nature portfolio

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Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.
For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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	No software used
Data analysis	We used matlab (version: R2019b)

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Main summary statistics that support the findings of this study are available in the Supplementary Data. Owing to company cohort data-sharing restrictions, individual data cannot be publicly posted. However, data are available from the authors upon request and with permission of KDDI Corporation. Data requests should be sent to the corresponding author, Toshinori Chiba, t.chiba0906@gmail.com, and will be responded to within 21 days.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	female: 46.8%
Reporting on race, ethnicity, or other socially relevant groupings	Japanese
Population characteristics	The main analysis used multidimensional psychiatric data taken immediately before and during the COVID-19 epidemic for 3,815 participants (mean age 47.1 years, 46.8% female).
Recruitment	From registrants of an online survey company (Macromill, INC; https://monitor.macromill.com/)
Ethics oversight	Ethics Committee of the Advanced Telecommunications Research Institute International

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	
Data exclusions	
Replication	
Randomization	
Blinding	

Behavioural & social sciences study design

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

Study description	Quantitative data from a longitudinal survey of 3,815 people by an Internet research company (Macromill) during the COVID-19 pandemic and over a long period of time after the pandemic were used for the psychological effects of COVID-19.
Research sample	A repeat internet survey was conducted in cooperation with Macromill, Inc.. The initial survey was conducted in December 2019. Since the first COVID-19 case was identified in Japan in January 2020, the data in this survey are considered baseline data (T0); following the COVID-19 epidemic, the subjects in this survey were invited to participate in August 2020 (T1), December 2020 (T2), April 2021 (T3), August 2021 (T4), and December 2021 (T5). These follow-up surveys added several items related to COVID-19: multidimensional psychiatric data taken just before and during the COVID-19 epidemic were collected from a total of 3,815 participants (mean age 47.1 years, 46.8% female). This number included some who responded to all of T1 to T5 and others who responded only to multiple timings of T1 to T5. The data used in this study are not representative.
Sampling strategy	We relied on Macromill, INC. (https://monitor.macromill.com/), the largest online research company in Japan for participant recruitment. This company maintains a participant pool of about 1.2 million individuals in Japan. Among this participant pool, 99,156 randomly chosen individuals, aged 18 and above, living in the Kansai region of Japan, were invited via e-mail to participate in screening for the original study before the COVID-19 pandemic (at T0). The email invitation to the survey included information on informed consent, and participants were considered to have consented to answer all questions in the survey.

The procedures were decided based on the original survey (at T0). At that time, we aimed to collect enough individuals with high scores in problematic smartphone (PS) use scores for a detailed survey. To do so, we performed a screening test (where participants reported demographics and PS score). Participants were then screened to include approximately equal numbers of individuals in each quintile relative to their PS score. This study does not include qualitative data. According to the post-hoc power analysis, our sample size of 50 data points was larger than a sample size of 20 data points that would be sufficient to achieve 99% power to detect an effect size of r = 0.7.

Data collection

Macromill collected information directly from the study participants and provided it to the researcher. The researcher was not present at the time of data collection. This study is not an intervention study; therefore, the researcher was not blinded to the experimental conditions or other factors.

Timing

The online surveys were conducted 6 times from the same population: once before the pandemic (December 2019: T0) and 5 times during the pandemic (August 2020: T1, December 2020: T2, April 2021: T3, August 2021: T4, and December 2021: T5).

Data exclusions

Participants were excluded if 1) they provided contradictory answers across items, e.g., to one question they answered that they never drink, but to another they answered that they sometimes drink, or across surveys (e.g. age differed more than two years within one year surveys).
2) they answered using only the maximum or minimum rating in questionnaires which include reverse items (e.g. CES-D and STAI-Y).
When the study period was divided into three periods: baseline T0, immediate post-pandemic T1, and post-pandemic T2-T5, 273 were excluded in T0, 216 in T1, and 1,651 in T2-T5.

Non-participation

No participants withdrew consent. The participants were able to participate in the online survey any number of times at their discretion. The current analyses included 3,815 responders at T0, 3,508 responders at T1, 2,680 responders at T2, 2,562 responders at T3, 2,022 responders at T4, and 1,806 responders at T5.

Randomization

As this is a longitudinal observational study of the impact of the worldwide COVID-19 pandemic, randomization is not relevant in this study.

Ecological, evolutionary & environmental sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing and spatial scale	
Data exclusions	
Reproducibility	
Randomization	
Blinding	

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	
Location	
Access & import/export	
Disturbance	

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 and archaeology
☑	☐ Animals and other organisms
☑	☐ Clinical data
☑	☐ Dual use research of concern
☑	☐ Plants

Methods

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

Antibodies

Antibodies used	

Validation

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	
Authentication	
Mycoplasma contamination	
Commonly misidentified lines (See ICLAC register)	

Palaeontology and Archaeology

Specimen provenance	
Specimen deposition	
Dating methods	

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	
Wild animals	
Reporting on sex	
Field-collected samples	
Ethics oversight	

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	
Study protocol	
Data collection	
Outcomes	

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☐	☐	Demonstrate how to render a vaccine ineffective
☐	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐	Increase transmissibility of a pathogen
☐	☐	Alter the host range of a pathogen
☐	☐	Enable evasion of diagnostic/detection modalities
☐	☐	Enable the weaponization of a biological agent or toxin
☐	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	
Novel plant genotypes	
Authentication	

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	
Files in database submission	
Genome browser session (e.g. UCSC)	

Methodology

Replicates	
Sequencing depth	
Antibodies	
Peak calling parameters	
Data quality	
Software	

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

Instrument

Software

Cell population abundance

Gating strategy

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type

Design specifications

Behavioral performance measures

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

(See Eklund et al. 2016)

Correction

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Graph analysis

Multivariate modeling and predictive analysis