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BRIEF COMMUNICATION

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Antibody responses to SARS-CoV-2 in patients with COVID-19

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We report acute antibody responses to SARS-CoV-2 in 285 patients with COVID-19. Within 19 days after symptom onset, 100% of patients tested positive for antiviral immunoglobulin-G (IgG). Seroconversion for IgG and IgM occurred simultaneously or sequentially. Both IgG and IgM titers plateaued within 6 days after seroconversion. Serological testing may be helpful for the diagnosis of suspected patients with negative RT–PCR results and for the identification of asymptomatic infections.

The continued spread of coronavirus disease 2019 (COVID-19) has prompted widespread concern around the world, and the World Health Organization (WHO), on 11 March 2020, declared COVID-19 a pandemic. Studies on severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) showed that virus-specific antibodies were detectable in 80–100% of patients at 2 weeks after symptom onset[1–6]. Currently, the antibody responses against SARS-CoV-2 remain poorly understood and the clinical utility of serological testing is unclear[7].

A total of 285 patients with COVID-19 were enrolled in this study from three designated hospitals; of these patients, 70 had sequential samples available. The characteristics of these patients are summarized in Supplementary Tables 1 and 2. We validated and used a magnetic chemiluminescence enzyme immunoassay (MCLIA) for virus-specific antibody detection (Extended Data Fig. 1a–d and Supplementary Table 3). Serum samples from patients with COVID-19 showed no cross-binding to the S1 subunit of the SARS-CoV spike antigen. However, we did observe some cross-reactivity of serum samples from patients with COVID-19 to nucleocapsid antigens of SARS-CoV (Extended Data Fig. 1e). The proportion of patients with positive virus-specific IgG reached 100% approximately 17–19 days after symptom onset, while the proportion of patients with positive virus-specific IgM reached a peak of 94.1% approximately 20–22 days after symptom onset (Fig. 1a and Methods). During the first 3 weeks after symptom onset, there were increases in virus-specific IgG and IgM antibody titers (Fig. 1b). However, IgM showed a slight decrease in the >3-week group compared to the ≤3-week group (Fig. 1b). IgG and IgM titers in the severe group were higher than those in the non-severe group, although a significant difference was only observed in IgG titer in the 2-week post-symptom onset group (Fig. 1c, $P=0.001$).

Sixty-three patients with confirmed COVID-19 were followed up until discharge. Serum samples were collected at 3-day intervals. Among these, the overall seroconversion rate was 96.8% (61/63) over the follow-up period. Two patients, a mother and daughter, maintained IgG- and IgM-negative status during hospitalization. Serological courses could be followed for 26 patients who were initially seronegative and then underwent seroconversion during the observation period. All these patients achieved seroconversion of IgG or IgM within 20 days after symptom onset. The median day of seroconversion for both IgG and IgM was 13 days post symptom onset. Three types of seroconversion were observed: synchronous seroconversion of IgG and IgM (nine patients), IgM seroconversion earlier than that of IgG (seven patients) and IgM seroconversion later than that of IgG (ten patients) (Fig. 2a). Longitudinal antibody changes in six representative patients of the three types of seroconversion are shown in Fig. 2b–d and Extended Data Fig. 2a–c.

IgG levels in the 19 patients who underwent IgG seroconversion during hospitalization plateaued 6 days after the first positive IgG measurement (Extended Data Fig. 3). Plateau IgG levels varied widely (more than 20-fold) across patients. IgM also showed a similar profile of dynamic changes (Extended Data Fig. 4). We found no association between plateau IgG levels and the clinical characteristics of the patients (Extended Data Fig. 5a–d). We next analyzed whether the criteria for confirmation of MERS-CoV infection

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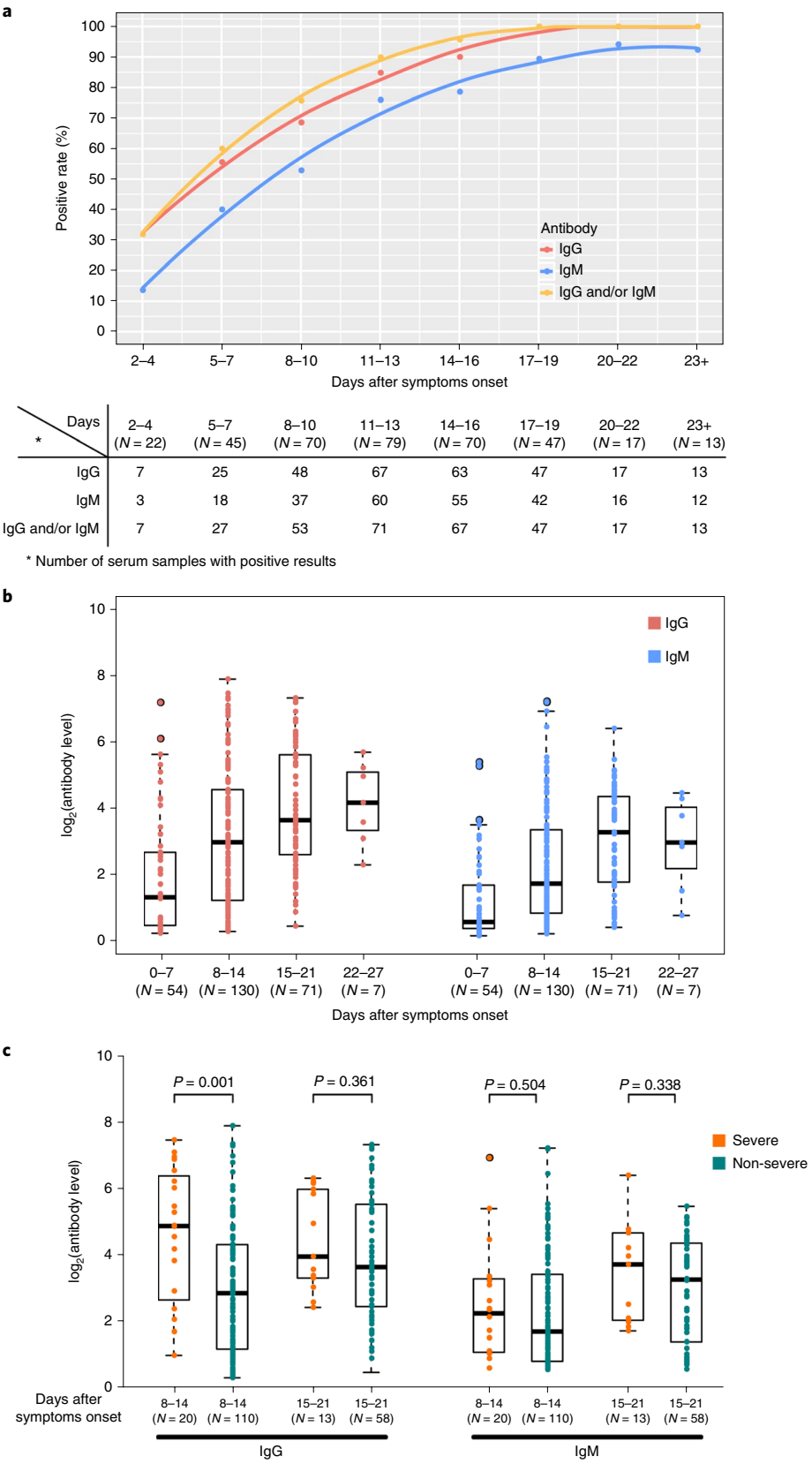

Days / *	2–4 (N = 22)	5–7 (N = 45)	8–10 (N = 70)	11–13 (N = 79)	14–16 (N = 70)	17–19 (N = 47)	20–22 (N = 17)	23+ (N = 13)
IgG	7	25	48	67	63	47	17	13
IgM	3	18	37	60	55	42	16	12
IgG and/or IgM	7	27	53	71	67	47	17	13

* Number of serum samples with positive results

Fig. 1 | Antibody responses against SARS-CoV-2. a, Graph of positive rates of virus-specific IgG and IgM versus days after symptom onset in 363 serum samples from 262 patients. **b**, Levels of antibodies against SARS-CoV-2 in patients at different times after symptom onset. **c**, Comparison of the level of antibodies against SARS-CoV-2 between severe and non-severe patients. The boxplots in **b** and **c** show medians (middle line) and third and first quartiles (boxes), while the whiskers show 1.5× the interquartile range (IQR) above and below the box. Numbers of patients (*N*) are shown underneath. *P* values were determined with unpaired, two-sided Mann–Whitney *U*-test.

