

PREDICTIVE COVID-19 DISEASE SEVERITY TEST



The test measures **host response to COVID-19** and, based on it, classifies and predicts disease severity.



It predicts whether the patients (1) are **likely to develop severe disease**, (2) will need **invasive ventilation** and (3) are likely to **survive if they have severe disease**.



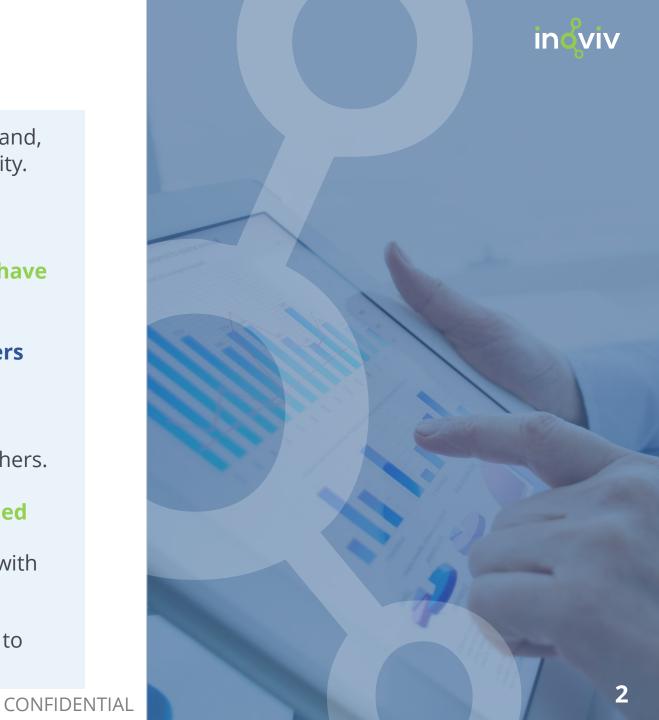
The test monitors **31 plasma protein biomarkers** simultaneously which span multiple aspects of COVID-19, including proteins that function in **inflammation**, **coagulation and vascular dysfunction**, **the complement cascade** and others.



This predictive biomarker signature was **identified** through **proteome screening** of **thousands of patient samples** at Charité University Hospital with **longitudinal** follow up.



Assay is being used on COVID-19 clinical studies to **demonstrate treatment efficacy**







| Disease Process/ Biomarker Category | Biomarker Name | Biomarker Name Abbreviation | Rationale for Inclusion in Panel | References |
|--|---|--------------------------------|----------------------------------|---|
| Inflammation | Complement C3 | С3 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | C-reactive protein | CRP | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Monocyte differentiation antigen CD14 | CD14 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Alpha-2-HS-glycoprotein | AHSG | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Lysozyme C, EC 3.2.1.17 | LYZ | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Inter-alpha-trypsin inhibitor heavy chain H1 | ITIH1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Immune Response | Proteoglycan 4 | PRG4 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Immunoglobulin heavy variable 5-51 | IGHV5-51 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Alpha-1-antichymotrypsin | SERPINA3 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Complement C1q subcomponent subunit C | C1QC | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |

INOVIV-CHARITÉ COVID-19 BIOMARKER PANEL

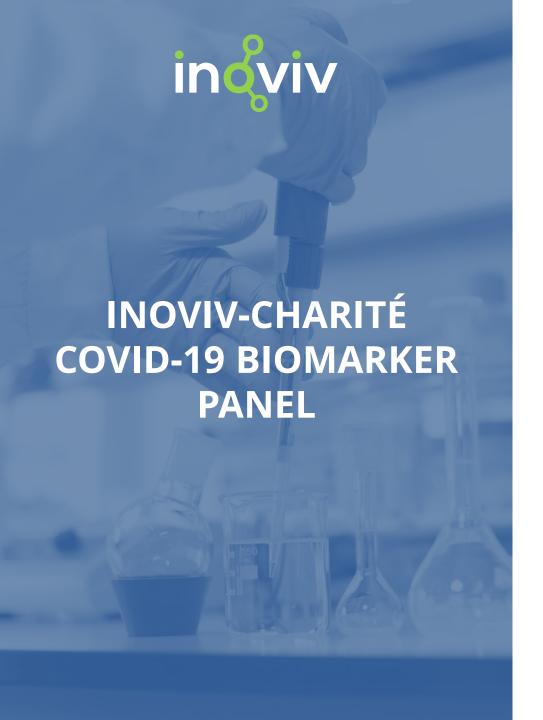


| Disease Process/ Biomarker Category | Biomarker Name | Biomarker Name Abbreviation | Rationale for Inclusion in Panel | References |
|--|---|--------------------------------|----------------------------------|---|
| Immune Response | N-acetylmuramoyl-L-alanine amidase, EC 3.5.1.28 | PGLYRP2 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Low affinity immunoglobulin gamma Fc region receptor III-A | FCGR3A | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Beta-2-microglobulin | B2M | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Coagulation & Vascular Dysfunction | Antithrombin-III | SERPINC1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Heparin cofactor 2 | SERPIND1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Protein ORM2 | ORM2 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Histidine-rich glycoprotein | HRG | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Plasma protease C1 inhibitor | SERPING1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | von Willebrand factor | VWF | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Plasma kallikrein, EC 3.4.21.34 | KLKB1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |

