***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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Information can be found in "Study Design" section of "Materials and Methods", page 20, as well as in legends of respective Figures and Supplemental Figure and Tables.

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* You should report how often each experiment was performed
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Information regarding replicates can be found in "Materials and Methods", as well as in legends of respective Figures and Supplemental Figures.

Whole transcriptomic data discussed have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE101112. (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE101112), as stated in " Whole transcriptome analysis" section of "Materials and Methods", pages 34 and 35.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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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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Information can be found in "Study Design" section of "Materials and Methods", page 20.

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* 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:

Supplementary Files 1, 2 and 3 contain source data on transcriptomics and metabolomics.