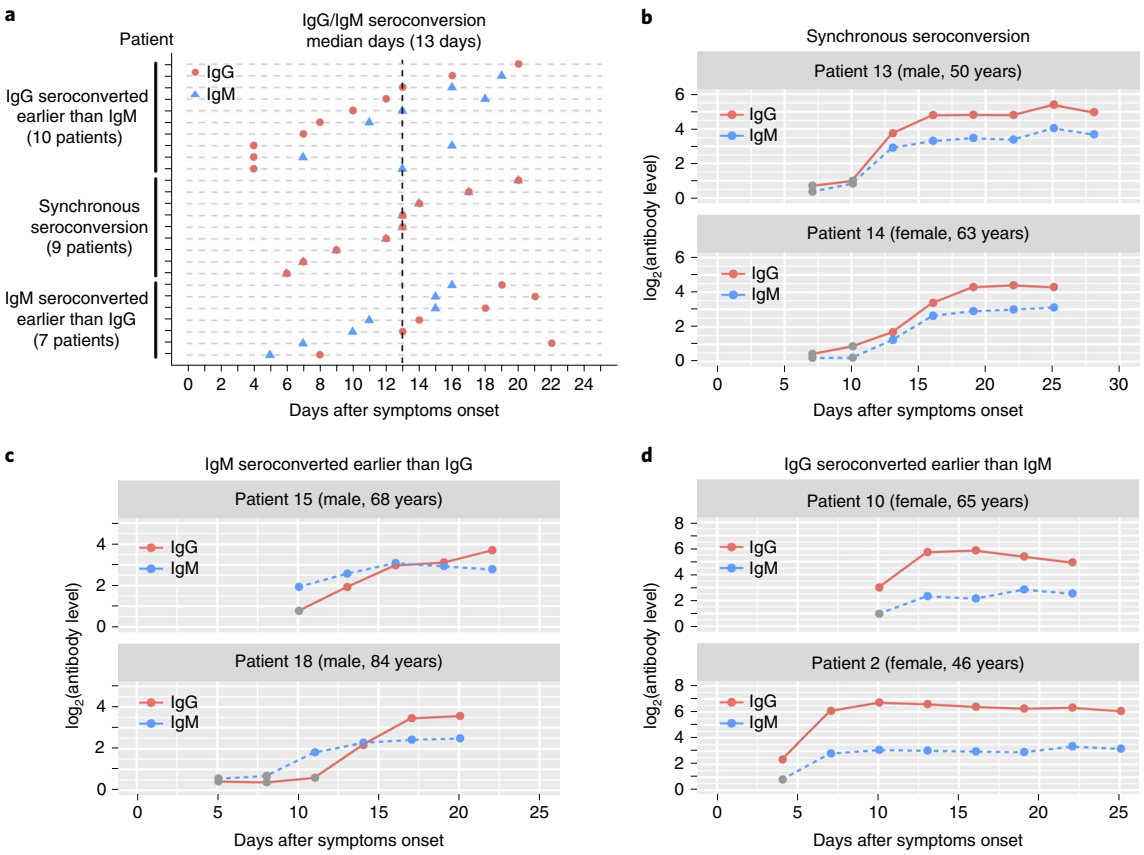

Fig. 2 | Seroconversion time of the antibodies against SARS-CoV-2. a, Seroconversion type of 26 patients who were initially seronegative during the observation period. The days of seroconversion for each patient are plotted. **b–d**, Six representative examples of the three seroconversion type: synchronous seroconversion of IgG and IgM (**b**), IgM seroconversion earlier than that of IgG (**c**) and IgM seroconversion later than that of IgG (**c**).

recommended by WHO, including (1) seroconversion or (2) a fourfold increase in IgG-specific antibody titers, are suitable for the diagnosis of COVID-19 (using paired samples from 41 patients). The initial sample was collected in the first week of illness and the second was collected 2–3 weeks later. Of the patients whose IgG was initially seronegative in the first week of illness, 51.2% (21/41) underwent seroconversion. A total of 18 patients were initially seropositive in the first week of illness; of these, eight patients had a fourfold increase in virus-specific IgG titers (Extended Data Fig. 6). Overall, 70.7% (29/41) of the patients with COVID-19 met the criteria of IgG seroconversion and/or fourfold increase or greater in the IgG titers.

To investigate whether serology testing could help identify patients with COVID-19, we screened 52 suspected cases in patients who displayed symptoms of COVID-19 or abnormal radiological findings and for whom testing for viral RNA was negative in at least two sequential samples. Of the 52 suspected cases, four had virus-specific IgG or IgM in the initial samples (Extended Data Fig. 7). Patient 3 had a greater than fourfold increase in IgG titer 3 days after the initial serology testing. Interestingly, patient 3 also tested positive for viral infection by polymerase chain reaction with reverse transcription (RT–PCR) between the two antibody measurements. IgM titer increased over three sequential samples from patient 1 (<4-fold). Patient 4 had 100-fold higher IgG and tenfold higher IgM titers than the cutoff values in two sequential samples. Patient 2 tested positive for both virus-specific IgG and IgM. An increase of IgG and/or IgM in sequential samples or a positive result in a single sample collected 2 weeks after symptoms suggest that these three patients were infected with SARS-CoV-2.

We further demonstrated the application of serology testing in surveillance in a cluster of 164 close contacts of patients with known COVID-19. Sixteen individuals were confirmed to be infected with SARS-CoV-2 by RT–PCR, with three cases reporting no symptoms. The other 148 individuals had negative RT–PCR results and no symptoms (Extended Data Fig. 8). Serum samples were collected from these 164 individuals for antibody tests ~30 days after exposure. The 16 RT–PCR-confirmed cases were all positive for virus-specific IgG and/or IgM. Moreover, 7 of the 148 individuals with negative RT–PCR results had positive virus-specific IgG and/or IgM, indicating that 4.3% (7/164) of the close contacts were missed by the nucleic acid test. Ten of the 164 close contacts who had positive virus-specific IgG and/or IgM were asymptomatic.

Our study showed that the criteria for the confirmation of MERS-CoV infection are suitable for most patients with COVID-19. However, a collection of the first serum sample as early as possible is required for some patients to meet these criteria, because 12.2% (5/41) of the patients had already plateaued in IgG titer within 7 days of symptom onset (Extended Data Fig. 6). For those patients who were not sampled during the ideal window, repeated serological tests would be needed to confirm an antibody response to SARS-CoV-2 infection.

Our study has some limitations. First, we did not test samples for virus neutralization and therefore the neutralizing activities of the detected IgG antibodies are unknown. Second, due to the small sample size of patients in severe and critical condition, it is difficult to determine the association between antibody response and clinical course.

RT–PCR-based viral RNA detection is sensitive and can effectively confirm early SARS-CoV2 infection[8]. Our data indicate that virus-specificantibodydetectionforCOVID-19couldbeimportant(1)

as a complement to nucleic acid testing for the diagnosis of suspected cases with negative RT–PCR results and (2) in surveying for asymptomatic infection in close contacts. Confirming suspected COVID-19 cases as early as possible with the help of serological testing could reduce exposure risk during repeated sampling and save valuable RT–PCR tests. In our small-scale survey, seven cases with negative nucleic acid results and no symptoms showed positive IgG and/or IgM. This highlights the importance of serological testing to achieve more accurate estimates of the extent of the COVID-19 pandemic.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41591-020-0897-1.

