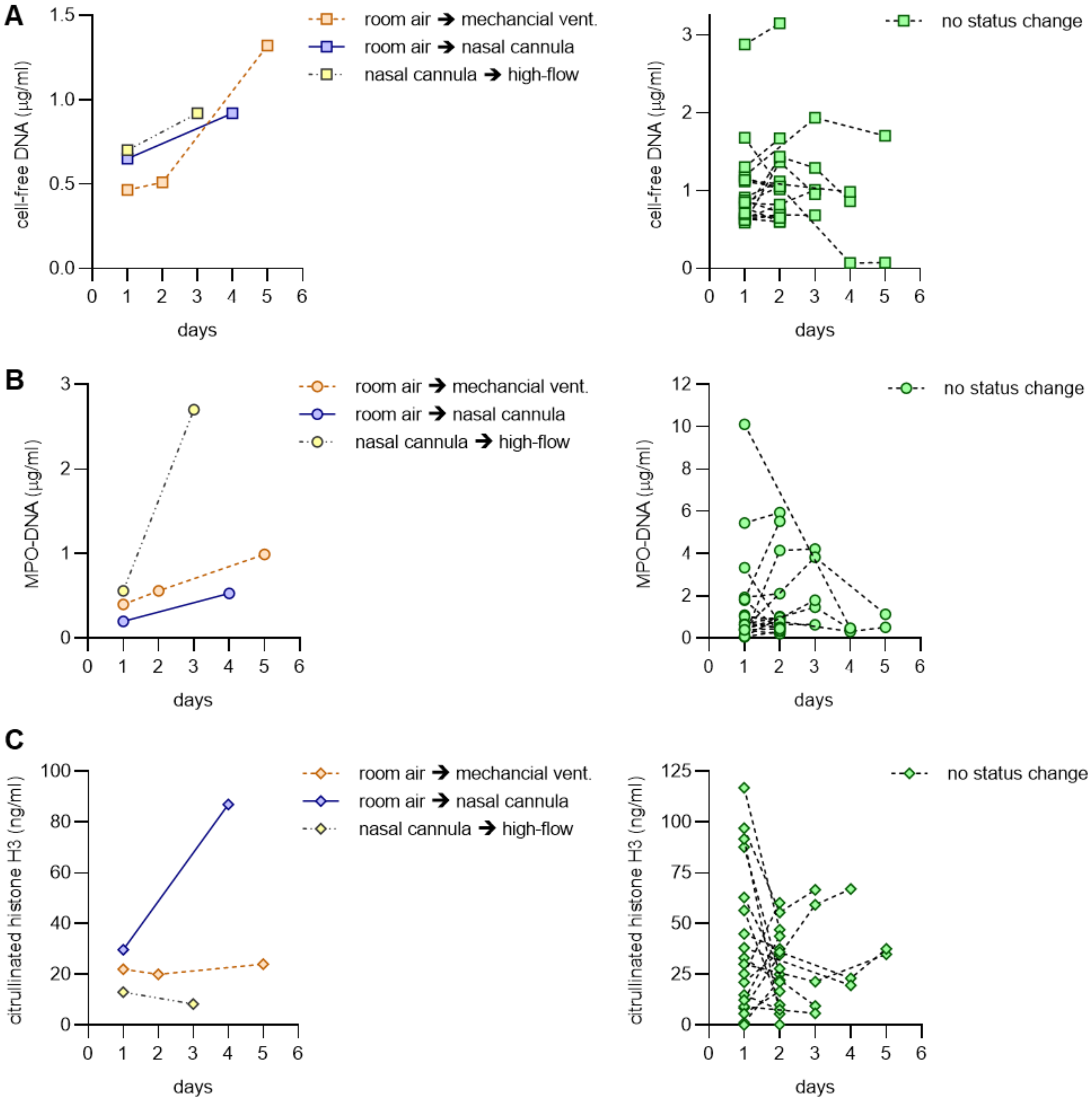
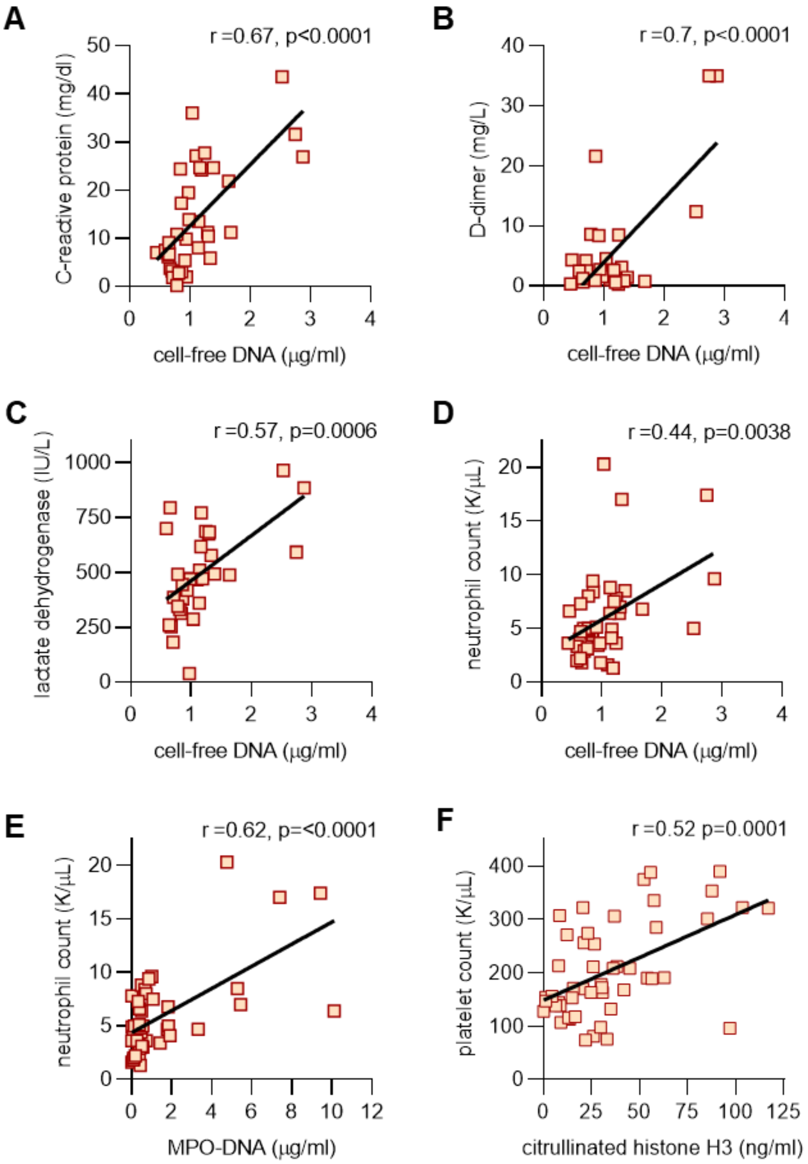
SUPPLEMENTAL MATERIAL

Neutrophil extracellular traps in COVID-19

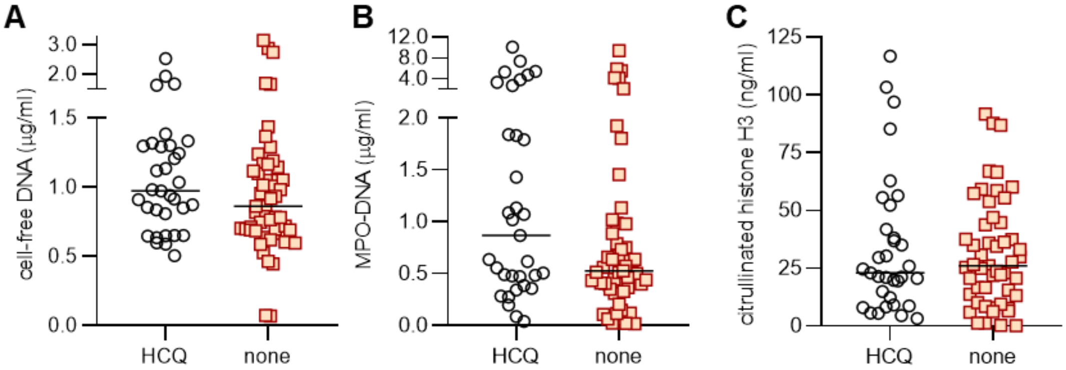
Zuo *et al.*



Supplemental Figure 1: Markers of NETs in longitudinal serum samples. For 22 patients, serum samples were available from multiple days. Data are plotted here for cell-free DNA (**A**), myeloperoxidase (MPO)-DNA complexes (**B**), and citrullinated histone H3 (**C**). “No status change” indicates no major change in oxygen requirement. As an example, a patient transitioning from room air to nasal-cannula oxygen *would* be considered to have had a status change.



Supplemental Figure 2: Association between NETs and clinical biomarkers with longitudinal data removed. Cell-free DNA was compared to clinical laboratory results (when available on the same day), and correlation coefficients were calculated for C-reactive protein (**A**, n=36), D-dimer (**B**, n=31), lactate dehydrogenase (**C**, n=32), and absolute neutrophil count (**D**, n=42). In panel **E** (n=42), MPO-DNA was compared to absolute neutrophil count and in **F** (n=49), citrullinated histone H3 was compared to platelet count. Pearson's correlation coefficients were calculated and are shown in the panels. No patient was included in this analysis more than once.



Supplemental Figure 3: Impact of hydroxychloroquine (HCQ) on NETs. Serum samples were grouped by HCQ treatment status (n=33 HCQ versus n=51 none) on the day of sample collection. Data are presented for cell-free DNA (**A**), myeloperoxidase (MPO)-DNA (**B**), and citrullinated histone H3 (**C**). No comparisons were statistically significant by either t test or Mann-Whitney test.