



## eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or the [ARRIVE guidelines](#) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: [editorial@elifesciences.org](mailto:editorial@elifesciences.org).

### Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

This information is included in Material and Methods under the section 'Statistical analysis for low throughput experiments'.  
Methods of analysis including statistical processing for RNA sequencing data quantification, differential expression analysis, cluster analysis and heatmap construction are described in Materials and Methods under the section 'Quantification and integration of expressed microRNAs and mRNAs'.

### 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
- If you encountered any outliers, you should describe how these were handled
- 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)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Number of biological independent replicates is indicated in figure legends. The use of biological replicates is clearly indicated in Material and Methods under the section 'Statistical analysis for low throughput experiments'.  
RNA sequencing data accession codes are included in manuscript and cover letter.



### 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)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Statistical method is described in Material and Methods under the section 'Statistical analysis for low throughput experiments'.  
Mean, SEM, N and p-value, are indicated in figure legends.  
Raw data are provided in source data files.  
Methods of analysis including statistical processing for RNA sequencing data quantification, differential expression analysis, cluster analysis and heatmap construction are described in Materials and Methods under the section 'Quantification and integration of expressed microRNAs and mRNAs'. Relevant details are also provided in respective figure legends. Information on statistical outcomes of differential expression analysis is provided in supplemental file 1 (p-values of selected genes) and also in the main manuscript in Results under the section 'Identification of miR-934 with species- and stage-specific expression during progenitor expansion and early neuron generation' (for miRNAs), and also under the section 'Inhibition of miR-934 during neural induction affects molecular pathways of neurogenesis and alters the expression of subplate-enriched genes'.

(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.)

### Group allocation

- 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
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

As indicated in the appropriate sections in the manuscript, samples are clearly allocated in experimental groups, according to stage of differentiation and/or treatment for miR934 perturbations.

### Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table



eLIFE

1st Floor  
24 Hills Road  
Cambridge CB2 1JP, UK

P 01223 855340  
W elifesciences.org  
T @elife

- Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Raw data are uploaded as source data files.