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Methods

Study design. A total of 285 patients with COVID-19 were enrolled in this cross-sectional study from three designated hospitals in Chongqing, a province-level municipality adjacent to Hubei Province, which was the starting point and epicenter of the COVID-19 epidemic. These three hospitals—Chongqing Three Gorges Central Hospital (TGH), Yongchuan Hospital Affiliated to Chongqing Medical University (CQMU) (YCH) and Chongqing Public Health Medical Center (CQPHMC)—were assigned by the Chongqing municipal people's government to admit patients from the three designated areas. All enrolled patients were confirmed to be infected with SARS-CoV-2 by RT–PCR assays on nasal and pharyngeal swab specimens. The median age of these enrolled patients was 47 years (IQR, 34–56 years) and 55.4% were males. Among them, 250 patients had an epidemiological history, while 262 patients had a clear record of symptom onset and 70 patients had multiple serum samples. A total of 363 serum samples from patients with a clear symptom onset history were included in the analysis. Of the 285 patients, 39 were classified as in a severe or critical condition according to the Diagnosis and Treatment Protocol for Novel Coronavirus Pneumonia (Trial Version 7), released by the National Health Commission & State Administration of Traditional Chinese Medicine. For the follow-up cohort, serum samples from 63 patients at YCH were taken at 3-day intervals from 8 February 2020 until hospital discharge. To analyze whether the serological criteria for MERS-CoV confirmation recommended by WHO were suitable for the diagnosis of COVID-19, two inclusion criteria were set to screen patients: (1) first serum sample collected within the first week of illness onset or (2) first serum sample collected within at least 7 days of illness onset but with negative IgG. Thirty-four patients met criterion 1 and seven patients met criterion 2.

To evaluate the potential of the serological test in COVID-19 diagnosis, we enrolled 52 patients with suspected COVID-19 admitted to Wanzhou People's Hospital (Chongqing, China) who had respiratory symptoms or abnormal pulmonary imaging, but negative RT–PCR results in at least two sequential tests. Serum samples were collected at the time indicated in Extended Data Fig. 7 and antibodies against SARS-CoV-2 were tested.

A serological survey was performed in a cluster of close contacts composed of 164 individuals, identified by the local center for disease control and prevention (Wanzhou, Chongqing). A couple who had traveled back from Wuhan city, and who were confirmed to be SARS-CoV-2 infected on 4 February 2020, were deemed the first-generation patients in this contact network. All other cases in this cohort had close contact (either directly or indirectly) with this couple in the period from 20 January to 6 February 2020. On 1 March, serum samples were collected from these 164 cases for antibody tests.

Definitions. Patients with epidemiologic history were defined as follows: Wuhan residents; recently been to Wuhan (30 days preceding symptom onset); local resident who had contact with confirmed cases. Seroconversion was defined as a transition of the test results for IgG or IgM against SARS-CoV-2 from negative to positive results in sequential samples. Antibody levels were presented as the measured chemiluminescence values divided by the cutoff (absorbance/cutoff, S/CO): $S/CO > 1$ was defined as positive and $S/CO \leq 1$ as negative.

Detection of IgG and IgM against SARS-CoV-2. To measure the level of IgG and IgM against SARS-CoV-2, serum samples were collected from the patients. All serum samples were inactivated at 56 °C for 30 min and stored at −20 °C before testing. IgG and IgM against SARS-CoV-2 in plasma samples were tested using MCLIA kits supplied by Bioscience Co. (approved by the China National Medical Products Administration; approval numbers 20203400183(IgG) and 20203400182(IgM)), according to the manufacturer's instructions. MCLIA for IgG or IgM detection was developed based on a double-antibody sandwich immunoassay. The recombinant antigens containing the nucleoprotein and a peptide from the spike protein of SARS-CoV-2 were conjugated with FITC and immobilized on anti-FITC antibody-conjugated magnetic particles. Alkaline phosphatase conjugated anti-human IgG/IgM antibody was used as the detection antibody. The tests were conducted on an automated magnetic chemiluminescence analyzer (Axceed 260, Bioscience) according to the manufacturer's instructions. All tests were performed under strict biosafety conditions. The antibody titer was tested once per serum sample. Antibody levels are presented as the measured chemiluminescence values divided by the cutoff (S/CO). The cutoff value of this test was defined by receiver operating characteristic curves. Antibody levels in the figures were calculated as $\log_2(S/CO + 1)$.

Performance evaluation of the SARS-CoV-2-specific IgG/IgM detection assay. The precision and reproducibility of the MCLIA kits were first evaluated by the National Institutes for Food and Drug Control. Moreover, 30 serum samples from patients with COVID-19 showing different titers of IgG (range 0.43–187.82) and IgM (range 0.26–24.02) were tested. Each individual sample was tested in three independent experiments, and the coefficient of variation (CV) was used to evaluate the precision of the assay. Finally, 46 serum samples from patients with COVID-19 were assessed using different batches of the diagnostic kit for SARS-CoV-2-specific IgG or IgM antibody; reproducibility was calculated based on the results from two batch experiments.

Cross-reactivity of antigens from SARS-CoV and SARS-CoV-2. Two recombinant SARS-CoV nucleocapsid (N) proteins from two different sources (Sino Biological, cat. no. 40143-V08B; Biorbyt, cat. no. orb82478), the recombinant S1 subunit of the SARS-CoV spike (Sino Biological, cat. no. 40150-V08B1) and the homemade recombinant N protein of SARS-CoV-2 were used in a chemiluminescence enzyme immunoassay (CLEIA), respectively. The concentration of antigens used for plate coating was 0.5 μg ml^{-1}. The dilution of alkaline phosphatase conjugated goat anti-human IgG antibody was 1:2,500. Five serum samples from patients with COVID-19 and five serum samples from healthy controls were diluted (1:50) and tested using CLEIA assays. The binding ability of antibody to antigen in a sample was measured in relative luminescence units.

Statistical analyses. Continuous variables are expressed as the median (IQR) and were compared with the Mann–Whitney *U*-test. Categorical variables are expressed as numbers (%) and were compared by Fisher's exact test. A P value of <0.05 was considered statistically significant. Statistical analyses were performed using R software, version 3.6.0.

Ethical approval. The study was approved by the Ethics Commission of Chongqing Medical University (ref. no. 2020003). Written informed consent was waived by the Ethics Commission of the designated hospital for emerging infectious diseases.

Reporting Summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

Raw data in this study are provided in the Supplementary Dataset. Additional supporting data are available from the corresponding authors on request. All requests for raw and analyzed data and materials will be reviewed by the corresponding authors to verify whether the request is subject to any intellectual property or confidentiality obligations. Source data for Fig. 1 and Extended Data Figs. 1 and 5 are available online.

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Author contributions

Conceptualization was provided by A.-L.H. The methodology was developed by X.-F.C., D.-Q.W., P. Liu, Q.-X.L., K.D. and M.-M.Z. Investigations were carried out by Q.-X.L., H.-J.D., J.C., J.-L.H., B.-Z.L., G.-C.W., K.D., Y.-K.C. and Y.H. The original draft of the manuscript was written by Q.-X.L., H.-J.D., J.C. and J.-L.H. Review and editing of the manuscript were carried out by Q.-X.L., H.-J.D., J.C., J.-L.H., Y.L. and A.-L.H. Funding acquisition was performed by A.-L.H. and J.-L.H. Resources were provided by P. Liao, Y.-Y.X., L.-H.Y., Z.M., F.G., X.-M.L., X.-X.Z., Z.-J.L., K.W., X.-L.Z., W.-G.T., C.-C.N., Q.-J.Y., J.-L.X., H.-X.D., H.-W.L., C.-H.L., X.-H.L., .S.-B.W., X.-P.C., Z.Z., J.W., C.-J.X., X.-F.L., L.W., X.-J.T., Y.Z., J.-F.Q., X.-M.L., L.H., J.-J.L., D.-C.Z., F.Z., J.-H.R., N.T., J.Y. and Q.L. A.-L.H. provided supervision.

