

***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:

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| We sampled as many cells per mouse and mice that were reasonable for a 4 year period.  A goal/guide for cell sample size per mouse was 30, based on previous studies from this and other labs (Wang, Dumont, Hassold, ) |

# 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:

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| -experiments are detailed in the Methods section  **Replicates**  (cells from the same mouse were replicates of the same genome  Multiple mice from the same genetic background  Experimental replicates -  **Outliers**  For **MLH1** staining (spreads)  Biological replicate- mouse of the same genetic background  Technical replicates- separate meiocyte spread from the same mouse (up to 3 made) (distributions of MLH1 counts from technical replicates were compared for a handful (3) of mice  (human quantification  **Total SC** – the total SC estimates per cell was quantified with an algorithm – using XX parameters – this // for time – it was intractable to optimize the parameters for each image – instead the skeletonized pixels per cell data was visualized for individual cells– and clear outliers were removed. |

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# 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:

|  |
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| Statistical analysis is explained in the Methods. The specific tests and values of N are listed in the text and tables  The raw data points are presented whenever possible in figures  Summary statistics such as means are displayed with error bars for the 2-/+ se (effectively a 95% CI) (detailed in figures and figure legends.  Figure 1 – shows +/- 2 s.d. (an approximation of a 95%)  Estimates of effect sizes (for foci) |

(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:

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| Image data for MLH1 foci counts was randomized within sex and a subset of mice during the quantification process.  (for some visualization, mice are pooled within groups) |

# 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:

|  |
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| Data files and analysis scripts will be uploaded to a public github repository.  (Because of the large size Image files are hosted on the NSF CyVerse and can be shared on request) |

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