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1. Frontiers Policies

1.1. Open Access and Copyright

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1.3. Authorship and Author Responsibilities



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(<http://www.icmje.org/recommendations/browse/roles-and-responsibilities/defining-the-role-of-authors-and-contributors.html>) guidelines which state that, in order to qualify for authorship of a manuscript, the following criteria should be observed:

- substantial contributions to the conception or design of the work; or the acquisition, analysis or interpretation of data for the work;
- drafting the work or revising it critically for important intellectual content;
- provide approval for publication of the content;
- agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Contributors who do not meet these criteria, but nonetheless provided important contributions to the final manuscript, should be included in the acknowledgement section. It is the author's responsibility to get written approval by persons named in the acknowledgment section.

Manuscripts prepared and written by commercial entities (fake-paper factories, "paper mills") on behalf of researchers listed as authors on the manuscript do not meet Frontiers' policies and will not be considered for publication. Frontiers will take proactive actions to reject suspicious manuscripts before peer review.

1.3.1. Author Contributions

In order to provide appropriate credit to all authors, as well as assigning responsibility and accountability for published work, individual contributions should be specified as an



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and is to be included upon submission. It can be up to several sentences long and should briefly describe the tasks of individual authors. Please list only 2 initials for each author, without full stops, but separated by commas (e.g. JC, JS). In the case of two authors with the same initials, please use their middle initial to differentiate between them (e.g. REW, RSW) or second letter of the last name (e.g., RWe, RWa). Please see an example here:

“AB, CZD, and EF contributed to conception and design of the study. AB organized the database. CYD performed the statistical analysis. EF wrote the first draft of the manuscript. GH, IJ, AB, and EF wrote sections of the manuscript. All authors contributed to manuscript revision, read, and approved the submitted version”.

1.3.2. Corresponding Author

The corresponding author takes primary responsibility for communication with the journal and editorial office during the submission process, throughout peer review, and during publication. The corresponding author is also responsible for ensuring that the submission adheres to all journal requirements including, but not exclusive to, details of authorship, study ethics and ethics approval, clinical trial registration documents, and conflict of interest declaration. The corresponding author should also be available post-publication to respond to any queries or critiques.

Requests to modify the author list after submission should be made to the editorial office using the Authorship Change form

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- **Fabrication and falsification:** Frontiers opposes both the fabrication of data or images (i.e. fake or made up data) and falsification of data or images (i.e. the intentional misrepresentation or deceptive manipulation of data).
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- **Plagiarism:** Plagiarism occurs when an author attempts to present previously published work as original content. Every manuscript submitted to Frontiers is screened for textual overlap by the software CrossCheck, powered by iThenticate. Manuscripts found to contain textual overlap are not considered for publication by Frontiers. For



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Frontiers checks all submitted manuscripts for plagiarism and duplication, and publishes only original content. Those manuscripts where plagiarism or duplication is shown to have occurred will not be considered for publication in a Frontiers journal. It is required that all submissions consist of content that has not been published previously. In accordance with COPE guidelines (<http://publicationethics.org/files/International%20standards>) we expect that "original wording taken directly from publications by other researchers should appear in quotation marks with the appropriate citations." This condition also applies to an author's own work.

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Frontiers allows the inclusion of content which first appeared in an author's thesis so long as this is the only form in which it has appeared, is in line with the author's university policy, and can be accessed online. If the thesis is not archived online, it is considered original, unpublished data and is subject to the unpublished data restrictions of some article types. Inclusion of material from theses or dissertations should be noted in the Acknowledgements section of the manuscript AND cited accordingly in the reference list. For some examples, please check our Manuscript Formatting Guidelines (<https://www.frontiersin.org/about/author-guidelines>).



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Manuscripts that first appeared as conference papers must be expanded upon if they are to be considered as original work. Authors are required to add a substantial amount of original content in the form of new raw material (experiments, data) or new treatment of old data sets which lead to original discussion and/or conclusions, providing value that significantly exceeds the original conference version. As a rule of thumb, at least 30% of the content must be original. Authors submitting such work are required to:

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- cite the conference in the Acknowledgements section, or the references section if applicable.

1.4.4. Blogs

Although permissible, extended manuscript content which previously appeared online in non-academic media, e.g. blogs, should be declared at the time of submission in the acknowledgements section of the manuscript.

1.4.5. Preprints

Frontiers' supportive preprint policy encourages full open access at all stages of a research paper, to share and generate knowledge researchers need to support their work. Authors publishing in Frontiers journals may share their work ahead of submission to a peer-reviewed journal, as well as during the Frontiers review process, on repositories or preprint



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1.5. Corrections

Frontiers recognizes our responsibility to correct scientifically relevant errors in previously published articles. Corrections can be submitted if:

- a small portion of an otherwise reliable publication proves to be misleading; OR
- there is an error in a figure that does not alter the conclusions; OR
- there is an error in statistical data not altering conclusions; OR
- there are mislabeled figures; OR
- the wrong slide of microscopy was provided; OR
- if the author / contributor list is incorrect when a deserving author has been omitted or somebody who does not meet authorship criteria has been included.

A correction must be submitted through our submission system (<https://www.frontiersin.org/submission/submit>) (check this link (<https://zendesk.frontiersin.org/hc/en-us/articles/115003295805-How-can-I-add-submit-a-Corrigendum->) for detailed instructions on how to submit a correction), and it is advised to use the following Word and LaTeX templates (https://www.frontiersin.org/design/zip/Frontiers_Corrigend)
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"Corrigendum: Title of original article".

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1.6. Retractions

As a member of the Committee on Publication Ethics (COPE) (<http://publicationethics.org/>), Frontiers abides by their guidelines and recommendations in cases of potential retraction.

Frontiers also abides by two other key principles, as recommended by COPE:

- retractions are not about punishing authors;
- retraction statements should be public and linked to the original, retracted article.

All potential retractions will be judged on their own merits and will be the subject of an internal investigation or, where satisfactory, the recommendations from the institutional investigation of the author(s). Frontiers considers the following reasons as giving cause for concern and potential retraction:

- clear evidence that findings are unreliable, either as a result of misconduct (e.g. data fabrication) or honest error (e.g. miscalculation or experimental error);
- findings have previously been published elsewhere without proper attribution, permission or justification (i.e. cases of redundant publication);
- major plagiarism;



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committee approval;

- legal issues pertaining to the content of the article, e.g. libelous content;
- major authorship issues, i.e. proven or strongly suspected cases of ghostwriting or sold ('gift') authorship;
- politically motivated articles where objectivity is a serious concern;
- the singling out of individuals or organizations for attack;
- faith issues (e.g. intelligent design);
- papers that have made extraordinary claims without concomitant scientific or statistical evidence (e.g. pseudoscience).

Readers who would like to draw the editors' attention to published work that might require retraction should contact the authors of the article and write to the journal, making sure to include copies of all correspondence with authors.

Please find more details on our comments and complaints policy here (<https://www.frontiersin.org/about/publishing-model>).

1.7. Ethical Concerns

For any ethical concerns, please contact us at editorial.office@frontiersin.org (<mailto:editorial.office@frontiersin.org>).

1.8 Territorial descriptions, maps, and affiliations.



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2. Editorial Policies

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All authors and members of Frontiers Editorial Boards are required to disclose any actual and potential conflicts of interest at submission or upon accepting an editorial or review assignment.

The Frontiers review system is designed to guarantee the most transparent and objective editorial and review process, and because the handling editor's and reviewers' names are made public upon the publication of articles, conflicts of interest will be widely apparent.

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during submission. A conflict of interest statement will be automatically generated, included in the generated PDF file for peer review, and in the final publication version of the article.

2.1.1. What Should I Disclose?

As an author, disclosure of any potential conflicts of interest should be done during the submission process. Consider the following questions and make sure you disclose any positive answers:

- Did you or your institution at any time receive payment or services from a third party for any aspect of the submitted work?
- Do you have financial relationships (such as commercial affiliation/employment, funding, intellectual property, etc.) with entities that could be perceived to influence, or that give the appearance of potentially influencing, what you wrote in the submitted work?
- Do you have any patents and/or copyrights, whether pending, issued, licensed, and/or receiving royalties related to the research?
- Do you have other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

If you failed to disclose potential conflicts of interest during submission, or in case of doubt, please contact the Frontiers Editorial Office at editorial.office@frontiersin.org (<mailto:editorial.office@frontiersin.org>) with the details of the potential conflicts as soon as possible.