Competing interests

The authors declare no competing interests.

Additional information

Extended data is available for this paper at https://doi.org/10.1038/s41591-020-0897-1.

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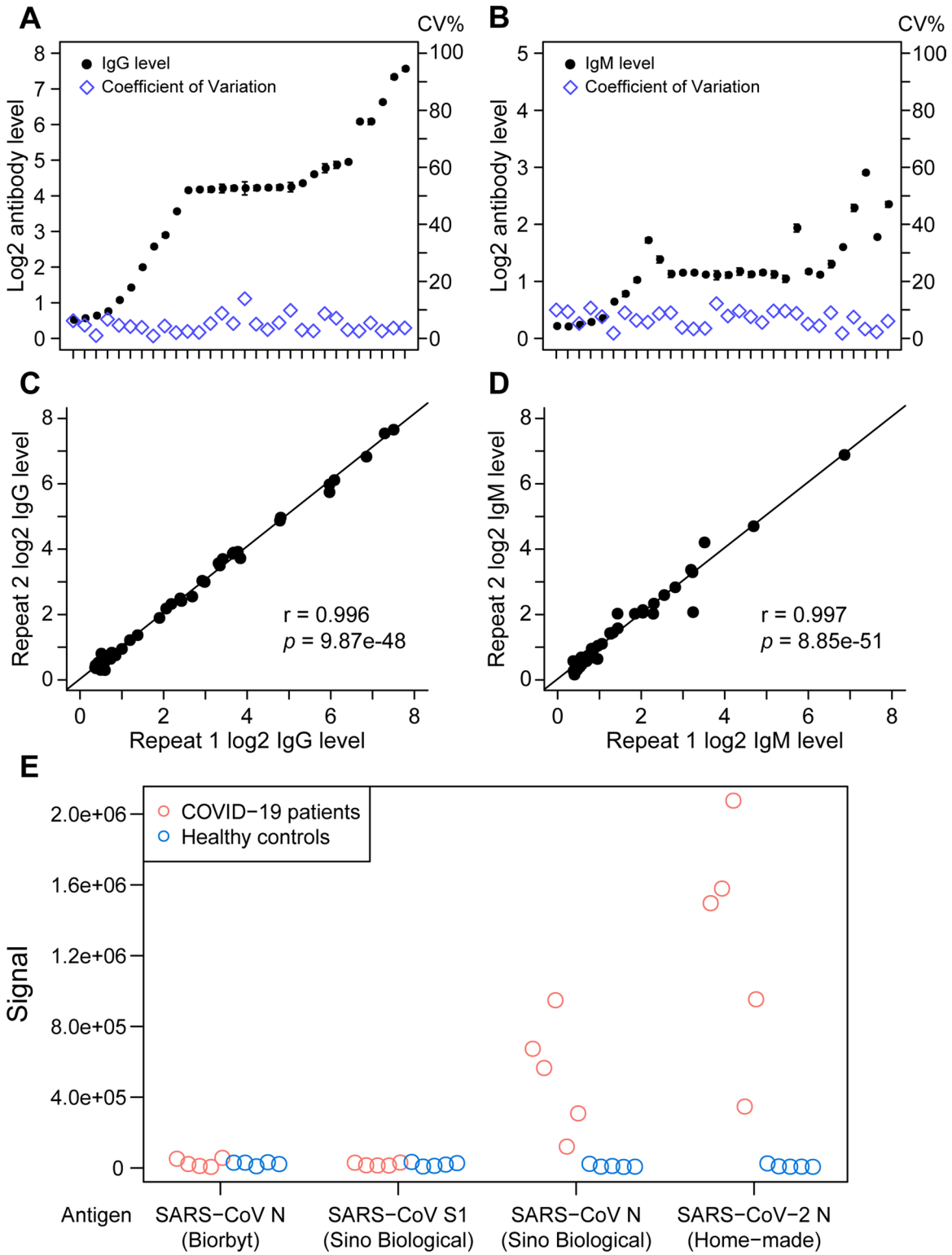
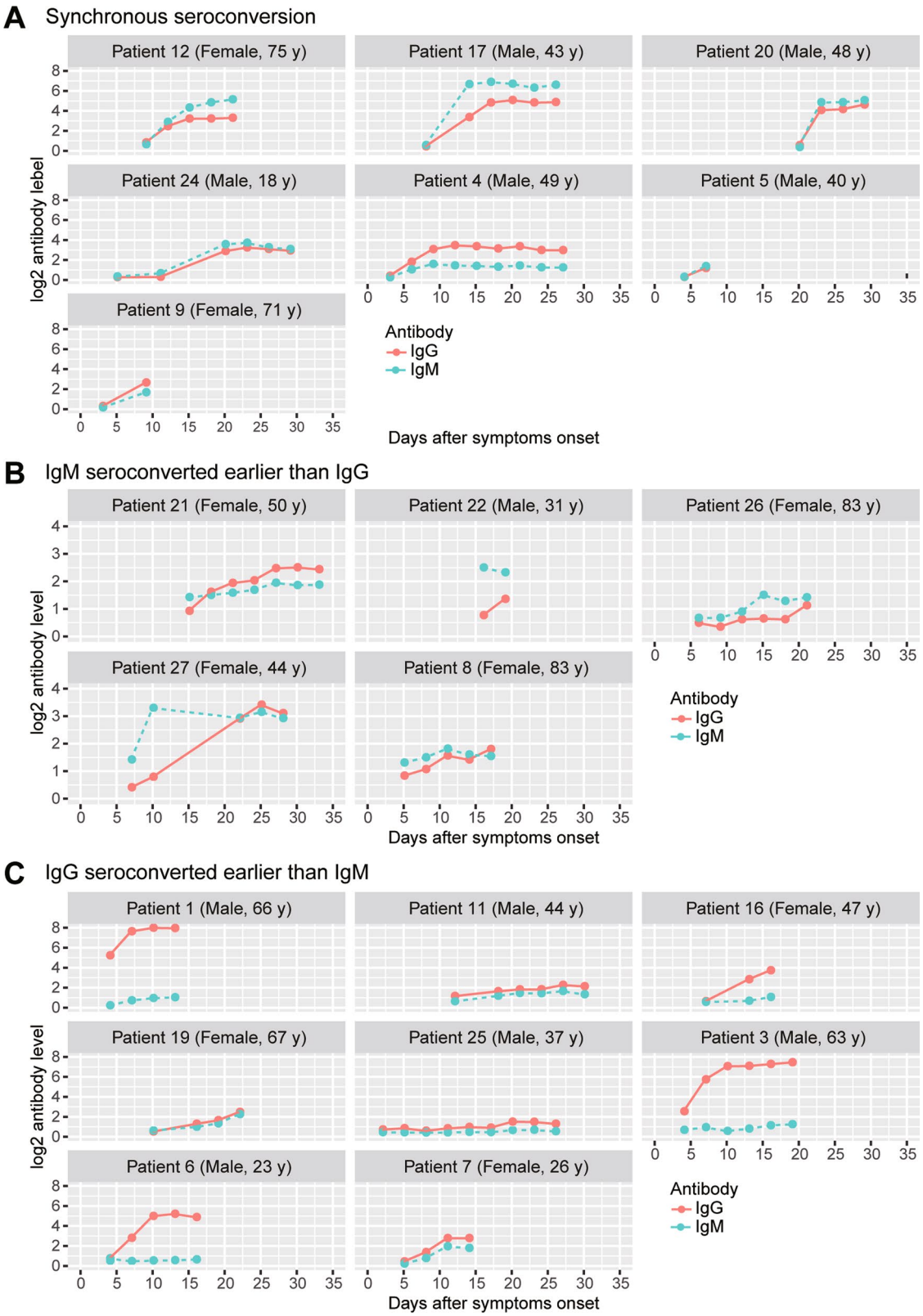
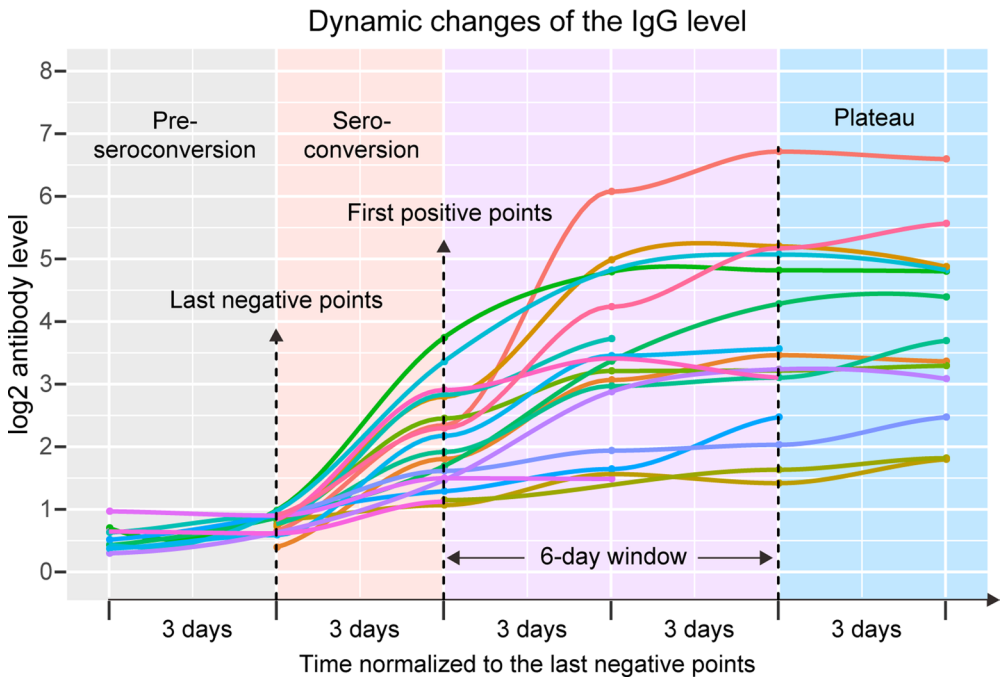


