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Correction

Cell-type-specific immune dysregulation in severely ill COVID-19 patients

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In the originally published version of this article, some scRNA-seq data analysis was presented for individual patients. Multiplexing of paired samples within each disease severity group was performed by “cell hashing” using barcoded antibodies, and sample demultiplexing was performed using CITE-seq-Count 1.4.3 and HTODemux, which assigned cells to one of the two samples based on their relative expression of the two barcode hashtags. Additional analyses performed after publication revealed that the hashing had not worked very efficiently and that some cells that were unstained by the hashing antibodies (negative, but otherwise passed quality control) had been inappropriately assigned to the two individual patient samples. The main text has now been corrected, and revised Figures 1D, S3, and S4 appear here and with the article online to present data as pairs of samples sequenced together instead of individual patients. This issue does not change the conclusions of our study because paired patients were from the same group and most analyses were performed by pooling all samples within each group.

The authors regret this error.

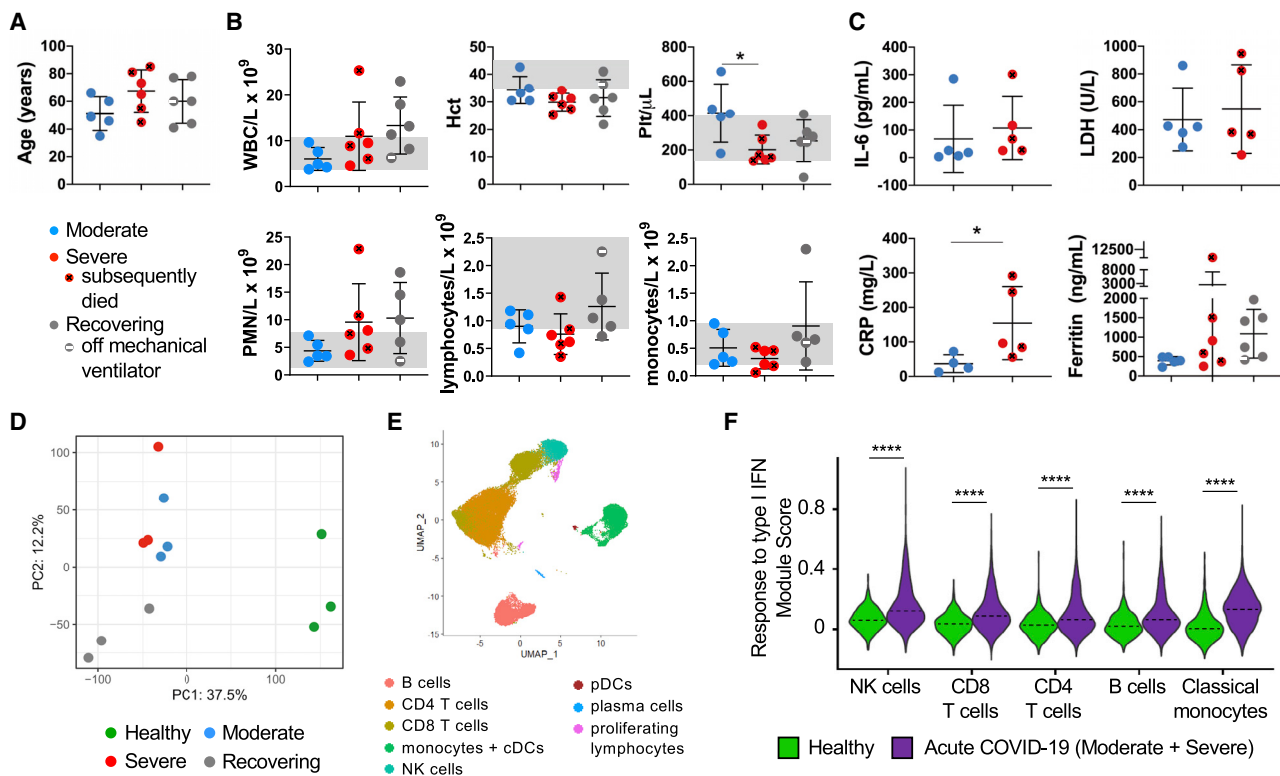


Figure 1. Evaluation of Blood Cells Subsets in Moderate, Severe (ARDS), and Recovering (post-ARDS) COVID-19 Patients (corrected)



