

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.

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:

Explicit power analyses were not used to establish sample size. For RNA and protein quantitation and for histology, we pre-determined a sample size of ≥ 3 biological replicates based on previous experience with these methods. It is also relevant to note that conclusions in this study typically depend on multiple genetic models. For example, phenotypes ascribed to H19 lncRNA are identified through 3 independent comparisons: wild type vs. loss of imprinting (LOI); LOI vs. LOI with H19 transgene rescue; and wild type vs. H19 mutation. For echocardiography, a sample size of 8-10 was selected based on preliminary analyses of 4 mice. Information on sample sizes is described in Figure legends.

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:

All N numbers reported in Figure legends describe biological replicates, meaning that samples were derived and analysed from that number of unique animals. We always collected samples from at least two independent litters.

For echocardiography, ex vivo analyses of blood vessels, immunoblotting, and RNA-sequencing, we analysed each animal/sample one time. For histology, we analysed >3 sections per animal, quantitated an average across the sections, and then present a representative section in the Figure. For RNA expression, we prepared one cDNA sample per animal and performed two technical replicates.

No data were excluded from our analyses. As described in the text, mutant mice display high variance in ventricular function but all data are displayed and included in our analyses.

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:

Data are presented according to these guidelines: see Figure legends.

(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:

Masking of genotypes was used by the pathologist who identified comparable tissue sections to be analysed and by the scientists performing echocardiography and in vivo analyses of blood vessels. The investigator performing RNA and protein quantitations did know the genotypes of the analysed samples.

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
- 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: