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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 our Editorial Policies 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	The medical imaging data is the raw output of the CT machines, which is in the Digital Imaging and Communication in Medicine (DICOM) format. Clinical metrics and follow-up questionnaires did not include any software for the data collection.
Data analysis	The data was analyzed with Python 3.6.7. The deep-learning module in this work was written with Pytorch 1.9.0. Our program is publicly available at https://github.com/LongxiZhou/DLPE-method

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 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

We declare that all the data supporting the novel lesions for COVID-19 inpatient and survivors are available at https://github.com/LongxiZhou/DLPE-method; Figure 1-4 in the main text and Supplementary Figure 4, 5, 8, 9, 16 are associated with the raw data.
The dataset for training the DLPE method is owned by Heilongjiang Tuomeng Technology Co. Ltd., Harbin, China, and is available upon request.
The trained DLPE models are available at https://github.com/LongxiZhou/DLPE-method, which can convert CT scans in DICOM into enhanced arrays (remove airways, blood vessels, provide the optimal window), or can be used as state-of-the-art segmentation models for the segmentation of COVID-19 lesions, lungs, airways and blood vessels.

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	The DLPE method is based on accurate segmentations for the lungs, airways and blood vessels. The segmentation models were trained over the dataset containing 3644 CT scans collected from patients from 5 different hospitals. We tested DLPE method on COVID-19 inpatient and survivors, in total 219 CT scans. The DLPE method generated satisfactory enhancement effects for all these scans (especially for patients with faint lesions).
Data exclusions	Data inclusion/exclusion criteria were described in the main text and discussed in details in Supplementary Section 1.1.1. In brief, we excluded data if the CT quality is very low, such as extensive artifacts and noises.
Replication	We tested the robustness of the DLPE method on CT scans collected under varies conditions, e.g., with contrast agents, extensive nosies, etc. The detail information is listed in Supplementary Section 1.1.4, 1.2.10 and 1.4.6.
Randomization	We conducted multi-fold cross validation during our model training.
Blinding	Blinding is not relevant as our study does not involve new clinical trials or group allocation of experimental subjects.

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
☐	☒ Human research participants
☐	☒ Clinical data
☒	☐ Dual use research of concern

Methods

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	COVID-19 patients of severe or critical conditions (requiring supplemental oxygen). These patients were infected from Feb to Apr, 2020. All clinical data were collected in Heilongjiang, China.
Recruitment	COVID-19 patients of severe or critical condition (requiring supplemental oxygen). Time: Feb to Apr, 2020. All clinical data were collected in Heilongjiang, China. Potential biases: we did not include light or mild patients, as these patients did not sample the clinical metrics we wanted to analyze, e.g., PaO2/FiO2 ratio, blood-gas data, etc. The participates were all Chinese and they were infected before the occurrence of the major SARS-CoV-2 variants.
Ethics oversight	The First Affiliated Hospital of Harbin Medical University, China; King Abdullah University of Science and Technology, Saudi Arabia

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	The study does not include new clinical trials. Our study analyzed the existing clinical data.
Study protocol	N/A. The study does not include new clinical trials.
Data collection	Recruitment: COVID-19 patients with severe or critical conditions (requiring supplemental oxygen). Time: Feb to Apr, 2020. All clinical data were collected in Heilongjiang, China.
Outcomes	N/A