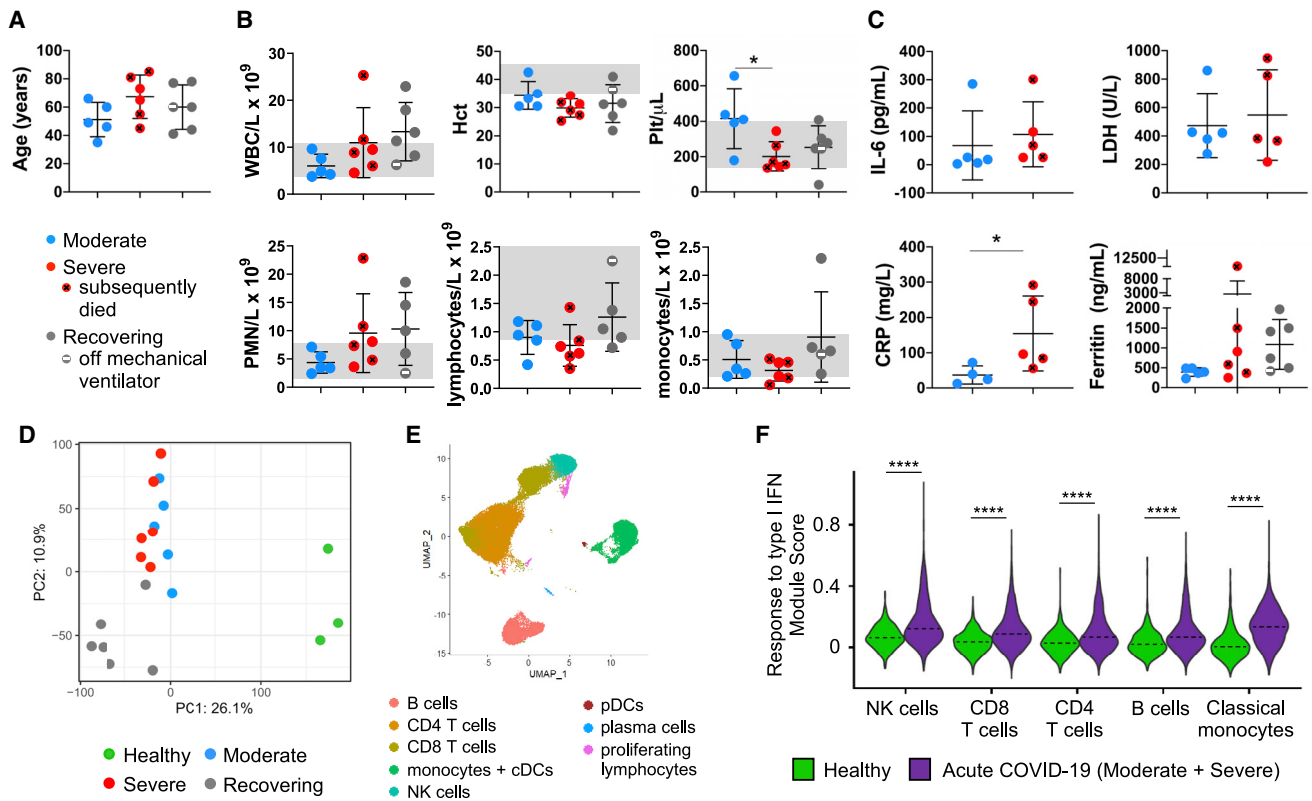


Figure 1. Evaluation of Blood Cells Subsets in Moderate, Severe (ARDS), and Recovering (post-ARDS) COVID-19 Patients (original)

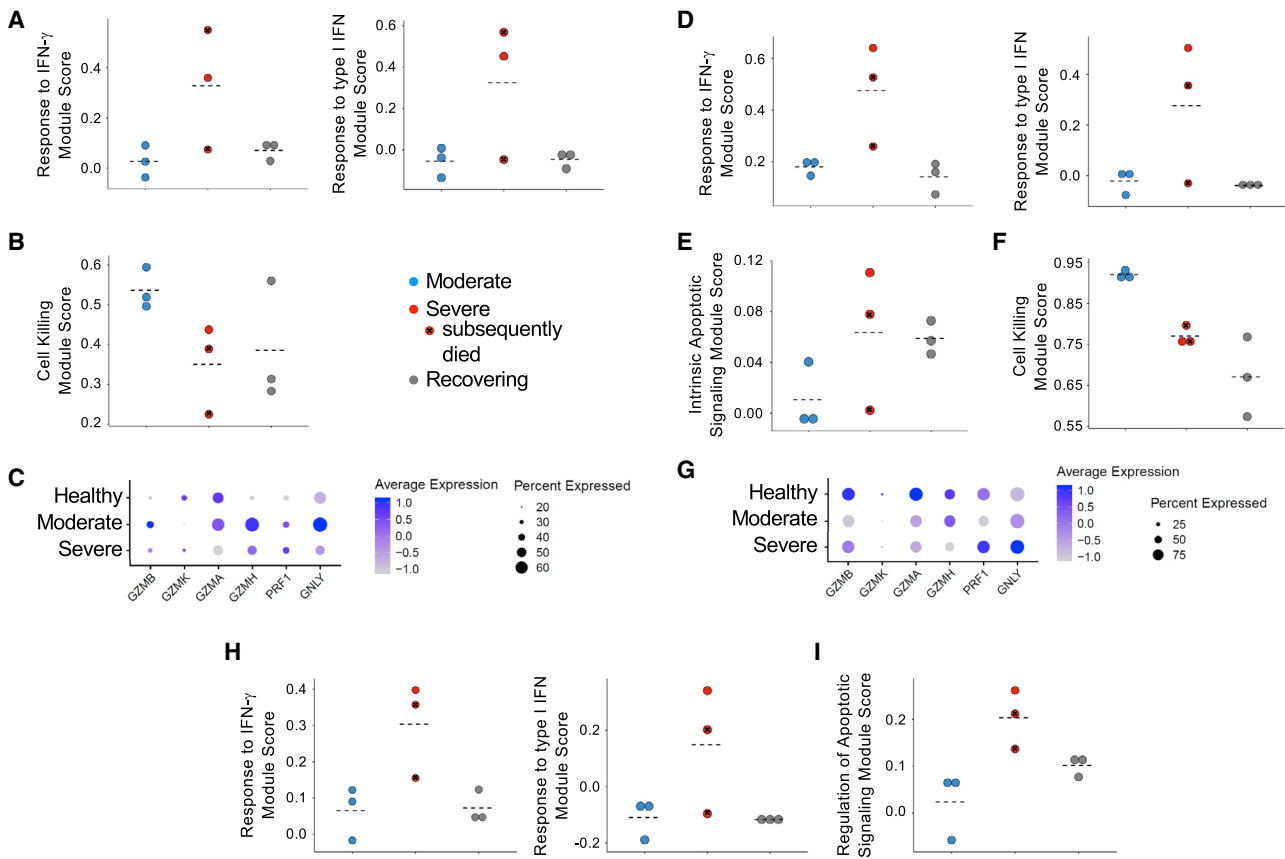


Figure S3. Comparison of NK and CD8 and CD4 T cell gene expression (corrected)

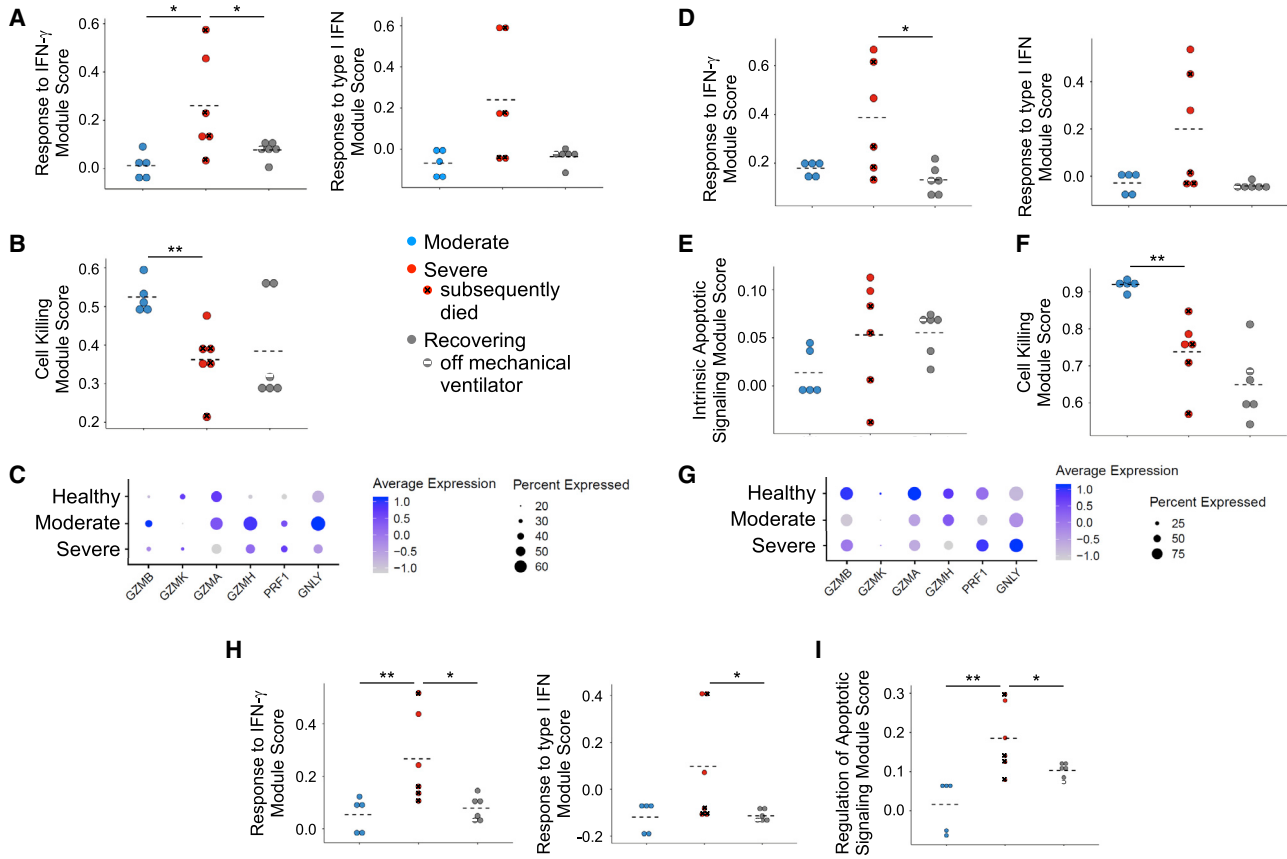


Figure S3. Comparison of NK and CD8 and CD4 T cell gene expression (original)

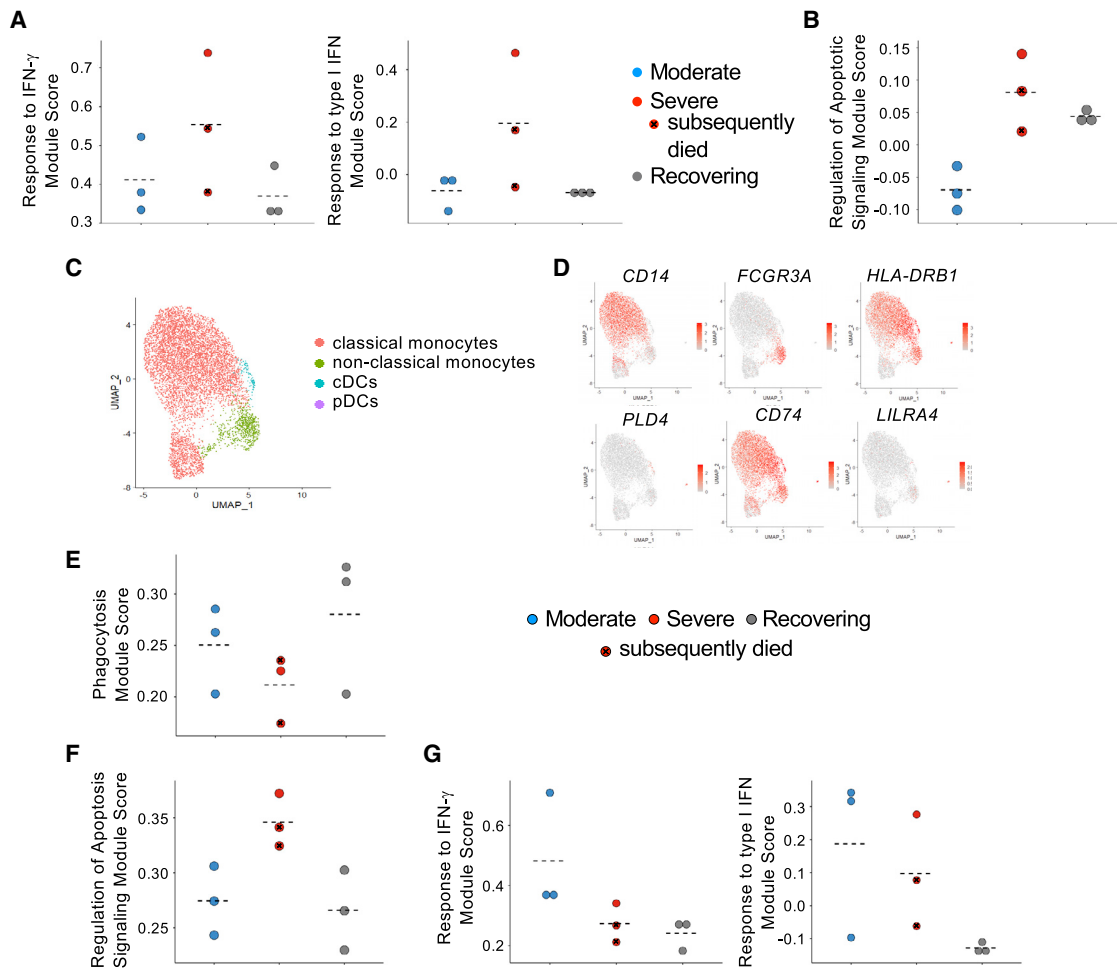


Figure S4. Comparison of B and plasma cell and monocyte gene expression (corrected)

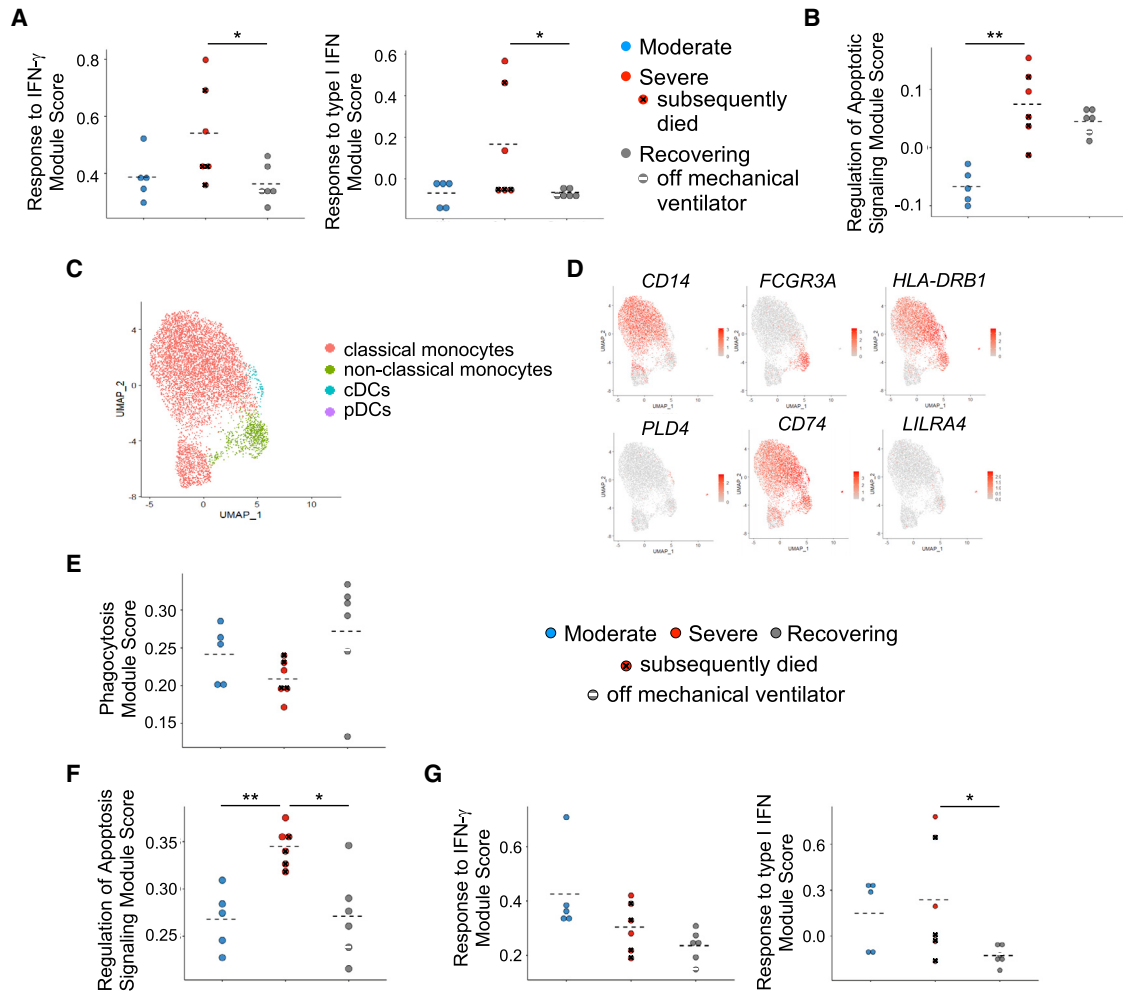


Figure S4. Comparison of B and plasma cell and monocyte gene expression (original)