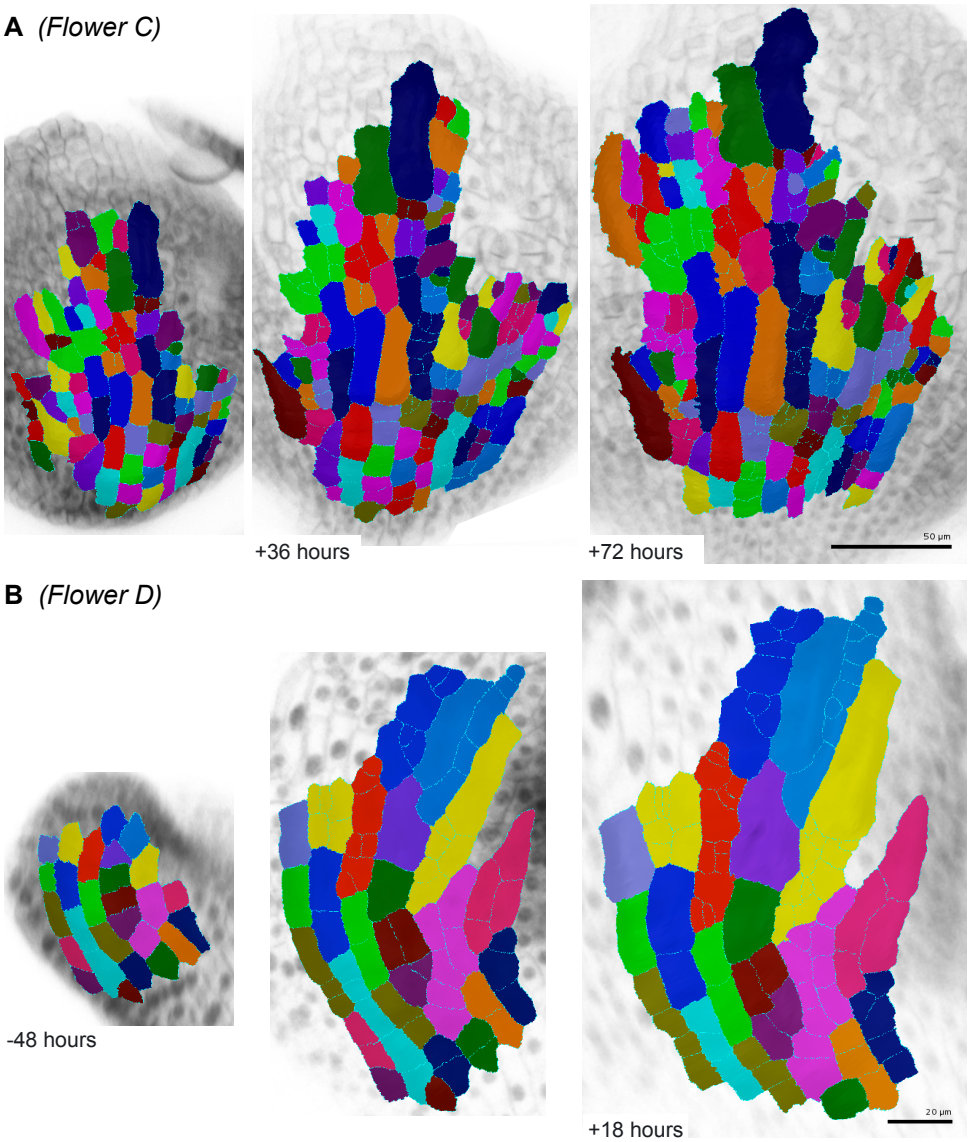

Fig. S1. Cell lineage tracking in live images of growing *Arabidopsis* sepals. Segmented cells and tracked cell lineages for a sepal in Flower C **(A)** and in Flower D **(B)**. Imaging for Flower D started at an earlier stage of growth than for Flowers A-C. One time point of the imaging session of Flower D was chosen such that the growth stage is comparable with the initial time point shown for the other flowers. Each segmented cell in the figure is colored according to the lineage, which means that cells with the same mother have the same color. More than one lineage can have the same color. The segmented cells (colored) are displayed on top of the original fluorescent plasma membrane and nuclear data (grey). Scales: 50 µm (**A**), 20 µm (**B**).