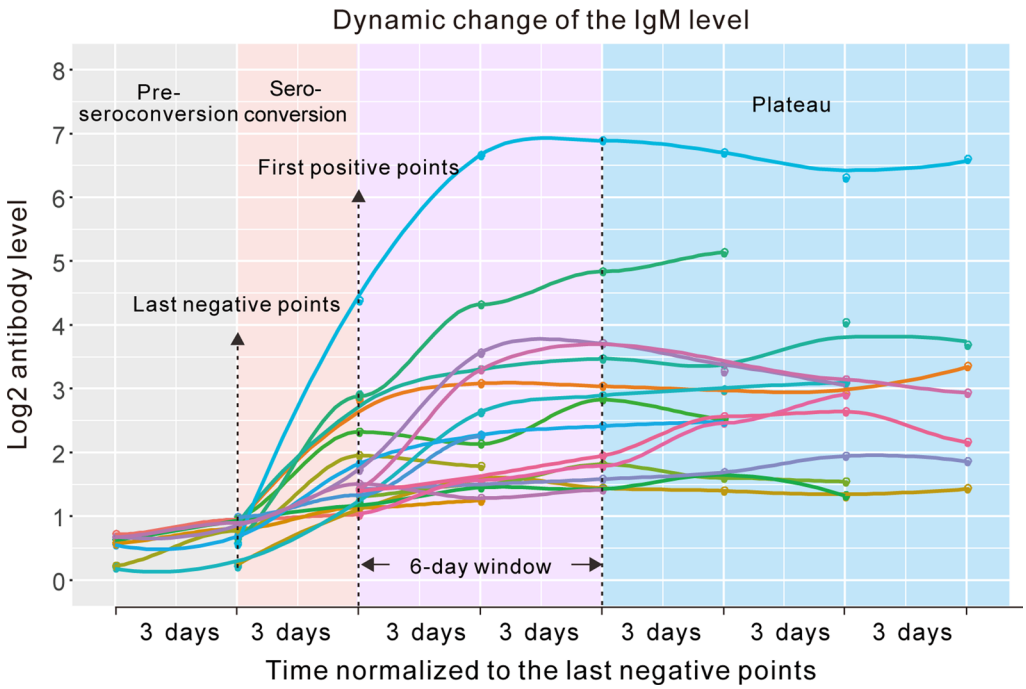
Extended Data Fig. 1 | The performance evaluation of the SARS-CoV-2 specific IgG/IgM detection assay. a,b. Thirty serum sample from COVID-19 patients showing different titers of IgG (**a**) (range from 0.43 to 187.82) and IgM (**b**) (range from 0.26 to 24.02) were tested. Each individual sample was tested in three independent experiment. CVs of titers of certain sample were calculated and presented. **c,d**. The correlation analysis of IgG and IgM titers serum samples from COVID-19 patients from 2 independent experiment. Forty-six serum samples from COVID-19 patients were detected using different batches of diagnostic kit for SARS-CoV-2 IgG (**c**) or IgM (**d**) antibody. Pearson correlation coefficients (R) are depicted in plots. For IgG, r = 0.996, *p* = 9.87e-48; For IgM, r = 0.997, *p* = 8.85e-51. **e**. The reactivity between COVID-19 patient serums (N = 5) and SARS-CoV S1, N (two sources) and SARS-CoV-2 N protein were measured by ELISA. Serum samples from COVID-19 patients showed no cross-binding to SARS-CoV S1 antigen, while the reactivity between COVID-19 patient serums and SARS-CoV N antigen from different sources was inconsistent.



