



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:

- measuring the relationship between cell area and LEC area for wt and *spike1*: see 'Results' section, subsection 'Lobeyness allows cells to increase their size while avoiding excessive stress', Figure 5A and Figure 5 – source data 1; Figure 5 – figure supplement 3 and Figure 5 – source data 2.

- average cell area and lobeyness in multi-species study: see Figure 6 – source data 1 and 'Results' section, subsection 'Cell shape and size across species'.

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:



- time-lapse imaging of cotyledons (wt, *p35S::LNG1* and *spike1*): see 'Results' section, subsections 'Isotropic tissue growth is correlated with puzzle-shaped cell formation' and 'A strategy for when lobes cannot be formed'.
- oryzalin treatment on NPA-grown meristems: see 'Results' section, subsection 'Experimental evidence that stress needs to be managed'.

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:

- correlation of growth anisotropy and lobeyness in cotyledons: see 'Results' section, subsection 'Isotropic tissue growth is correlated with puzzle-shaped cell formation'
- comparison of growing wt and *spike1* cotyledons (Kolmogorov-Smirnov test): see Figure 5-figure supplement 1 and 'Materials and Methods' section, subsection 'Comparison of the distributions of cellular quantities between WT and *spike1*'
- correlation of lobeyness and cell area for each species in the multi-species study (Pearson's correlation coefficient): see Figure 6 and 'Results' section, subsection 'Cell shape and size across species'.

(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:

- phenotyping of *p35S::LNG1* T1 plants: see Figure 4.

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:

- Figure 5 (Source Data 1, Source Data 2)
- Figure 6 (Source Data 1)

Source data files have been listed at the end of the manuscript PDF (section 'Supplementary files')