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*“Author XXXXXXXX was employed by the company
XXXXXXX.*

*The remaining authors declare that the research was
conducted in the absence of any commercial or
financial relationships that could be construed as a
potential conflict of interest”.*

For commercial funding, the role of the funder must be
declared. We recommend the following statements:

*“The authors declare that this study received funding
from XXXXXXXX. The funder had the following
involvement with the study: XXXXXXXX”.*

*“The authors declare that this study
received funding from XXXXXXXX. The funder was not
involved in the study design, collection, analysis,
interpretation of data, the writing of this article or the
decision to submit it for publication”.*

2.1.2. What About Editors and Reviewers?

Handling editors and reviewers will be asked to consider the
following potential conflicts of interest before accepting any
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FAMILY	1. Are any of the authors a spouse or significant other, a member of the same family or a very close personal friend? Review Editors should also not be a member of the same family as the handling editor.
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2. Are you currently hosting or have hosted a Frontiers Research Topic with any of the

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3. Are you currently collaborating or have you collaborated on a research project or a publication with any of the authors within the past 2 years?

4. Are you currently collaborating or have you collaborated with any of the authors as an advisor or in any other direct supervisory capacity in the past five years?

5. Are you currently collaborating or have you collaborated with any of the authors as a student or in any other direct subordinate capacity in the past five years?

Note: Review Editors should not accept assignments if they have a close professional relationship with the handling editor, which in their view could affect the objectivity of the review.

AFFILIATION

6. Are you affiliated with the same institution as any of the authors? If so, has this resulted in interactions, collaborations or mutual interests with the authors that would compromise your impartiality in conducting this review?

7. Are you a current member of a committee or department that coincides with an affiliation with any of the authors?

FINANCIAL

8. Do you have a business or professional partnership with any author?

9. Do you have financial interests or business relations with any organization involved in this research or in the preparation of the manuscript?

10. Do you have any financial interest or competing interests in the content of the manuscript that might affect your ability to perform an objective review?



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2.3.1. Studies Involving Animal Subjects



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In order to protect subject anonymity, identifying information should not be included in the manuscript unless such information is absolutely necessary for scientific purposes AND explicit approval has been granted by the subjects.

2.3.3. Inclusion of Identifiable Human Data

Frontiers follows the ICMJE recommendations (<http://www.icmje.org/recommendations/browse/roles-and-responsibilities/protection-of-research-participants.html>) on the protection of research participants, which state that patients have a right to privacy that should not be violated without informed consent. We require nonessential identifiable details to be omitted from all manuscripts, and written informed consent will be required if there is any doubt that anonymity can be maintained.

It is the responsibility of the researchers and authors to ensure that these principles are complied with, including the obtaining of written informed consent for publication of any potentially identifiable data or images.

Written informed consent can be documented on a form provided by an institution or ethics committee, and it must clearly state how the identifiable data will be used. Frontiers makes available its own form (<https://www.frontiersin.org/files/pdf/FrontiersConsentForm>) which may be used for this purpose, although not required if an alternative form of consent, meeting the ICMJE recommendations (<http://www.icmje.org/recommendations/browse/roles->



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such as the Transparency and Openness (<https://cos.io/our-services/top-guidelines/>) (TOP) guidelines, and the joint declaration of data citation principles produced by FORCE 11 (<https://www.force11.org/group/joint-declaration-data-citation-principles-final>).

2.4.1. Availability of Materials

Authors are required to make all materials used to conduct their research available to other researchers. Research materials necessary to enable the reproduction of an experiment should be clearly indicated in the Materials and Methods section. Relevant materials such as protocols, analytic methods, and study material should preferably be uploaded to an online repository providing a global persistent link/identifier. If this is not possible, authors are strongly encouraged to make this material available upon request to interested researchers, and this should be stated in the manuscript.

2.4.1.1. Resource Identification Initiative

Authors wishing to participate in the Resource Identification Initiative (<https://www.force11.org/group/resource-identification-initiative>) should cite antibodies, genetically modified organisms, software tools, data, databases, and services using the corresponding catalog number and RRID in your current manuscript. For more information about the project and for steps on how to search for an RRID, please [click here](#) (https://www.frontiersin.org/files/pdf/letter_to_author.pdf).

2.4.2. Availability of Data



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Frontiers requires that authors make the “minimal data set” underlying the findings described and used to reach the

conclusions of the manuscript, available to any qualified researchers. The data should be FAIR—findable, accessible, interoperable, and reusable—so that other researchers can locate and use the data. However, exceptions are granted if data cannot be made publicly available for legal or ethical reasons.