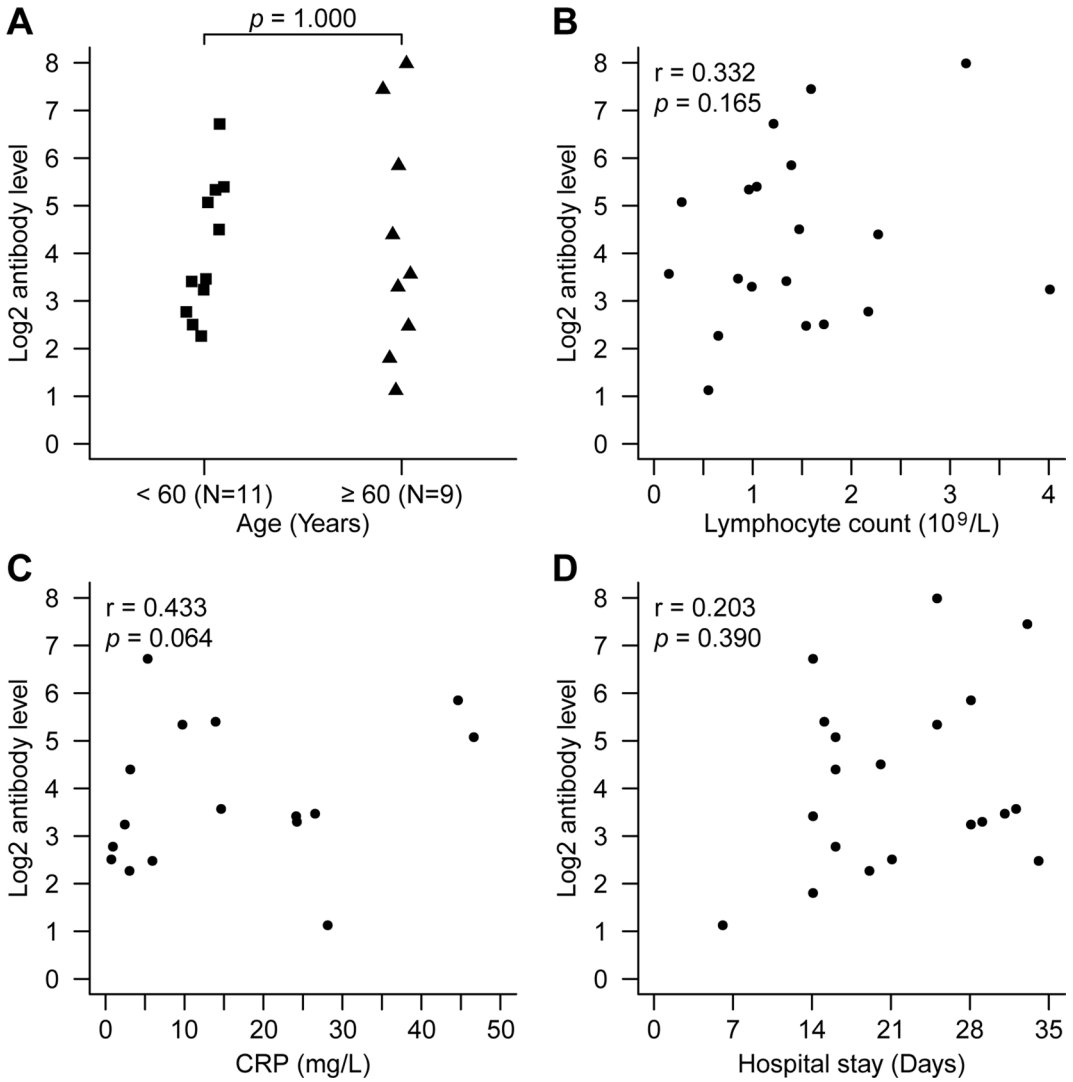
Extended Data Fig. 2 | Three types of seroconversion. a. Patients with a synchronous seroconversion of IgG and IgM (N = 7). **b**. Seroconversion for IgG occurred later than that for IgM(N = 5). **c**. Seroconversion for IgG occurred earlier than that for IgM (N = 8).



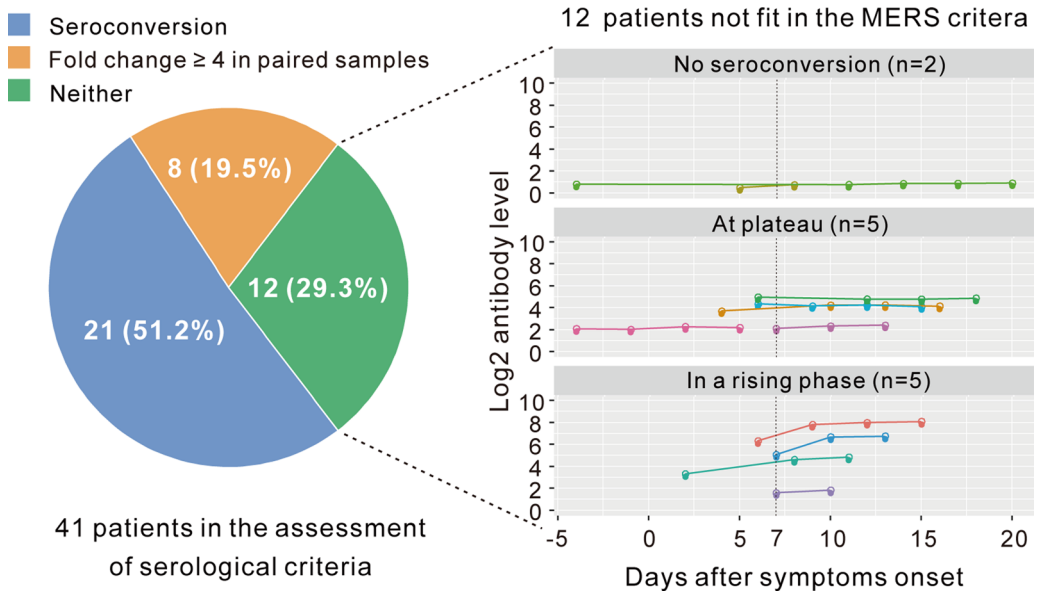
Extended Data Fig. 3 | Dynamic changes of the SARS-CoV-2 specific IgG. Time course of the virus-specific IgG level in 19 patients experienced IgG titer plateau. IgG in each patient reached plateau within 6 days since IgG became positive.



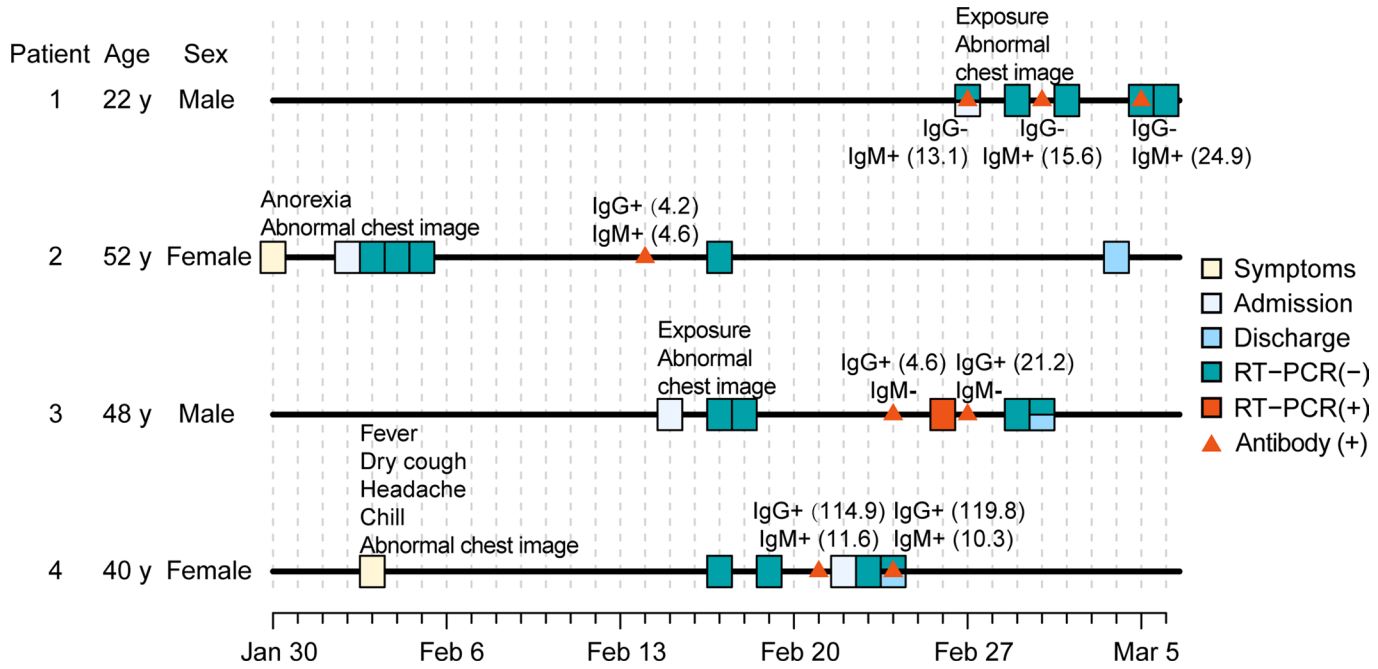
Extended Data Fig. 4 | Dynamic changes of the SARS-CoV-2 specific IgM. Time course of the virus-specific IgM level in 20 patients experienced IgM titer plateau. IgM in each patient reached plateau within 6 days since IgM became positive.



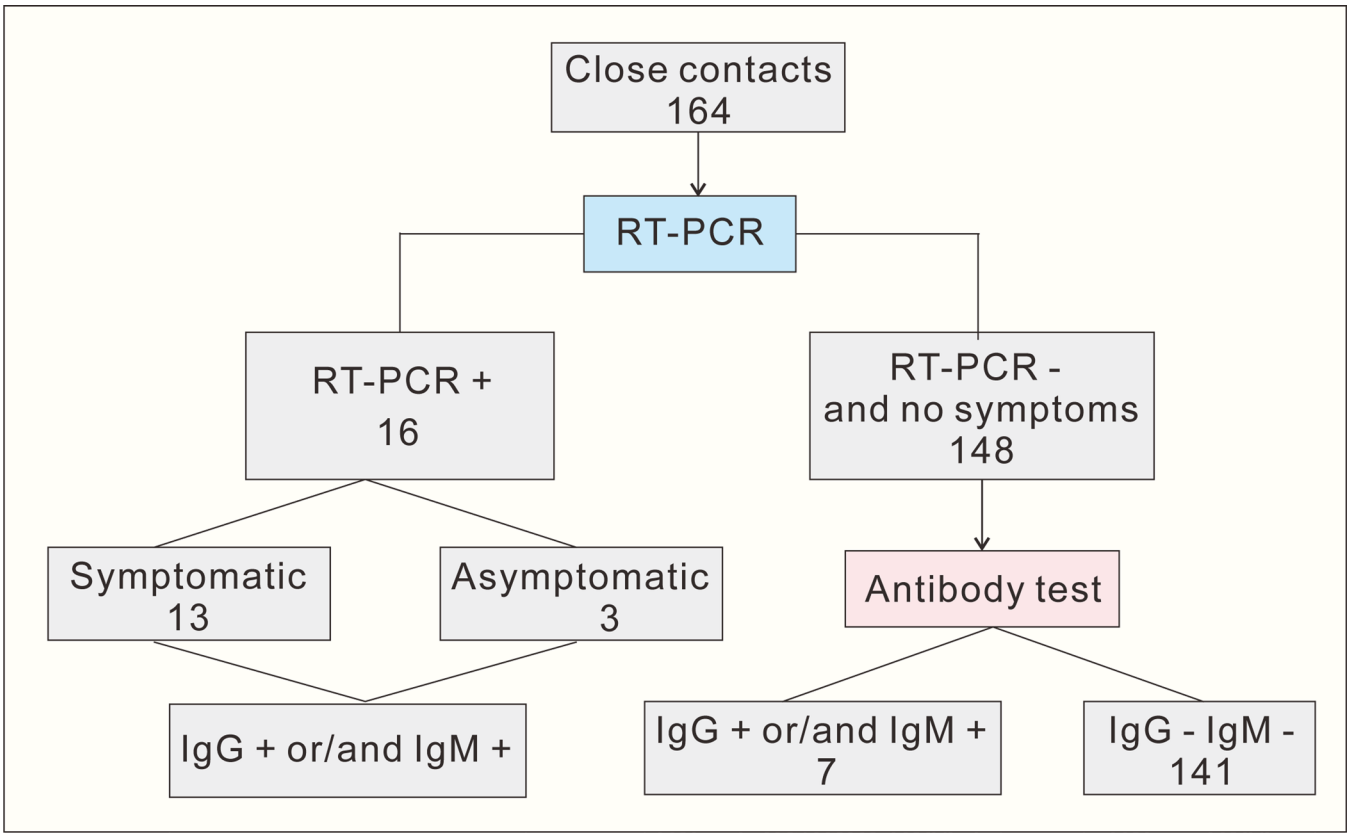
Extended Data Fig. 5 | The association between the IgG levels at the plateau and clinical characteristics of the COVID-19 patients. a. No significant difference in the IgG levels at the plateau was found between < 60 y group (N = 11) and ≥ 60 y group (N = 9). Unpaired, two-sided Mann-Whitney U test, p = 1.000. **b–d**. No association was found between the IgG levels at the plateau and lymphocyte count (**b**) or CRP (**c**) or hospital stay (**d**) of the patients (N = 20). Pearson correlation coefficients (r) and *p* value are depicted in plots.



Extended Data Fig. 6 | The assessment of MERS serological criteria for COVID-19. The assessment of MERS serological criteria for COVID-19 confirmation were carried out in 41 patients with sequential samples. All 41 patients were classified into three groups based on IgG change from sequential samples, including (1) seroconversion, (2) fold change ≥ 4-fold in paired samples, (3) neither.



Extended Data Fig. 7 | Serology testing in identification of COVID-19 from 52 suspected cases. Chronology of symptom onset, RT-PCR and serology testing in 4 cases developing positive IgG or/and IgM were presented.



Extended Data Fig. 8 | Serological survey in close contacts with COVID-19 patients. A cluster of 164 close contacts of known COVID-19 patients were tested by RT-PCR followed by serology testing. Serum samples were collected from these 164 individuals for antibody tests approximately 30 days after exposure.

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Reporting Summary

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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 commercial, open source software, custom code was used in data collection.
Data analysis	Statistical analyses were performed using R software, version 3.6.0.

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

Raw data in this study are provided in the Supplementary Dataset. Additional supporting data are available from the corresponding authors on request. All request for raw and analyzed data and materials will be reviewed by the corresponding authors to verify whether the request is subject to any intellectual property or confidentiality obligations.

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	We did not perform statistical analyses to predetermine sample sizes. By 12th Feb, 2020, a total of 426 confirmed COVID-19 patients were admitted to three designated hospitals. 124 patients were reluctant to offer their blood samples while 17 Samples from 17 patients are not qualified for serology testing (hemolysis, lipemia). Therefore, 285 COVID-19 patients were included in this study.
Data exclusions	All patients and serum were included.
Replication	Precision and reproducibility experiments were conducted in triplicate or duplicate. The magnetic chemiluminescence enzyme immunoassay (MCLIA) for virus-specific antibody detection was proved with admirable precision and reproducibility. The antibody titer was tested one time for each serum sample in our study.
Randomization	Our study is an observation study, so no randomization is needed here.
Blinding	Serum extraction and antibody detection were performed independently by researchers blind to samples information, data analysis were performed by two trained researchers.

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	Alkaline Phosphatase–conjugated Affinipure Goat Anti-Human IgG, Catalog number: SA00002-8, Proteintech.
Validation	The antibody was only used for the application as indicated and organisms verified by the manufactures.

Human research participants

Policy information about studies involving human research participants

Population characteristics	For the cross-sectional cohort, the median age was 47 years, ranged from 7 months to 84 years, and 158 of 285 were male. For the follow up cohort, the median age was 49 ranged from 11 to 84 years, and 36 of 63 were male.
Recruitment	1) Confirmed COVID-19 patients (two positive RT-PCR results from nasal and pharyngeal swab specimens). 2) Patients were recruited from 3 designated hospitals in Chongqing city, China. 3) Patients agreed to be enrolled.
Ethics oversight	Chongqing Medical University

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

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SUPPLEMENTARY INFORMATION

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In the format provided by the authors and unedited.

Antibody responses to SARS-CoV-2 in patients with COVID-19

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Supplemental Information

Supplementary Table 1. Baseline characteristics of patients from the cross-sectional study.

	Number (%)			
	All (N=285)	ICU (N=39)	Non-ICU (N=246)	*p* value
Age - years (median, IQR)	47 (37-56)	54 (46-77)	46 (36-55)	**1.63E-04**
Gender				
Female	127 (44.6%)	18 (46.2%)	109 (44.3%)	0.863
Male	158 (55.4%)	21 (53.8%)	137 (55.7%)	
Epidemiologic history				
From Wuhan	115 (40.3%)	15 (38.5%)	100 (40.6%)	0.243
close contacts	135 (47.4%)	16 (41.0%)	119 (48.4%)	
Unknown	35 (12.3%)	8 (20.5%)	27 (11.0%)	
Incubation period - days (median, IQR)	8 (5-12)	9 (8-10)	7 (5-12)	0.586
Comorbidities				
Hypertension	41 (14.4%)	7 (17.9%)	34 (13.8%)	0.468
Cardiovascular disease	9 (3.2%)	3 (7.7%)	6 (2.4%)	0.111
Diabetes	22 (7.7%)	7 (17.9%)	15 (6.1%)	**0.019**
Malignancy	3 (1.1%)	1 (2.6%)	2 (0.8%)	0.358
COPD	4 (1.4%)	2 (5.1%)	2 (0.8%)	0.092
Chronic kidney disease	2 (0.7%)	0 (0.0%)	2 (0.8%)	1
Chronic liver disease	17 (6.0%)	5 (12.8%)	12 (4.9%)	0.066
Hyoxemia	4 (1.4%)	2 (5.1%)	2 (0.8%)	0.092
Tuberculosis	6 (2.1%)	1 (2.6%)	5 (2.0%)	0.59
Total	87 (30.5%)	19 (48.7%)	68 (27.6%)	**0.014**
Signs and symptoms				
Fever	168 (58.9%)	24 (61.5%)	144 (58.5%)	0.861
Fatigue	79 (27.7%)	20 (51.3%)	59 (24.0%)	**8.52E-04**
Dry cough	157 (55.1%)	22 (56.1%)	135 (54.9%)	0.864
Anorexia	66 (23.2%)	18 (46.2%)	48 (19.5%)	**7.56E-04**
Myalgia	35 (12.3%)	5 (12.8%)	30 (12.2%)	1
Dypnea	19 (6.7%)	14 (35.9%)	5 (2.0%)	**5.76E-10**
Expectoration	66 (23.2%)	14 (35.9%)	52 (21.1%)	0.064
Pharyngalgia	30 (10.5%)	2 (5.1%)	28 (11.4%)	0.397
Diarrhea	25 (8.8%)	4 (10.3%)	21 (8.5%)	0.76
Nausea	17 (6.0%)	4 (10.3%)	13 (5.3%)	0.265
Dizziness	24 (8.4%)	6 (15.4%)	18 (7.3%)	0.115
Headache	30 (10.5%)	4 (10.3%)	26 (10.6%)	1
Vomiting	7 (2.5%)	2 (5.1%)	5 (2.0%)	0.246
Abdominal pain	6 (2.1%)	2 (5.1%)	4 (1.6%)	0.192
Chill	43 (15.1%)	7 (17.9%)	36 (14.6%)	0.63
Nasal congestion	10 (3.5%)	2 (5.1%)	8 (3.3%)	0.632

Rhinorrhea	13 (4.6%)	2 (5.1%)	11 (4.5%)	0.694
Chest stuffiness	42 (14.7%)	8 (20.5%)	34 (13.8%)	0.328
Onset of symptom to (median day, IQR)				
Hospital admission	6 (3-8)	7 (5-9)	5 (3-8)	**0.024**
Severe	8 (6-11)	8 (6-11)	NA	NA
Heart rate (median bpm, IQR)	88 (80-97)	89 (84-96)	87 (78-97)	0.345
Respiratory rate (median, IQR)	20 (20-21)	22 (20-25)	20 (20-21)	**4.04E-04**
Mean arterial pressure, (median mm Hg, IQR)	93.3 (85.7-103.3)	94.9 (86.0-100.7)	93.3 (85.9-103.5)	0.809

COPD, chronic obstructive pulmonary disease.

Continuous variables were expressed as the median (interquartile range, IQR) and compared between ICU and non-ICU groups with the unpaired, two-sided Mann-Whitney U test. Categorical variables were expressed as numbers (%) and compared between ICU and non-ICU groups by the Fisher's exact test.

Supplementary Table 2. Laboratory findings of the patients from the cross-sectional study on admission to hospital.

	Median, IQR				
	Normal Range	All (N=285)	severe (N=39)	Non-severe (N=246)	*p* value
White blood cell count,$\times 10^{9}$ /L	3.5~9.5	5.3 (4.5-6.6)	6.3 (4.8-9.5)	5.2 (4.4-6.5)	**6.70E-03**
Neutrophil count, $\times 10^{9}$ /L	1.8~6.3	3.5 (2.6-4.6)	4.6 (3.7-7.8)	3.4 (2.5-4.3)	**1.19E-05**
Lymphocyte count, $\times 10^{9}$ /L	1.1~3.2	1.2 (0.9-1.6)	0.8 (0.6-1.1)	1.3 (1.0-1.6)	**2.15E-07**
Monocyte count, $\times 10^{9}$ /L	0.1~0.6	0.4 (0.3-0.5)	0.4 (0.3-0.6)	0.4 (0.3-0.5)	7.74E-01
Platelet count, $\times 10^{9}$ /L	125.00~350.00	210.0 (146.0-265.0)	203.0 (129.0-297.5)	210.5 (149.0-259.8.0)	7.35E-01
Prothrombin time, s	8~14	11.4 (10.8-12.5)	11.7 (11.2-12.5)	11.3 (10.8-12.5)	9.41E-02
Activated partial thromboplastin time, s	20~40	30.0 (26.0-37.5)	29.3 (25.5-35.4)	30.0 (26.0-37.7)	6.52E-01
D-dimer, mg/L	<0.55	0.4 (0.2-0.6)	0.7 (0.6-1.3)	0.3 (0.2-0.5)	**1.64E-09**
Creatine kinase, U/L	40~200	57.0 (39.3-92.3)	69.5 (39.8-128.8)	56.6 (39.4-86.5)	1.43E-01
Lactate dehydrogenase, U/L	120~250	221.5 (168.0-266.8)	332.5 (231.3-383.5)	202.0 (162.3-251.0)	**1.46E-09**
Alanine aminotransferase, U/L	7~40	22.7 (14.9-41.3)	32.3 (20.1-48.5)	22.0 (14.6-39.0)	**3.00E-02**
Aspartate aminotransferase, U/L	13~35	23.7 (18.0-35.0)	32.0 (22.4-45.0)	22.7 (17.8-33.0)	**2.42E-03**
Total bilirubin, μmol/L	0~21	10.7 (7.1-16.8)	12.0 (8.2-16.9)	10.6 (7.0-16.7)	1.84E-01
Creatinine, μmol/L	57~111	65.5 (56.0-79.0)	62.0 (53.5-72.5)	66.5 (57.0-80.0)	5.85E-02
Hypersensitive troponinI, ng/mL	0.001~0.014	0.005 (0.004-0.008)	0.007 (0.005-0.012)	0.004 (0.003-0.006)	**1.96E-03**
Procalcitonin, ng/mL	<0.046	0.050 (0.031-0.072)	0.068 (0.048-0.100)	0.050 (0.029-0.070)	**7.70E-04**
C-reactive protein, mg/L	0~5	9.1 (2.7-33.3)	18.8 (5.1-63.7)	8.0 (2.5-29.9)	**8.09E-03**

Continuous variables were expressed as the median (interquartile range, IQR) and compared

between severe and non-severe groups with the unpaired, two-sided Mann-Whitney U test.

Supplementary Table 3. A summary of the CVs of the assay for the detection of SARS-CoV-2 specific IgG or IgM antibody from the reports of National Institutes for Food and Drug Control.

Antibody	CV of within-run	CV of between-run	Report number
IgM	4%	7%	RZ202000929
IgM	5%	7%	RZ202000930
IgM	5%	7%	RZ202000931
IgG	6%	6%	RZ202000932
IgG	6%	6%	RZ202000933
IgG	2%	6%	RZ202000934

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Corresponding author(s): Ai-Long Huang

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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.

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☒	☐ Clinical data

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