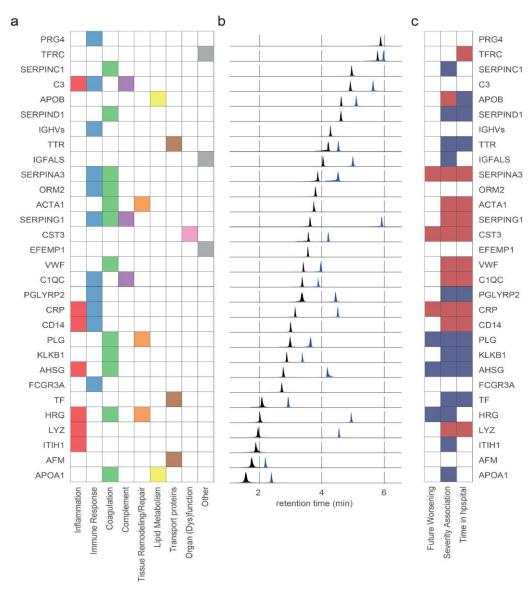




| Disease Process/ Biomarker Category | Biomarker Name | Biomarker Name Abbreviation | Rationale for Inclusion in Panel | References |
|--|---|--------------------------------|----------------------------------|---|
| Tissue Remodelling / Repair | Actin, aortic smooth muscle; Actin, cytoplasmic 1; Actin, cytoplasmic 2; Actin, gamma-enteric smooth muscle | ACTA2;ACTB;ACTG1; ACTG2 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Plasminogen, EC 3.4.21.7 | PLG | lnoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Lipid Metabolism | Apolipoprotein A-I | APOA1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Apolipoprotein B-100 | APOB | lnoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Transport Proteins | Serotransferrin | TF | lnoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Transthyretin | TTR | lnoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Afamin | AFM | lnoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Organ Dysfunction | Cystatin-C | CST3 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| Other Proteins Related to COVID-19 | EGF-containing fibulin-like extracellular matrix protein 1 | EFEMP1 | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Insulin-like growth factor-binding protein complex acid labile subunit | IGFALS | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |
| | Transferrin receptor protein 1 | TFRC | Inoviv generated data | Messner et al., 2020; Demichev et al., 2021; Wang et al., 2022 |





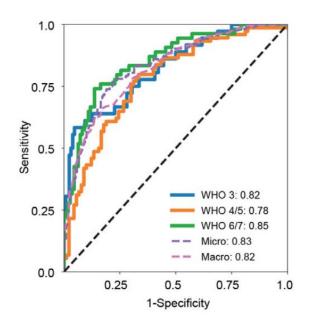


CONFIDENTIAL

Wang et al., 2022

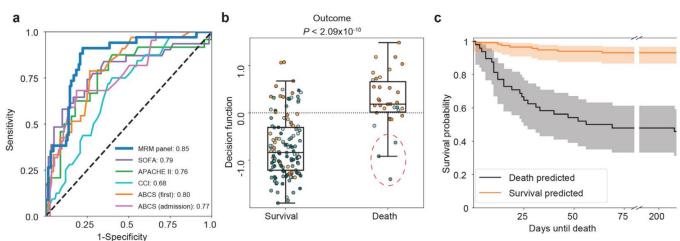
JZZ

PREDICTIVE COVID-19 DISEASE SEVERITY TEST



✓ ROC curves for the prediction of the WHO severity group from the first time point measured for every patient

✓ (n=36 (WHO 3), n=47 (WHO 4), n=27 (WHO 5), n=16 (WHO 6), n=38 (WHO7)



✓ Outperformed current clinical assessments for survival prediction



For research use only. Not for use in diagnostics procedures.



High throughput LC-MS/MS stratification of plasma proteome response to SARS-CoV-2 infection

Using the SCIEX Triple Quad 7500 system, powered by SCIEX OS software

Catherine S. Lane¹, Daniel Blake¹, Adam Cryar², Jacob Harris², Ernestas Sirka², Markus Ralser³, Ziyue Wang³, Johannes Harti³. Michael Mülleder⁴

¹SCIEX, Alderley Edge, UK, ²Inoviv, London, UK, ³Institute of Biochemistry, Charité Universitätsmedizin Berlin, Germany, ⁴Core Facility - High-Throughput Mass Spectrometry, Charité Universitätsmedizin Berlin, Germany

Multi-faceted research into the nature of the COVID-19 disease caused by the SARS-CoV-2 virus is ongoing, as scientists strive to increase understanding of the disease and stratify and predict the impact it has on everyday life globally. One important area of research is to investigate the severity of the disease and



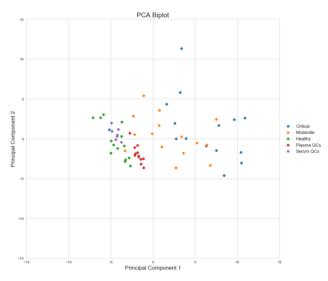


Figure 2 PCA Biplot of quantification results from all 52 peptides monitored, showing disease state stratification.



indviv