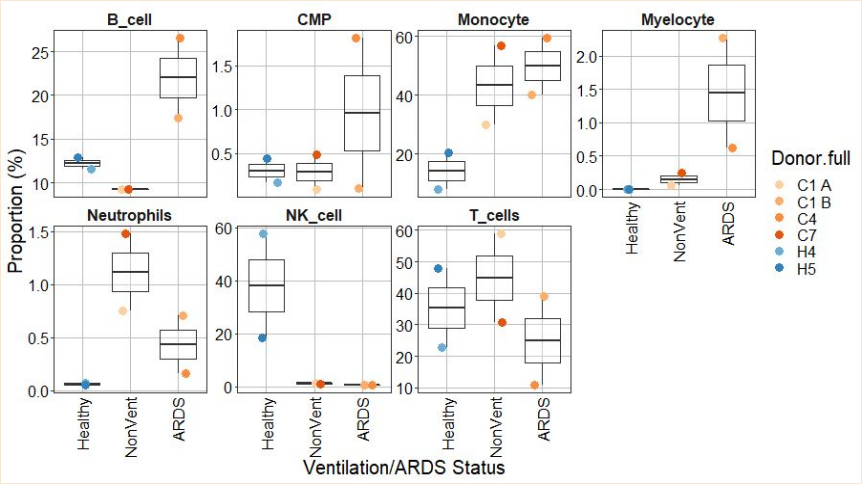
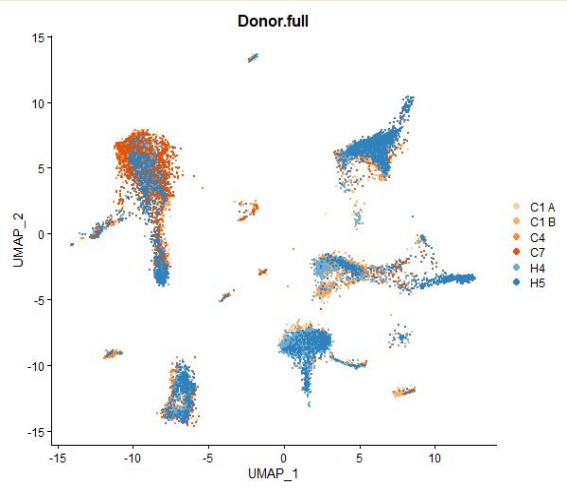
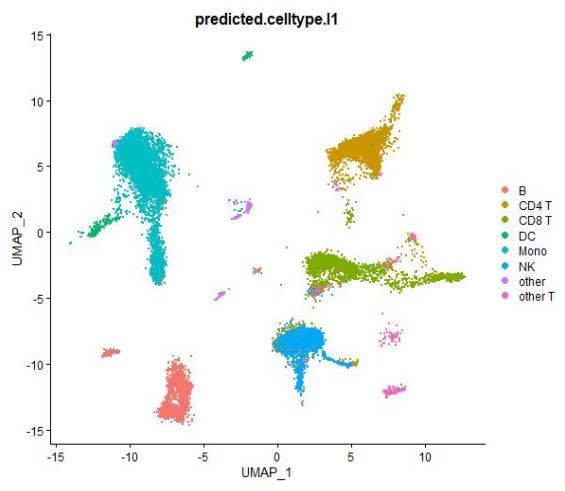
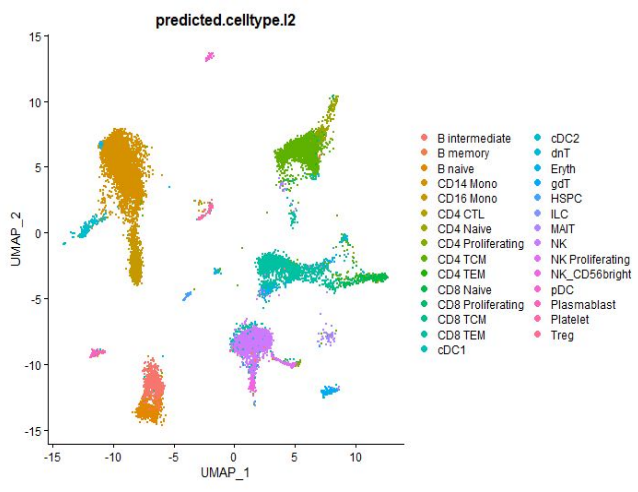


