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Profiling of COVID-19 Patients Reveals Key Factors in the Path to Recovery

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The COVID-19 pandemic, caused by SARS-CoV-2, has triggered a global health crisis with profound socio-economic repercussions. While numerous proteomics-based studies have investigated differentially expressed proteome profiles in COVID-19 patients with varying disease severities (e.g., mild vs. severe), few have focused on the molecular determinants associated with recovery from severe conditions. In this study, we profiled the serum proteome of a cohort consisting of 20 COVID-19 patients with divergent clinical outcomes and 5 healthy controls. Patients were categorized based on their clinical progression. Our analysis identified 181 proteins, with 14 showing differential expression between deteriorating patients and those who recovered. Network and pathway analyses of these proteins unveiled potential biological processes, notably complement regulation, central to COVID-19 recovery. Complement C2 could be an early marker to detect clinical deterioration in patients with COVID-19. Our findings provide novel molecular insights into the recovery process and suggest potential predictive markers to guide clinical decisions for patients in severe conditions.