Supplementary Figures

Title: Longitudinal whole blood transcriptomic analysis characterizes neutrophil activation and interferon signaling in moderate and severe COVID-19.

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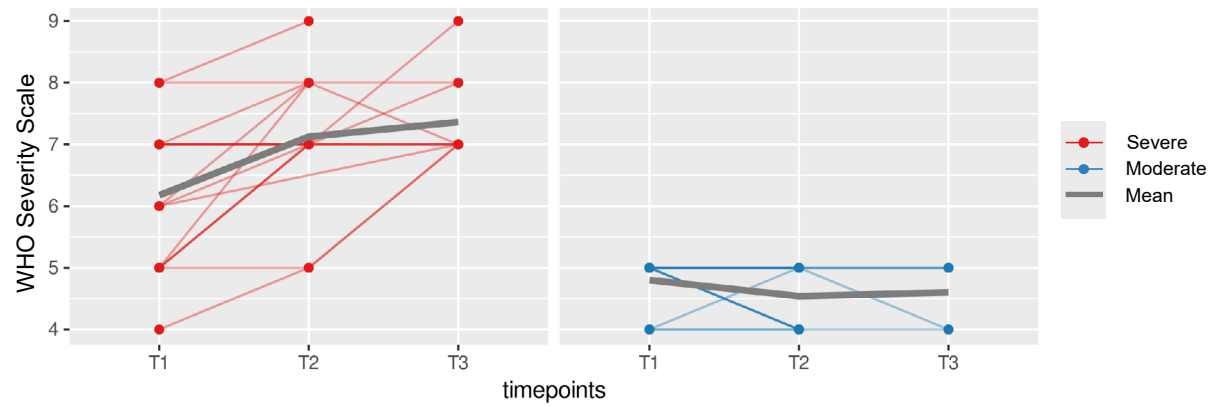Torben Lüders
Christine Jonassen
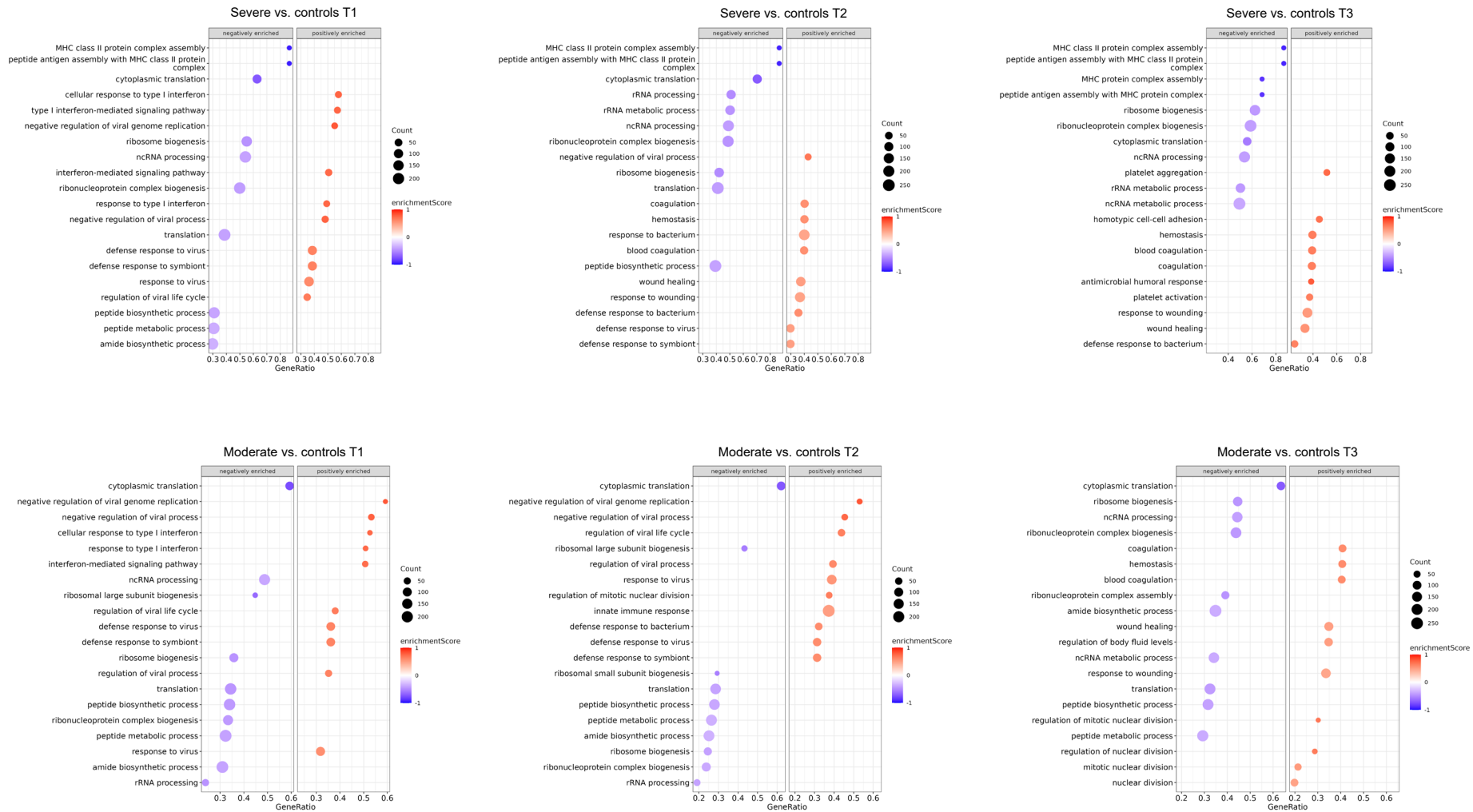Anita Blomfeldt
Torbjørn Omland
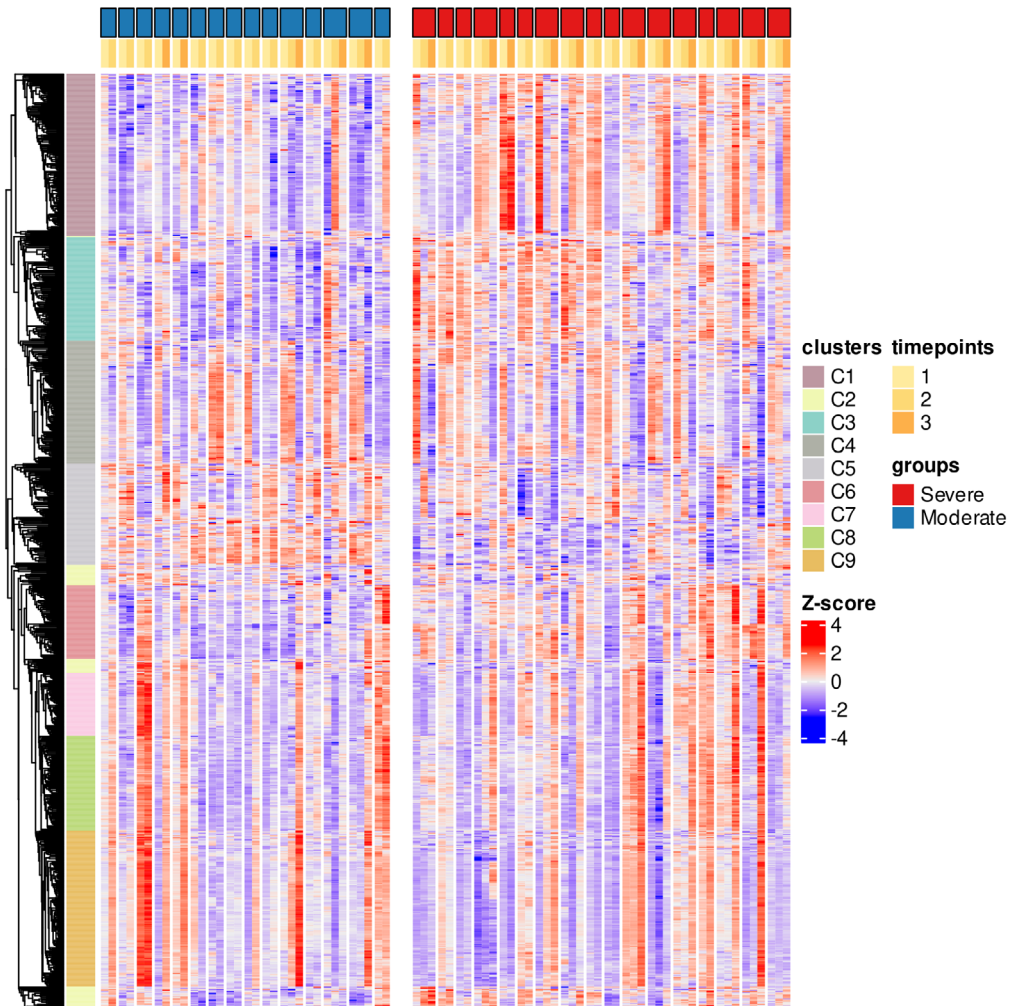Hilde Nilsen
Jan-Erik Berdal