UMAP original data Azimuth







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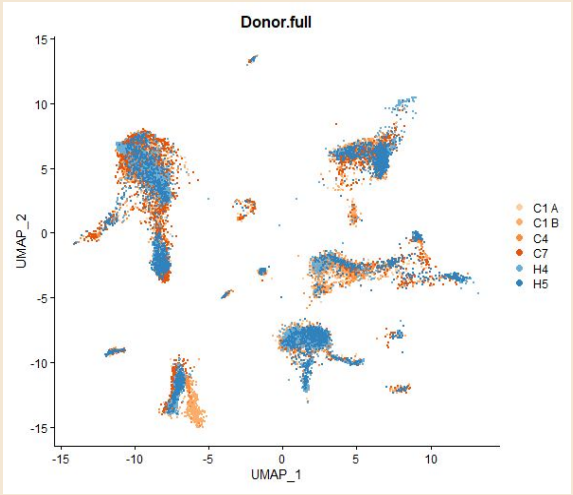
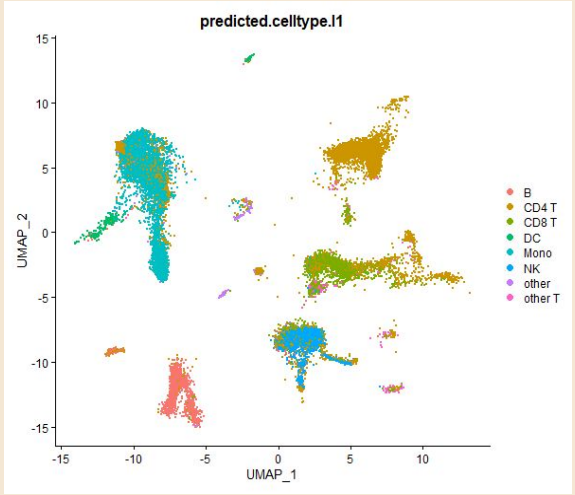
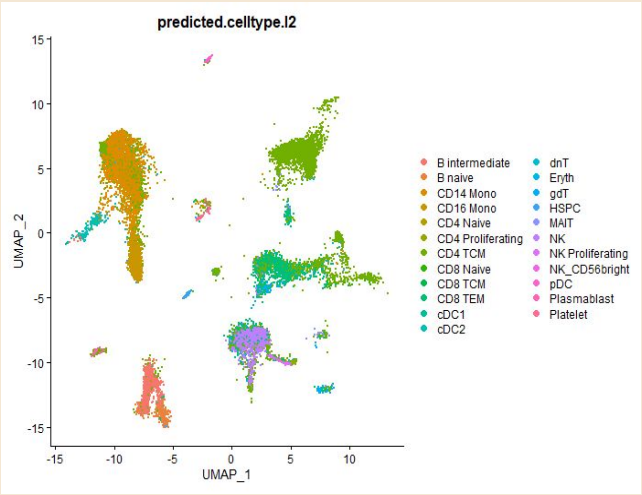
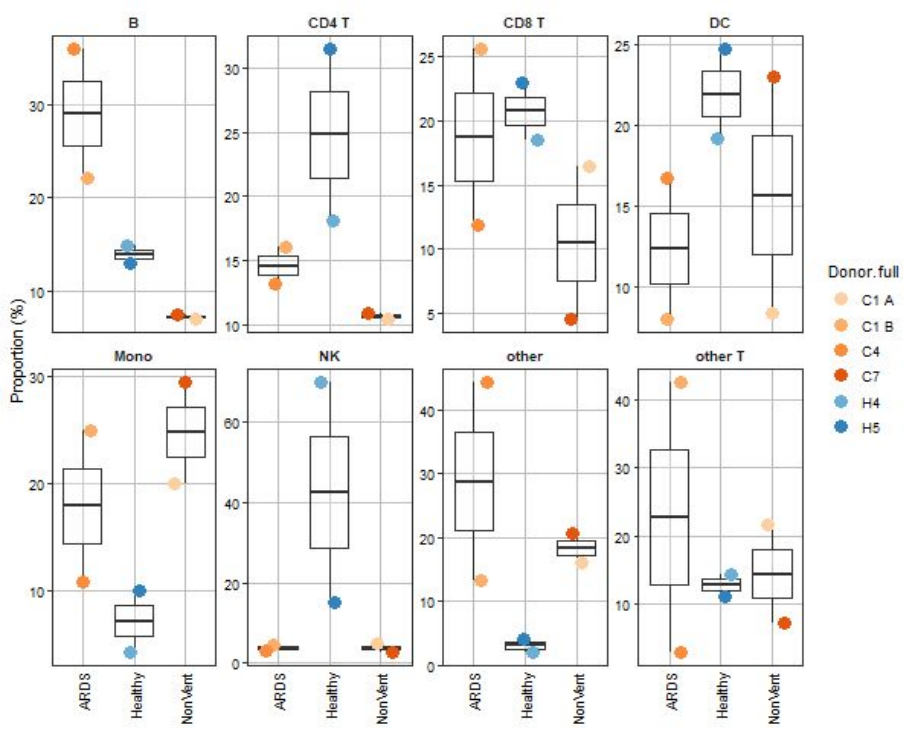
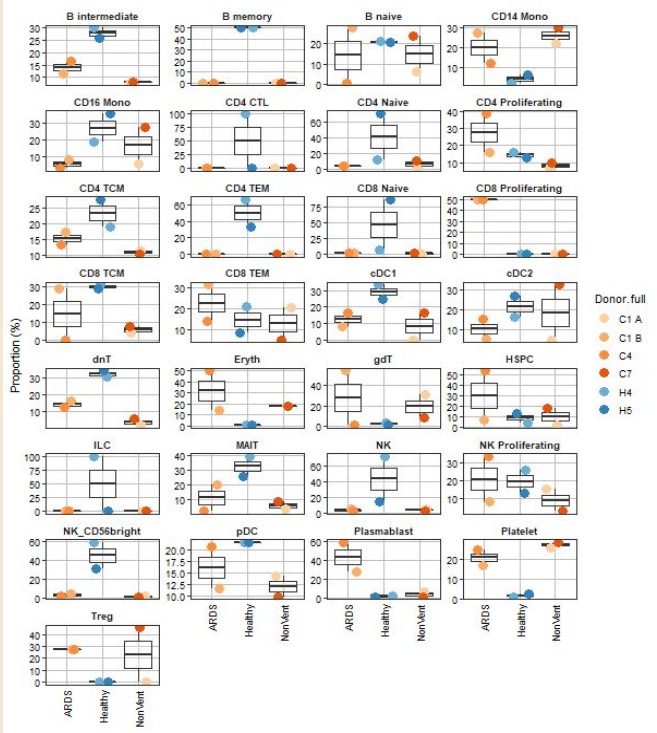




