***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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The information regarding sample size selected for the analysis is provided under Materials and methods, Sub-heading: Statistical Analysis.

**Replicates**

* 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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* Criteria for exclusion/inclusion of data should be clearly stated
* 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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We have not performed any high-throughput sequencing analysis. Our RT-PCR experiment was performed as per previously published work Subramanian and Schilling 2014.

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* Statistical analysis methods should be described and justified
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Source data was not generated for this analysis. Image data analysis was performed using standard plugins available on ImageJ. The information is provided under Materials and methods, Sub-heading: Microscopy and Image Analysis.