

Additional checklist for *Nature* Biology Articles

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Title: Spatiotemporal transcriptome of the human brain

These points are additional to those in the production checklist at http://mts-nature.nature.com/letters/ms_checklist.pdf. Please note that we cannot accept your paper unless you have completed and returned BOTH checklists and confirmed that your manuscript meets all of the relevant formatting and accessibility/reproducibility criteria.

1. Formatting

Please confirm that all of the following points are correctly formatted in your manuscript.

Formatting:	Yes
The paper is within the 5 page length limit for Articles (please use the provided macro to help you determine the length of your paper).	*1.
The methods summary is less than 300 words and the full methods are provided in the SAME word document as the main text, after the figure legends (the numbering of references used only in the full methods section continues from the main references).	*2.
All error bars are defined in the figure legends.	√
The <i>n</i> is noted in all figure legends, where appropriate.	√
Figures do not contain tables as sub-panels. (Tables should be provided as separate display items.)	√
Where possible the SI is combined and submitted as a single PDF.	√
All SI files (including movies and large data sets) have been uploaded on this version. (Production cannot access files provided with earlier versions.)	√
No more than 10 SI files (including sound/movie files) are submitted. Each individual file (including combined, single PDFs) is no larger than 30 MB, and the cumulative size of the files is no larger than 150 MB.	√
The figure legends in the SI are displayed under the individual figures.	√

*1. The paper length is 7 pages approved by Editor.

*2. The full method is provided in the supplementary information.

2. Accessibility/Reproducibility

Please confirm that your manuscript meets each of the relevant criteria below, by ticking either “yes” or “not applicable”.

Accessibility/Reproducibility	Yes	N/A
All small RNA sequences are provided.		√
Microarray data are in MIAME format.		√
Full chemical characterization (including structure) is provided for small molecules.		√
<i>Nature</i> standard table has been used for X-ray crystallography/NMR structural data.		√
Accession numbers are provided for protein structure/cryoEM structure/ microarray/gene sequences/small RNA sequences.	√	