Title: Immunological misfiring and sex differences/similarities in early COVID-19 studies: missed opportunities of making a real IMPACT

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**Supplementary Figures S1-4**. **Changed immunological and biological measures in COVID-19 patients.**

**Figure. S1**

Scatter plots (left) and bar charts (right) for cytokines that exhibited stronger correlations in females than in males, including between IFNα2 and IFNγ, for CCL21 with CCL1 and fractalkine, and for CCL8 with CCL1. Goodness-of-fit (R2), Person’s r, and p-values shown for each group. CCL1, CCL21, and CXCL10 appear in several correlations between different measures in this cohort and may be significant for predicting disease progression. Number next to the groups denote actual numbers of patients in which each measure was detected. N/group: HCW♀: 87; Non-ICU♀: 30; ICU♀: 16; Non-ICU♂: 33; ICU♂: 14; HCW♂: 27.

**Figure. S2**

PCAs for significantly changed symbols in non-ICU **(a)**, ICU **(b)**, deceased **(d)** and coagulopathy-affected **(f)** COVID-19 patients versus healthy controls, and in ICU **(c)**, deceased **(e)** and coagulopathy-affected **(g)** COVID-19 patients versus non-ICU patients: donut plots showing the primary components necessary to explain at least 90% of the group’s variance, and the 9 symbols most correlated with each of the first four primary components (left), and PCA biplots for the first two components (right), with the color of points denoting log2 fold change versus the respective control group.

**Figure. S3**

Volcano plots for non-ICU **(a)**, ICU **(b)** and deceased **(c)** COVID-19 patients versus healthy controls, and for ICU **(d)** and deceased **(e)** COVID-19 patients versus non-ICU patients; Venn diagram contrasting significantly changed measures between non-ICU and ICU patients compared to healthy controls **(f)**, and between ICU and deceased patients compared to non-ICU patients **(g)**.

**Figure. S4**

Scatter plots showing correlations for IL6 with ICU admission, treatment count and clinical score; plasmacytoid dendritic cells (pDCs) with clinical score and treatment count, and nonclassical monocytes (ncMono) with clinical score and treatment count, with goodness-of-fit (R2), Person’s r, and p-values shown for each group.

**Supplementary Tables S1-4 Legends:**

**Table S1**. SARS-CoV-2 viral load in nasopharyngeal (Np) and saliva samples in IMPACT Cohort patients.

Breakdown of a total of 179\* data points from a total of 98 patients. Two or more longitudinal data points were collected from a total of 59 patients that were hospitalized in Yale between March and May of 2020. \*: DFSO for a few patients were missing/not reported and hence those patients were not included in our analysis for DFSO. Numbers in parenthesis (0) indicates patients with confirmed 0 values for viral load in both saliva and Np samples. Missing values represent samples was not collected and/or tested. The numbers of datapoints/patients shown in the middle column were used in our reanalysis.

**Table S2**. All Characteristics. All biological and clinical measures’ correlations of COVID-19+ patients (sex aggregated) with each other using heath care workers (HCW) as comparison group.

**Table S3**. All significantly changed (p<0.05) biological and clinical measures in COVID-19+ patients (sex aggregated) versus heath care workers (HCW) as comparison group. Most significantly changed measures are shown in descending order.

**Table S4**. All significantly changed (p<0.05) biological and clinical measures in COVID-19+ non-ICU patients (sex aggregated) versus heath care workers (HCW) as comparison group. Most significantly changed measures are shown in descending order.

**Table S5**. All significantly changed (p<0.05) biological and clinical measures in COVID-19+ ICU patients (sex aggregated) versus heath care workers (HCW) as comparison group. Most significantly changed measures are shown in descending order.