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* 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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Study.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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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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Information for replicates, where applicable, has been described in figure legends and methods.

High-throughput sequencing data have been deposited at the GEO (GSE196458).

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* Statistical analysis methods should be described and justified
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Source data have been deposited as processed data at the GEO (GSE196458).