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

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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
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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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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