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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Tune 2.9-290033/2.9.0.2926, Xcalibur 4.0
Data analysis	Microsoft Excel 2016, OriginPro 2020, Proteome Discoverer 2.4, Perseus 1.6.5.0., Python 3.6, numpy 1.15.4, scipy 1.3.0,pandas 0.23.4, Cytoscape 3.7.1, BiNGO 3.0.3, EnrichmentMap 3.1.0, ReactomeFI 6.1.0

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All mass spectrometry data is available via the PRIDE repository under the accession PXD017710 and processed data under http://corona.papers.biochem2.com/.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size was chosen balancing technical capacities during large scale proteomic experiments and statistical power. For each analysis at least 3 independent biological replicates have been used.
Data exclusions	No data has been excluded from analysis.
Replication	Reproducibility of results has been assessed by at least three independent biological replicates and was tested by statistical tests as stated in methods and figure legends.
Randomization	Experiments have been carried out using cell culture systems, making randomization not necessary. To control technical covariates, technical sample preparations have been carried out in parallel and samples have been multiplexed, where applicable.
Blinding	Investigators have not been blinded for the experiments, since data analysis and acquistion methods are unbiased by investigator. Data from different groups was analyzed together to ensure same handling and eliminate analysis bias.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	SARS-CoV-2 Nucleoprotein, Sino Biological, CAT #40143-R019-100ul
Validation	Antibody has been validated by manufacturer for WB,ELISA,IHC-P,FCM,ICC/IF and IP with recombinant SARS-CoV-2 protein.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Caco-2: DSMZ (ACC. 169)
Authentication	Cell lines have been used without further validation, Authentication certificate was delivered by DSMZ
Mycoplasma contamination	Cell line used in this study was tested negative for mycoplasma infection
Commonly misidentified lines (See ICLAC register)	None