***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
* 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

Sample sizes indicate the number of independent biological replicates and can be found in the figure legends.

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Whenever possible, we provide the measurements for each cell as a dot plot, so that the sample size and raw distribution is directly visible in each figure. Otherwise, the information about sample sized can be found in the figure legends.

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* You should report how often each experiment was performed
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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.

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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.)

**Group allocation**

One tailed Fisher’s exact test is used where we made statistical claims. The information, as well as mean, SD or SEM, can be found in the figure legends.

In some of the analyses, samples were designated “1-budded” or “2-budded”, etc, according to the obvious outcomes of the cell cycles of interest. These information can be found in the results section.

Source code files for numerical simulations for all of our models are provided as source code files. Model definition and full parameter lists can be found in the methods section.

* 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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* 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
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