To comply with best practice in their field of research, authors are required to make certain types of data available to readers at the time of publication in specific, stable, community-supported repositories such as those listed below. Authors are encouraged to contact our data availability office at datapolicy@frontiersin.org (<mailto:datapolicy@frontiersin.org>) prior to submission with any queries concerning data reporting.

2.4.2.1. Exceptions Related to Availability of Data

We strongly encourage sharing the maximal amount of data; however where ethical, legal or privacy issues are present the data should not be shared. In cases where some or all data cannot be shared for legal, ethical or privacy restrictions, the authors should make these limitations clear in the Data Availability Statement at the time of submission.

Possible limitations to making data publicly available include patient confidentiality and participant privacy. Authors should ensure that the data shared are in accordance with the ethical consent provided by participants on the use of confidential/identifiable human data. We require that the authors demonstrate that publication of such data does not compromise the anonymity of the participants or breach local data protection laws.



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The original contributions presented in the study are publicly available. This data can be found here: [link/accession number].

2. Existing datasets are available in a publicly accessible repository:

Publicly available datasets were analyzed in this study. This data can be found here: [link/accession number].

3. Information for existing publicly accessible datasets are contained within the article (e.g. for studies using greater than 10 accession numbers):

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/supplementary material.

4. All relevant data is contained within the article:

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author/s.

5. Restrictions apply to the datasets:

The datasets presented in this article are not readily available because [VALID REASON]. Requests to access the datasets should be directed to [text input].

6. Data has been obtained from a third party:



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The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

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Authors are required to deposit the following mandatory data types in public, community-supported repositories, such as those listed below, prior to publication of an associated Frontiers manuscript:

Data-type	Required Repositories	Metadata Standard
Genetic and genomic sequence (DNA/RNA)^	GenBank DNA Data Bank of Japan (DDBJ) European Nucleotide Archive (ENA)	MiXS
Metagenomic sequence	EBI Metagenomics	MiXS
DNA and RNA trace or short-read sequencing data	NCBI Trace Archive NCBI Sequence Read Archive	MiXS



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Data-type	Required Repositories	Metadata Standard
Genetic polymorphism data, including SNP and CNV data	dbSNP dbVar European Variation Archive DGVa	MiXS
Gene expression data; chromatin immunoprecipitation data (deep-sequencing or microarray)	ArrayExpress Gene Expression Omnibus (GEO)	MIAME / MINSEQE
Data linking genotype to phenotype	dbGaP	
Protein sequence data	UniProt	
Proteome profiling data	PRIDE PeptideAtlas ProteomeXchange	MIAPE
Small molecule, protein, protein complex data structural data	Crystallography Open Database Cambridge Structural Database wwPDB (Protein DataBank) Electron Microscopy Databank	CIF
Taxonomy data	Zoobank	

^ Genetic sequence variants should be annotated according to the guidelines established by the Human Variome Project (<http://www.humanvariomeproject.org/resources/genetics-and-genomics-journals.html>).



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Authors are encouraged to consider deposition in public, community-supported repositories of the data-types listed below:
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Data-type	Recommended Repositories	Metadata Standard
Protein-protein interaction data	Database of Interacting Proteins (DIP)	MIMIx
Metabolite and metabolome profiling data	MetaboLights Human Metabolome Database	MSI
Small-molecule screening data; chemical compound data	PubChem	CIF
Flow cytometry data	Flow Repository	
Brain imaging data; neuroimaging data	OpenNeuro INDI NITRC NeuroVault [Statistical maps]	BIDS
Trait data	TRY database	
Phenology data	National Phenology Network	
Any data	Figshare Dryad Digital Repository	None

2.4.7. Inclusion of RNAseq Data



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Studies employing RNASeq for comparative transcriptomic analyses must contain at least three biological replicates



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(unless otherwise justified). Each biological replicate should be represented in an independent library, each with a unique barcode if libraries are multiplexed for sequencing. Validation on a number of key transcripts highlighted in the study is also highly recommended.

