***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 sample sizes for each experiment was described in Figure Legends or Methods section. No statistical method was used to predetermine sample sizes. Standard practices in the field were used to determine sample sizes.

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* You should report how often each experiment was performed
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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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Detailed information was described in Figure Legends or Methods section. We observed the same findings within each animal (mouse) studied. All experiments were repeated two or more times in independent trials. No data was excluded from experiments. GEO information is located at the end of the Methods section.

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* Statistical analysis methods should be described and justified
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* 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.

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P values can be found in Results and Figure Legends. Statistical analysis methods can be found in Methods section.

(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
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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:

Mice of the correct genotype and age were randomly selected for inclusion in the study. RNA-seq and ChIP-seq analysis were performed using automated scripts, but with experimenter knowledge of sample IDs necessary to run the code. Cell counts of TdTomato+ cells between control and conditional knock-out animals were performed using a computer program that permited blinded manual cell counting. Details can be found in Methods section.

**Additional data files (“source data”)**

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

Raw ChIP-seq data GEO accession: GSE74315. RNA-seq data generated in this study and ChIP-seq analysis are deposited in NCBI GEO under accession code GSE130514.