Supplementary Figure 1:

Clinical trajectories. WHO severity scale over time in severe (red) and moderate (blue) patients. Mean values in grey.
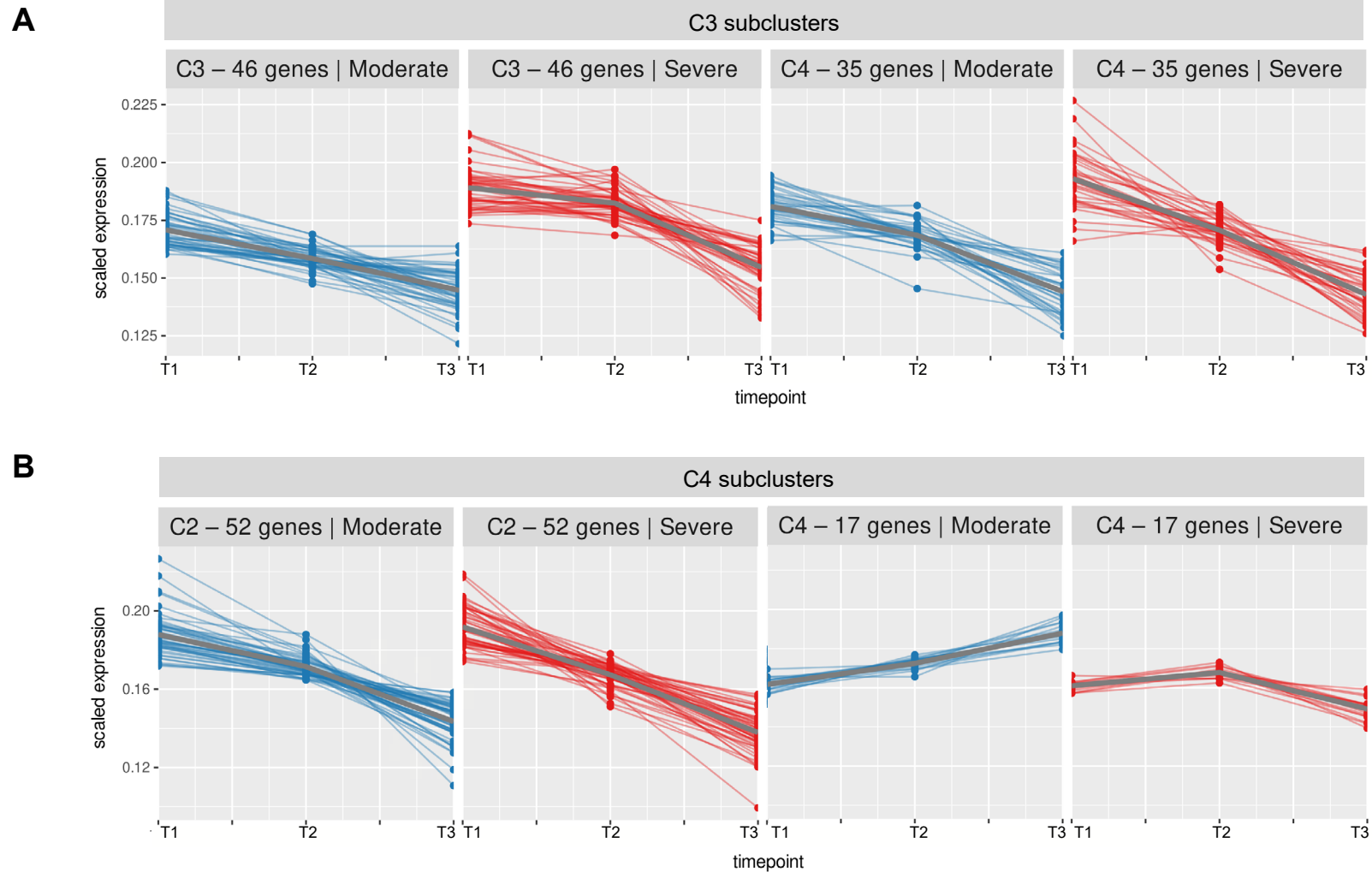
Supplementary Figure 2:

Gene set enrichment analysis (GSEA) in severe and moderate patients vs. healthy controls. Top 20 GO terms for each comparison indicated.
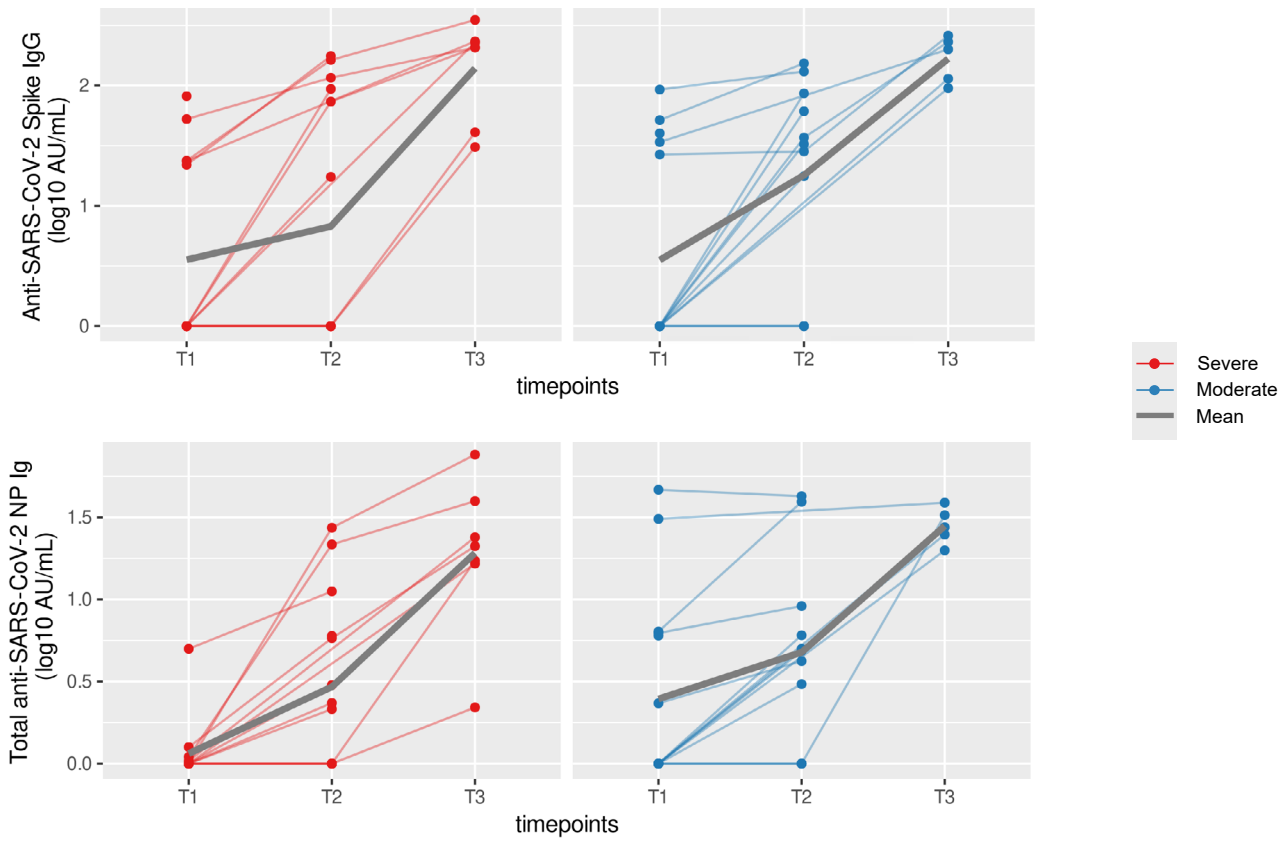
Supplementary Figure 3:

Time Series heatmap. Heat map showing the results of
PART clustering in the time series analysis.
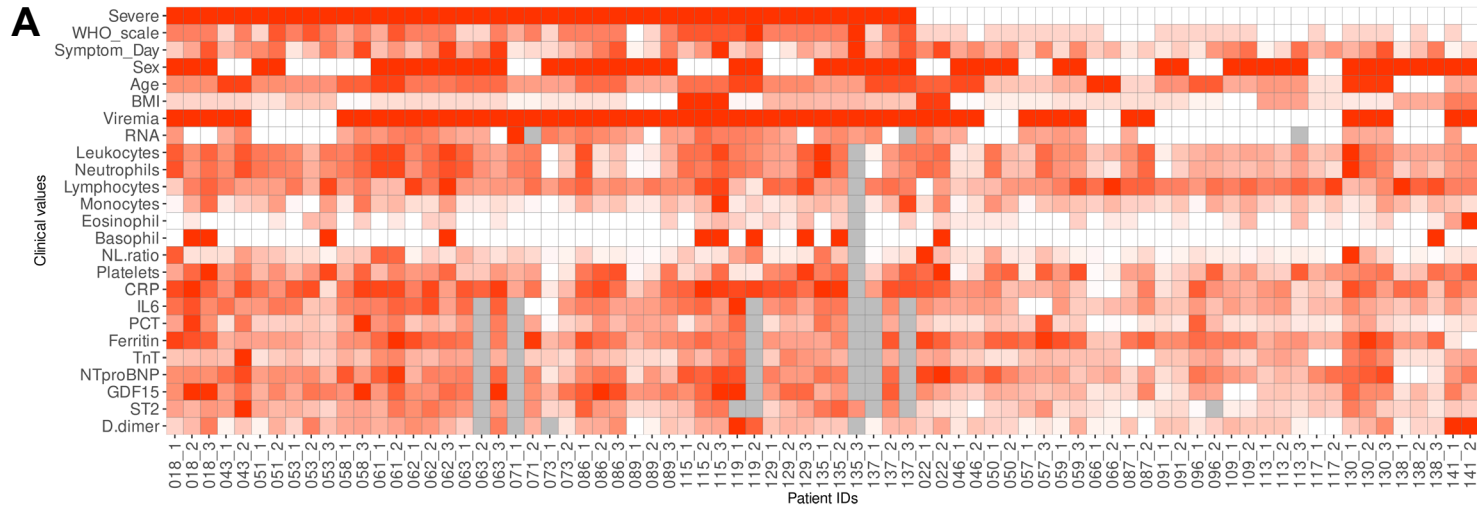
Supplementary Figure 4:

Time series subclusters. Trajectories of subclusters in A: C3 and B: C4. Patients with severe disease in red, moderate disease in blue. Mean scaled expression in grey.
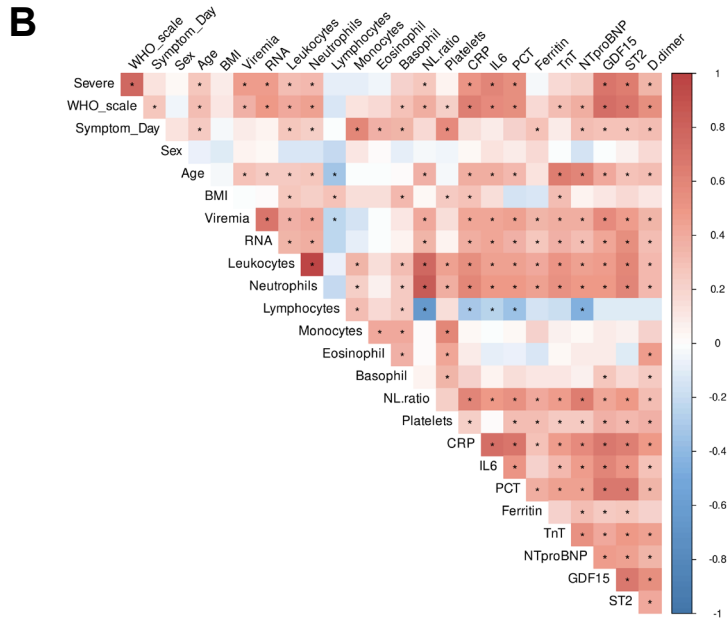
Supplementary Figure 5:

SARS-CoV-2-specific antibody levels. Levels of SARS-CoV-2-specific antibodies in serum samples, per patient, timepoint and severity group. Mean value per group in grey.
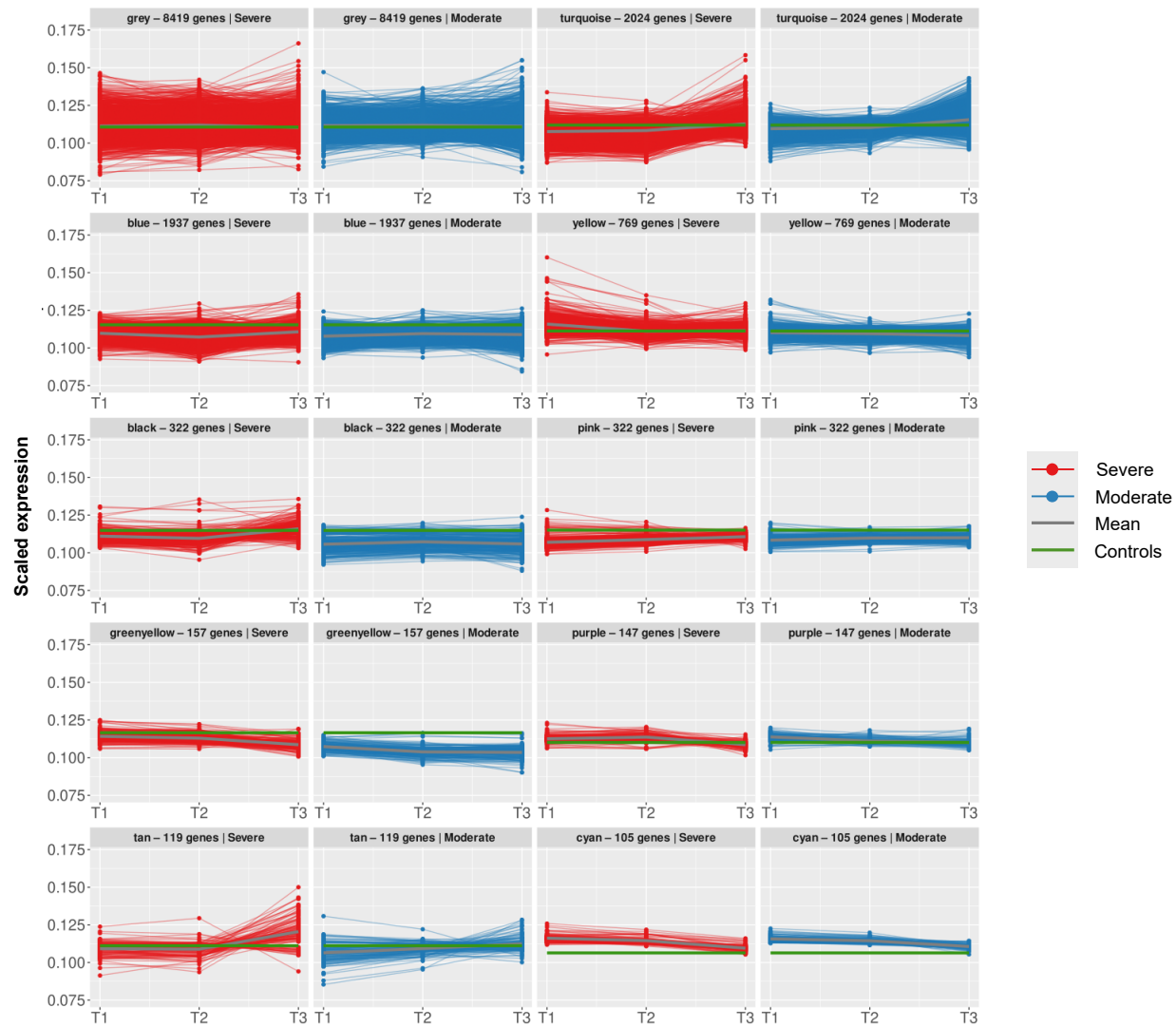
Supplementary Figure 6:

A

Clinical trait heatmap. Heat map of clinical traits and biomarkers for each sample. Biomarker variables are log-transformed. Grey boxes indicate missing data.
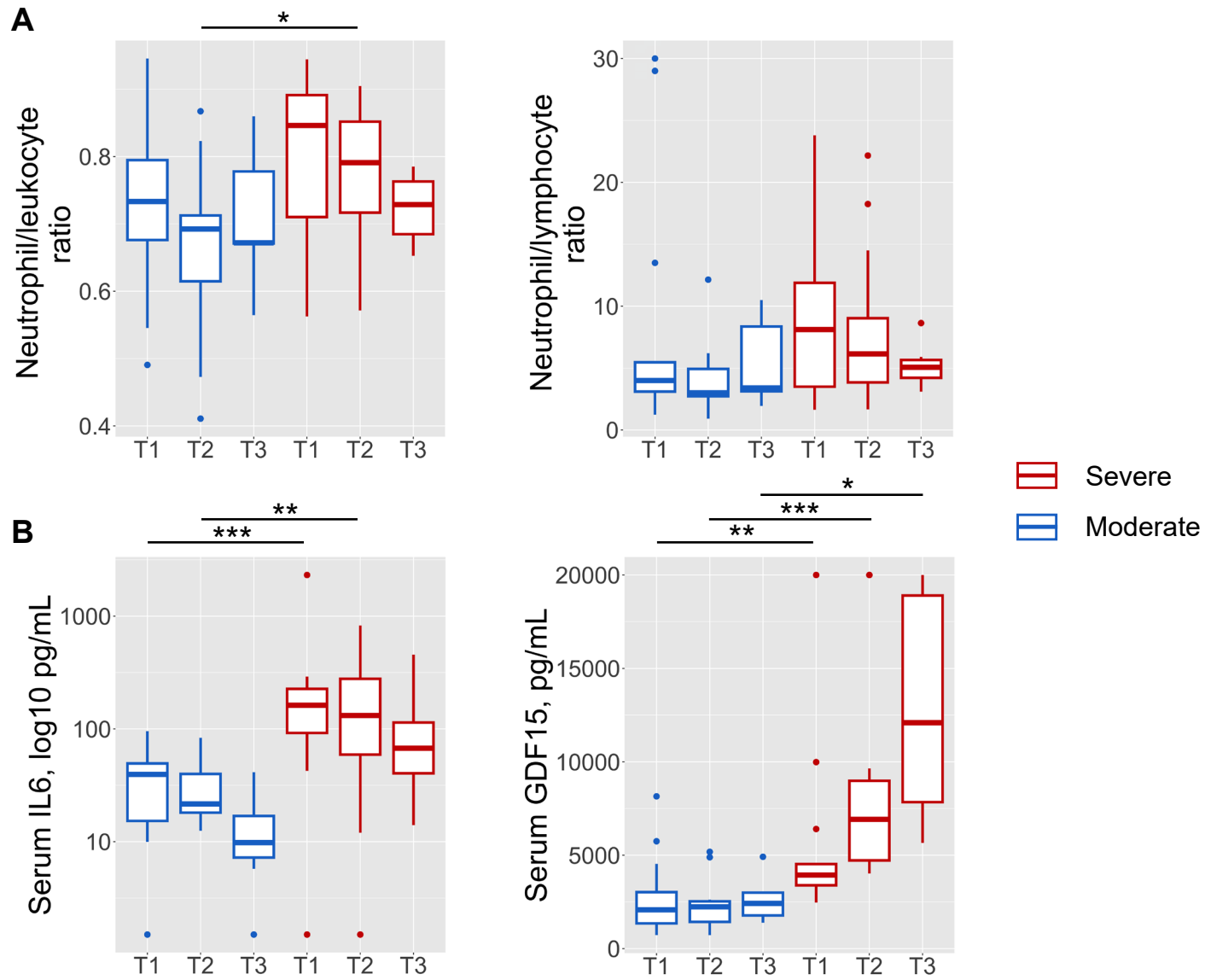
B

Correlation between clinical traits and biomarkers. Color indicates the correlation statistic, scale on the right. Dots indicate a p-value < 0.05.

Supplementary Figure 7:

Remaining WGCNA module trajectories. Gene trajectories over time in severe (red) and moderate (blue) patients. Mean scaled expression in patients and healthy controls in grey and green, respectively.

Biomarkers: A: Leukocyte ratios by clinical cytometry and B: serum concentrations of cytokines, per severity group and timepoint. Moderate in blue, severe in red. *: p<0.05 **: p<0.01 ***: p<0.001