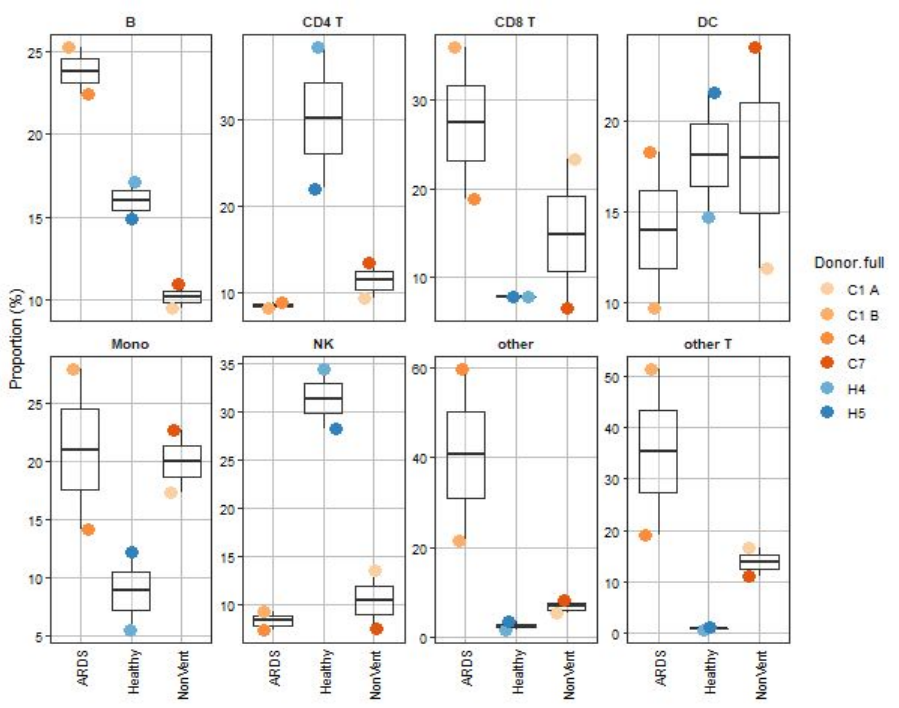


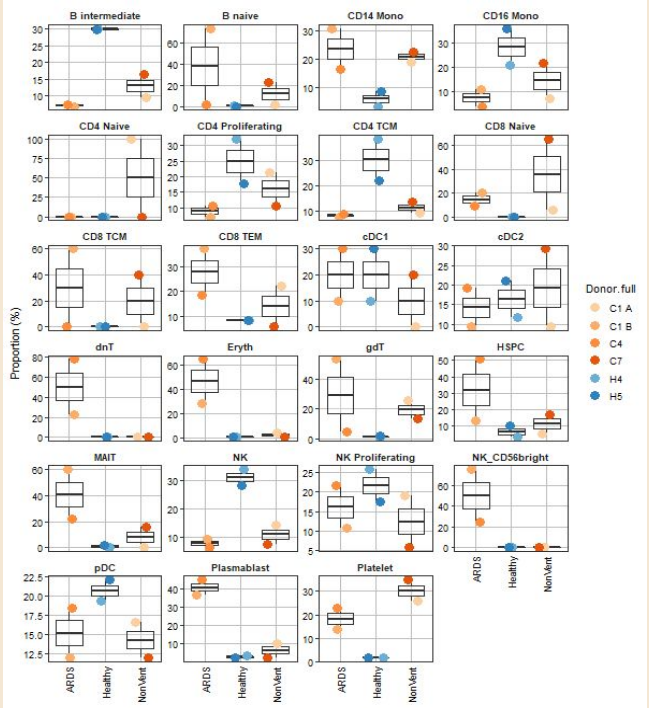
Cell proportions original data Azimuth





Cell proportions data after ComBat Azimuth





Thank you for your attention

Source:

Wilk, A.J., Rustagi, A., Zhao, N.Q. et al.
A single-cell atlas of the peripheral immune response in patients with severe COVID-19.
Nat Med 26, 1070–1076 (2020).

Integrated analysis of multimodal single-cell data
Yuhan Hao, Stephanie Hao, Erica Andersen-Nissen, William M. Mauck III, Shiwei Zheng, Andrew Butler, Maddie J. Lee, Aaron J. Wilk