Full data accompanying these experiments must be made available to reviewers at the time of submission in a freely accessible resource, e.g the sequence read archive (SRA) (<https://www.ncbi.nlm.nih.gov/sra>) or European Nucleotide Archive (ENA) (<https://www.ebi.ac.uk/ena>). Depending on the question addressed in a manuscript, de novo assemblies of transcriptomes may also require multiple replicates, and assembled sequences together with sequence annotation must be made freely available, e.g figshare (<https://figshare.com/>) or dryad (<https://datadryad.org/>).

2.4.8. Inclusion of Proteomics Data

Authors should provide relevant information relating to how peptide/protein matches were undertaken, including methods used to process and analyze data, false discovery rates (FDR) for large-scale studies, and threshold or cut-off rates for peptide and protein matches. Further information should include software used, mass spectrometer type, sequence database and version, number of sequences in database, processing methods, mass tolerances used for matching, variable/fixed modifications, allowable missed cleavages, etc.

Authors should provide as supplementary material the information used to identify proteins and/or peptides. This should include information such as accession numbers, observed mass (m/z), charge, delta mass, matched mass, peptide/protein scores, peptide modification, miscleavages,



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peptide sequence, match rank, matched species (for cross-species matching), number of peptide matches, etc.
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Ambiguous protein/peptide matches should be indicated.

For quantitative proteomics analyses, authors should provide information to justify the statistical significance, including biological replicates, statistical methods, estimates of uncertainty, and the methods used for calculating error.

For peptide matches with biologically relevant post-translational modifications (PTMs) and for any protein match that has occurred using a single mass spectrum, authors should include this information as raw data or annotated spectra, or submit data to an online repository (recommended option; see table below).

Raw or matched data and 2-DE images should be submitted to public proteomics repositories such as those participating in ProteomeXchange. Submission codes and/or links to data should be provided within the manuscript.

2.4.9. Code

Frontiers is committed to open science and open data; we require that authors make available all code used to conduct their research available to other researchers. Code necessary to enable the reproduction of an experiment should be clearly indicated in the Materials and Methods section, and where possible code should be uploaded to an online repository (such as github.com or [code ocean](https://codeocean.com)) providing a global persistent link/identifier.

Our policies on code availability are informed by community-driven standards, which Frontiers endorses, such as the Transparency and Openness (TOP) (<https://cos.io/our-services/top-guidelines>) guidelines, and the joint declaration of data citation principles produced by FORCE 11 (<https://www.force11.org/>).



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We strongly encourage sharing original code where possible. In situations where custom code is proprietary, an exception will be granted providing that all relevant software needed to replicate the results of the study are available commercially for researchers. Details of the proprietary software used should be listed in the materials and methods section.

At submission, authors should declare any intellectual property relating to the code and themselves in a conflict of interest statement.

2.5. Statistics

Frontiers requires that all statements concerning quantitative differences should be based on quantitative data and statistical testing. For example, if a quantitative statement is made regarding the abundance of a certain protein based on a western blot, we request that the blot be scanned and the abundance assessed quantitatively using the correct analytic software (e.g. ImageJ) and statistics in order to support that statement.

Statistics should/must be applied for independent experiments. The number of independent samples and the deviation parameters (e.g. standard error of the mean, standard deviation, confidence intervals) should be clearly stated in the Methods or the Figure legends. In general, technical replicates within a single experiment are not considered to be independent samples. Where multiple comparisons are employed (e.g. microarray data or genome-wide association studies), any analysis should correct for false positive results. Descriptions of statistical procedures should include the software and analysis used, and must be sufficiently detailed to be reproduced.



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Authors are required to specifically state in their legends how many times experiments were performed (in general we require $n=3$ as a minimum) and what specific statistical analysis was performed.



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2.6. Image Manipulation

Frontiers takes concerns regarding image manipulation seriously. We do not accept that individual features within an image are modified (e.g. enhanced, obscured, moved, recycled, removed or added). Image processing methods (e.g. changes to the brightness, contrast or color balance) must be applied to every pixel in the image and the changes should not alter the information illustrated in the figure. Cropped images should be avoided where possible for gels and blots. Where cropped images are shown in figures, a full scan of the entire original gel(s) must be submitted as part of the supplementary material. Where control images are re-used for illustrative purposes, this must be clearly declared in the figure legend. If any form of image processing is legitimately required for the interpretation of the data, the software and the enhancement technique must be declared in the methods section of the manuscript. Image grouping and splicing must be clearly stated in the manuscript and the figure text.

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2.7. Support

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