***eLife’s* transparent reporting form**

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* You should state whether an appropriate sample size was computed when the study was being designed
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Our work developed a novel sequencing method and bioinformatics software. So this information is not applicable.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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The experiment was described in the 2nd section of the Result. Data preprocessing procedures were described in Methods.

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* Statistical analysis methods should be described and justified
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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Code for analysing sequencing data are available at https://github.com/yangence/circfull. The data for reproducing all figures are available at https://doi.org/10.6084/m9.figshare.14265650.v1. Sequencing data are available at https://www.ncbi.nlm.nih.gov/sra/PRJNA722575