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

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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Details on sample sizes and number of experimental and simulation replicates can be found in the relevant Figure Legends.

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* You should report how often each experiment was performed
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* 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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* Include model definition files including the full list of parameters used
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The code used for the computational simulations is available from the github repository with the identifier: <https://github.com/FrancisCrickInstitute/CohesinModel>