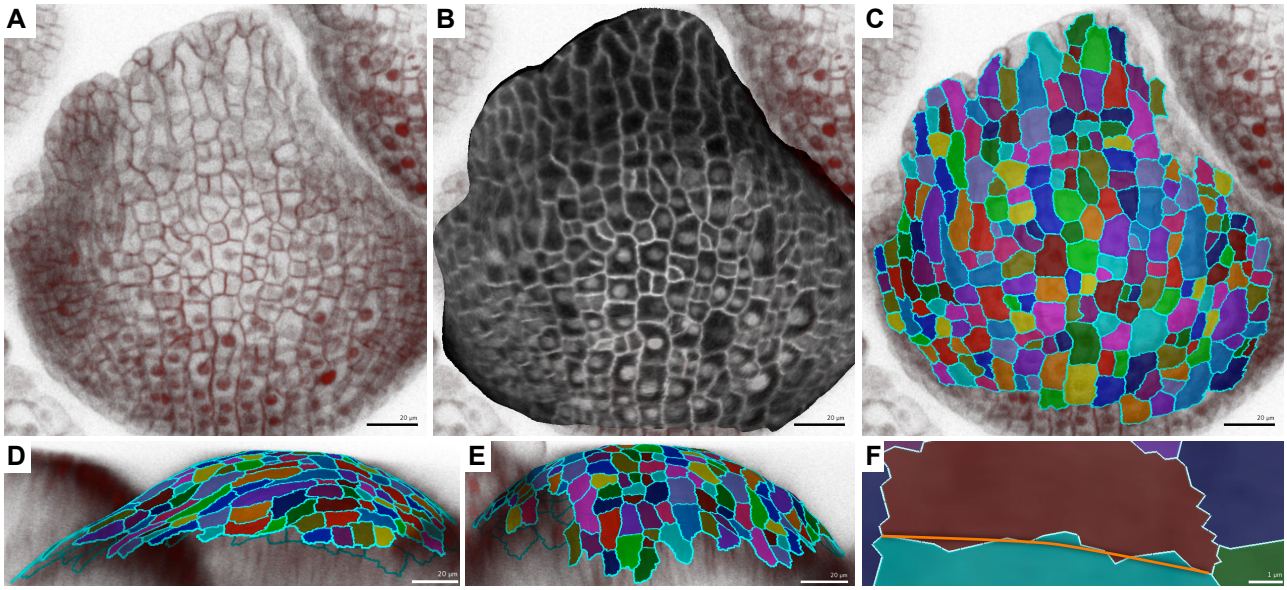

Fig. S2. Image processing workflow. The input data is a 3D stack with fluorescent nuclei and membranes **(A)**, whose intensities are projected on a curved surface mesh **(B)**, which is segmented into cells **(C)**. Side **(D)** and front **(E)** views illustrate the curvature of the sepal. We measure wall lengths **(F)** by fitting a quadratic function (sketched in orange) to reduce errors due to the zig-zag shape of the segmented cell border. Scale: 20 µm **(A-E)**, 1 µm **(F)**.

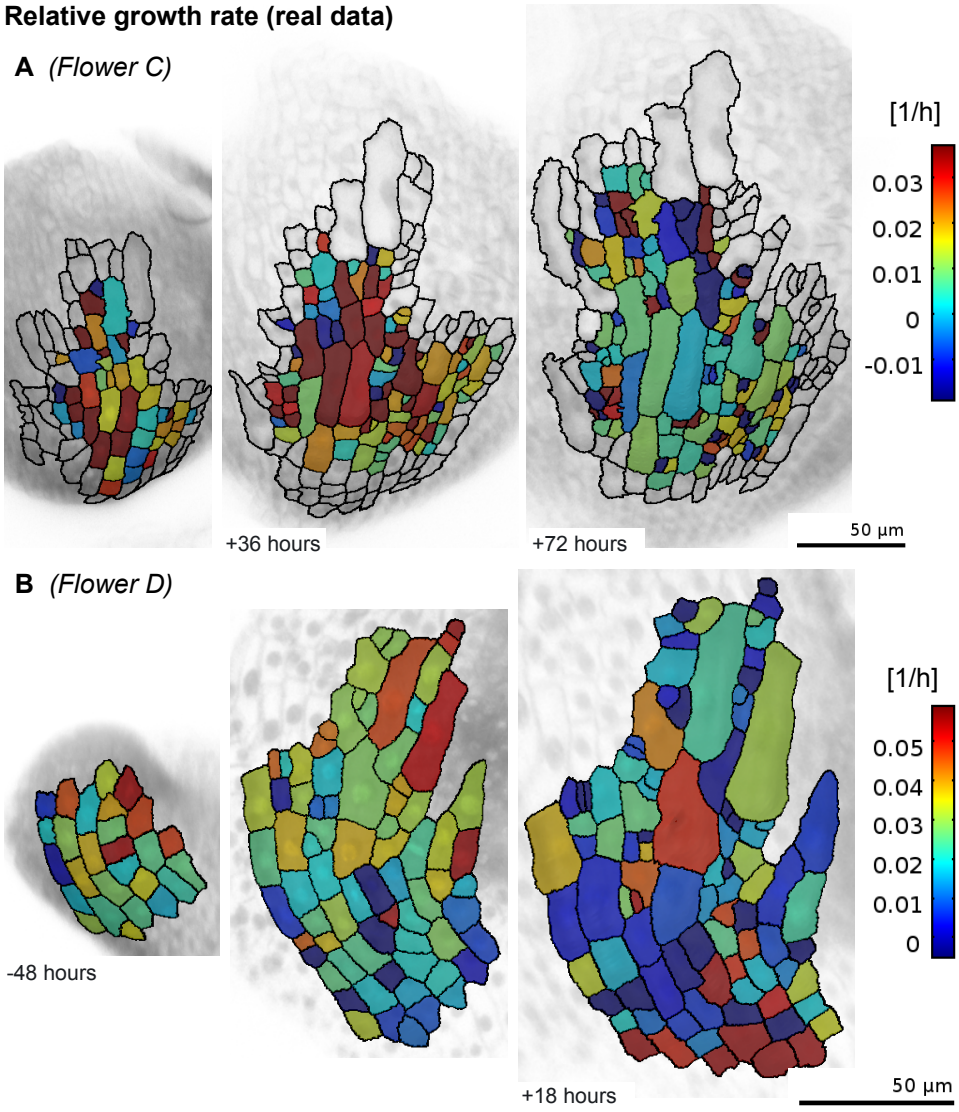

Fig. S3. The relative growth rate is noisy. The relative growth rate for each cell/lineage computed over a 6-hour interval for Flowers C **(A)** and D **(B)** is noisy varying greatly from cell to cell. The colormap displays the average relative growth rate RGR_i, which is computed by comparing cell areas A_i and A_{i+1} at two subsequent time points t_i and t_{i+1} as $RGR_i = \ln(A_{i+1} / A_i) / (t_{i+1} - t_i)$. RGR_i is displayed on the cells of the sepal at time t_i, showing the growth in the following time interval.

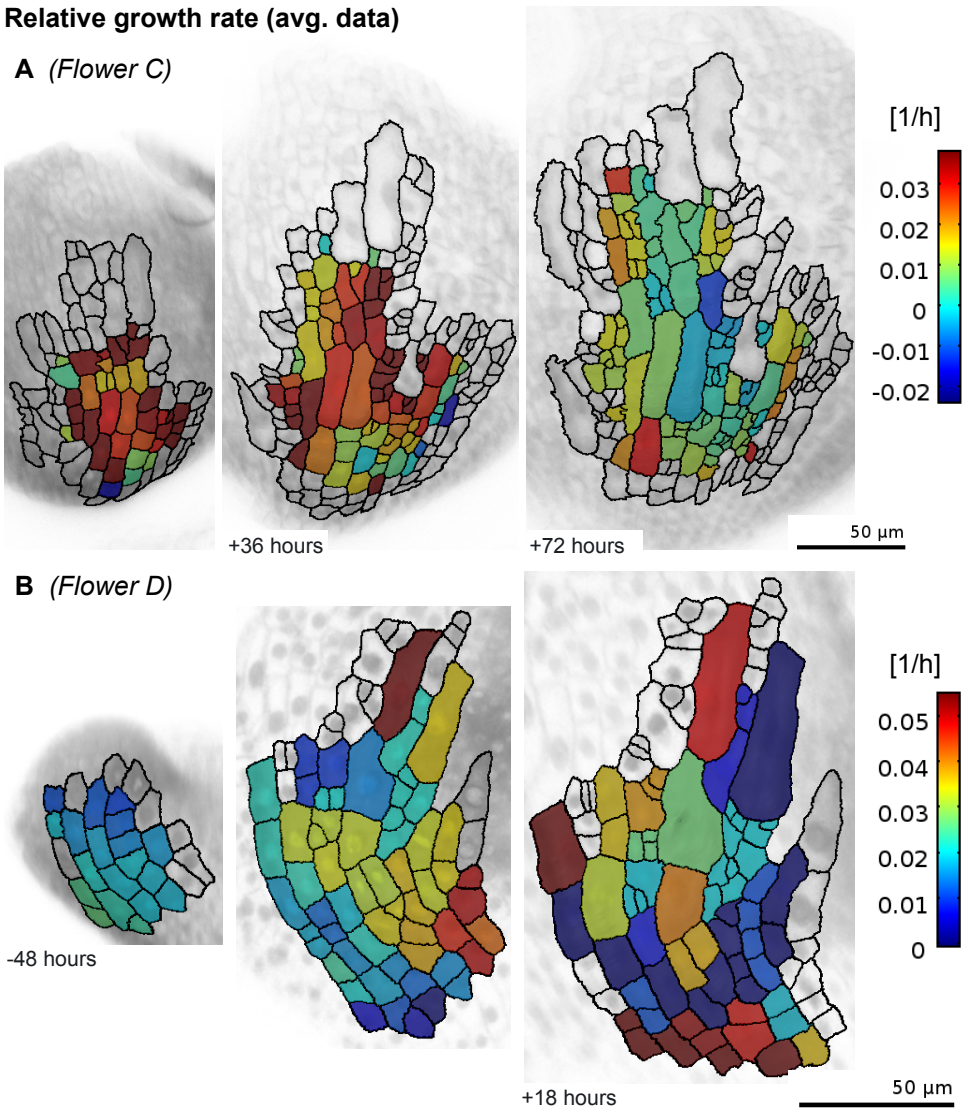

Fig. S4. A low order displacement field smoothens growth. The relative growth rate for each cell lineage using the spatially averaged data for Flowers C **(A)** and D **(B)** is considerably less noisy than the same quantity extracted from the real data (Fig. S3). The colormap displays the average relative growth rate $RGR_i = \ln(A_{i+1} / A_i) / (t_{i+1} - t_i)$. The cell areas A_i and A_{i+1} at two subsequent time points t_i and t_{i+1} are computed with the low-order displacement fields $u(X, t_i)$ and $u(X, t_{i+1})$, respectively. RGR_i is displayed on the cells of the sepal at time t_i, showing the growth in the following time interval.

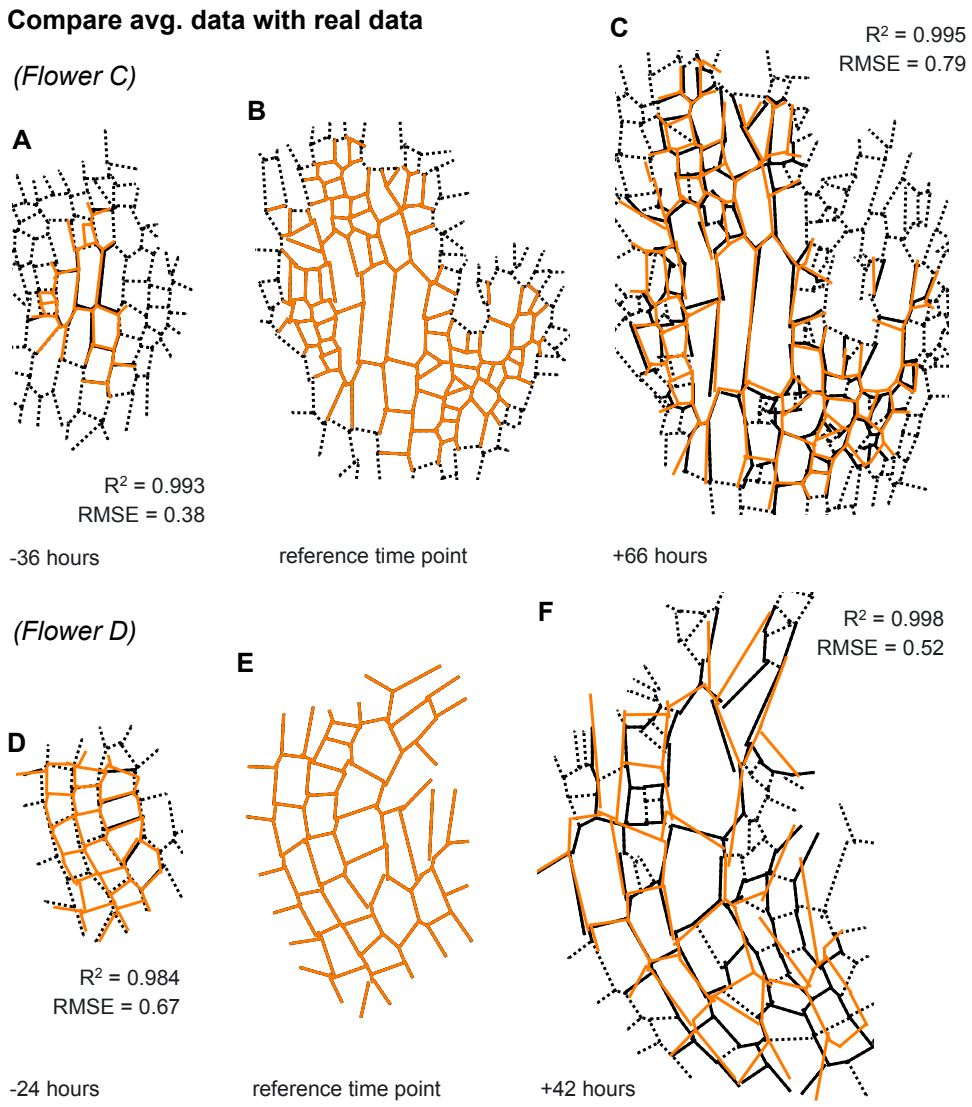

Fig. S5. Spatially averaged kinematics fit the real data well. Comparison of the predicted cell lineage growth using the continuous low-order displacement fields $u(X, t_j)$ (solid orange lines) with the real imaging data (black solid lines) at time points 36 hours before **(A)** or 66 hours after **(C)** the reference time point **(B)** for Flower C and 24 hours before **(D)** or 42 hours after **(F)** the reference time point **(E)** for Flower D. Note that the predicted and real data match remarkably well as the coefficient of determination (R^2) is close to 1 and the root mean squared error (RMSE) is low. To simplify the comparison visually in the figure, each wall segment is represented as a straight line. The prediction is for cell lineages and does not take into account cell division. At time points before the reference time, the predicted data contain cells, which have not divided yet in the real data, such that two predicted cells may match one real cell. At time points after, the opposite is the case, such that several real cells may match one predicted cell. For the real imaging data we show these additional walls as black dashed lines. We do not expect the prediction to match these walls, as they did not exist in the reference time point.

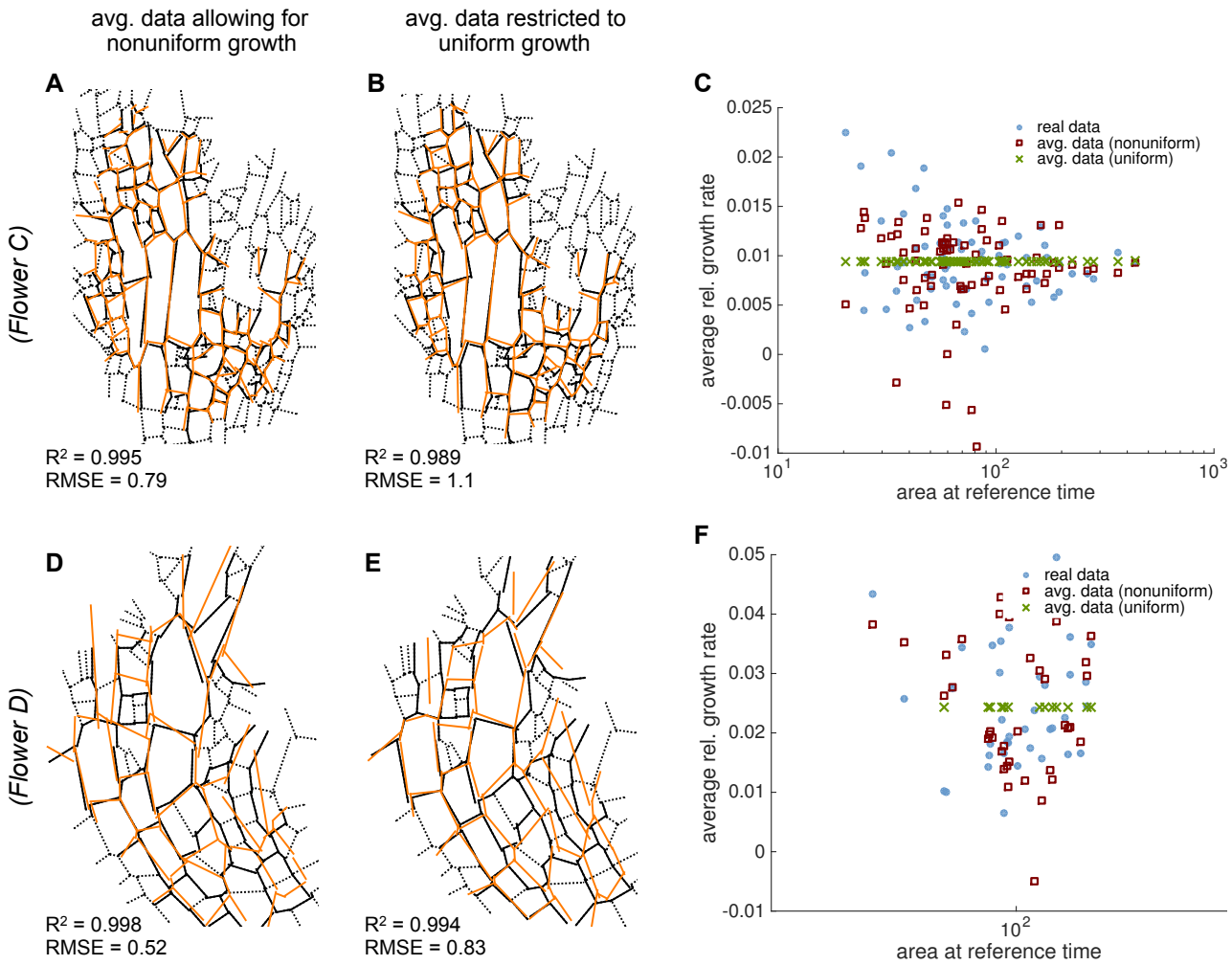

Fig. S6. Uniform growth in space predicts cellular growth. Comparison of various growth prediction methods (orange lines) with the real imaging data (black solid lines). **(A, D)** The continuous low-order displacement field prediction (orange lines) for Flowers C **(A)** and D **(D)** best match the data (black lines). These images replicate C and F from Fig. S5. **(B, E)** