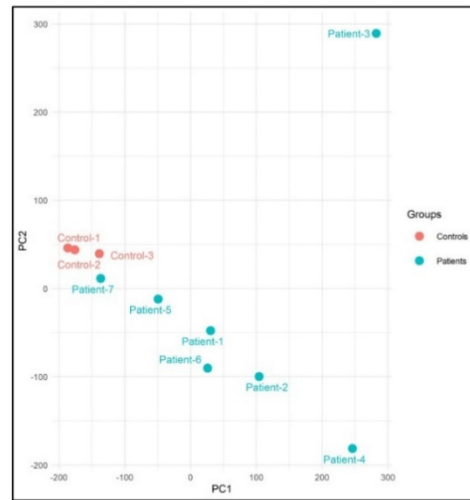


(a)



(b)

Signaling enrichment analysis

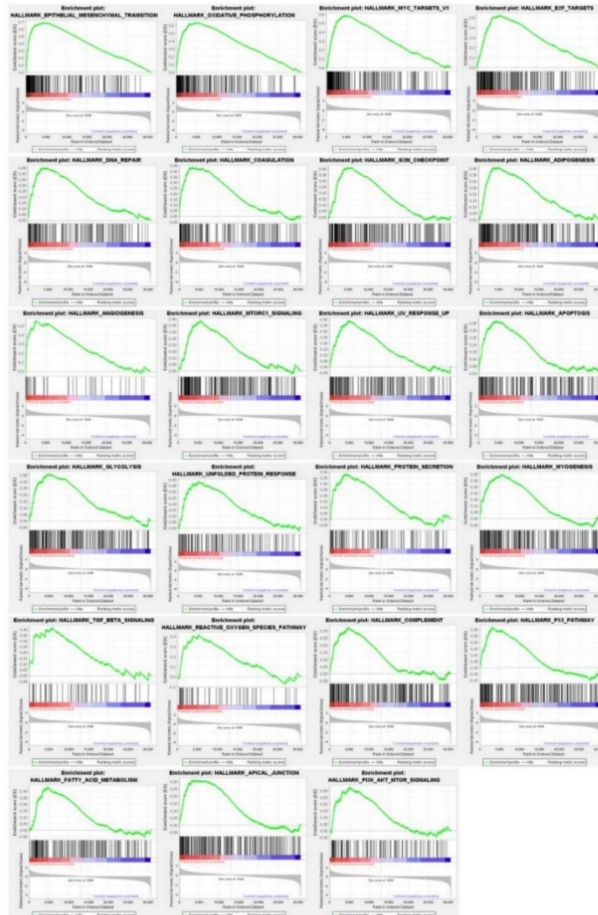
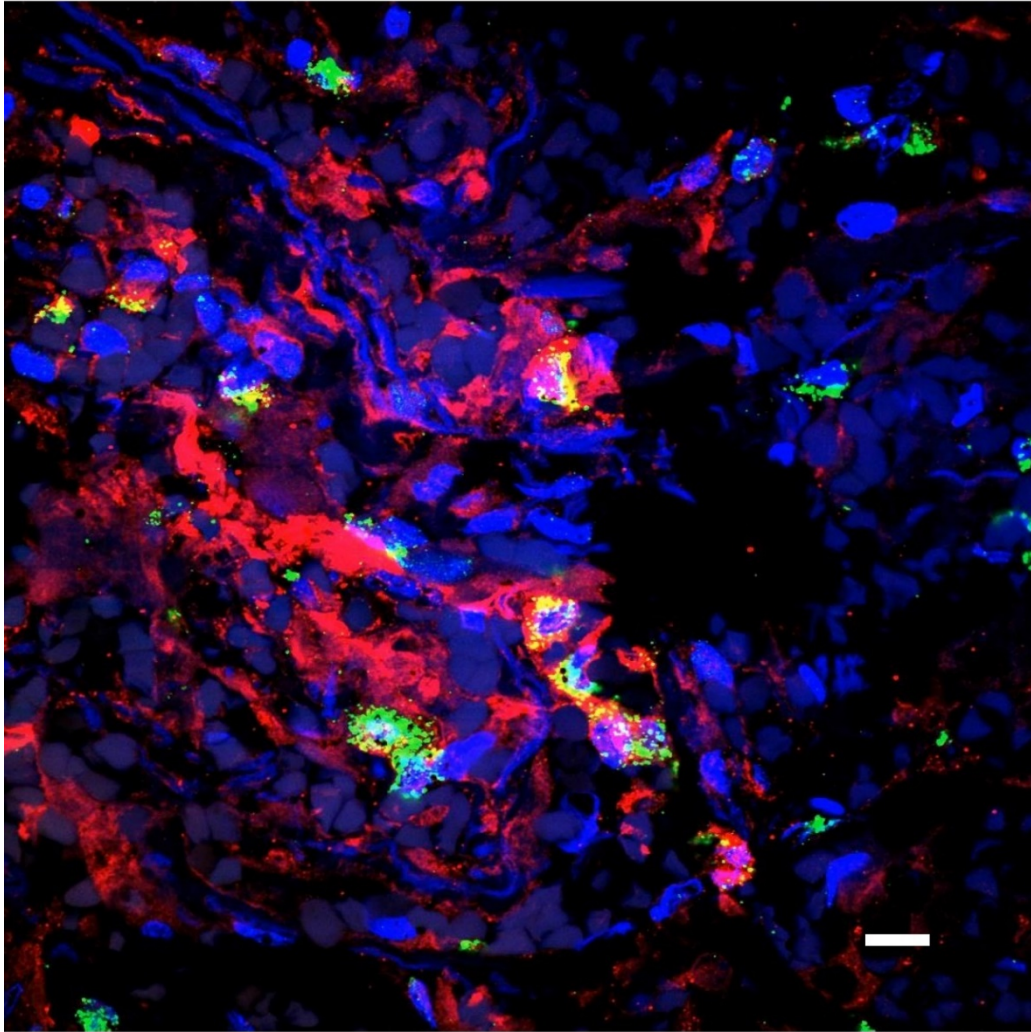


Figure S1: Principal-component analysis and signaling enrichment analysis.

(a) The scatterplot of principal-component analysis using normalized gene expression value of samples to indicate a distinct overlap of patients and controls. (b) Enriched signaling pathways with normalized p value < 0.001 in patients versus control individuals based on the hallmark gene set collection.



Supplementary Movie S1. NETs are co-localized with lipid oxidation marker 4-HNE.

Demonstration of extracellular DNA (Hoechst 33342, blue) and neutrophil granule protein (MPO, green) deposition together with the marker of lipid oxidation (4-HNE, red) under in vivo conditions (SARS-CoV-2 lung infection), with an interval of 0.1 μm , slices were taken throughout the z axis (z stacks) with 10 (left) and 15 (right) slices per stack in order to show extracellular DNA in their full extension. Scale bar, 10 μm , (n=3).

Table S1. List of differentially expressed genes between COVID-19 patients and healthy donors with corresponding logFCs and adjusted *p* values.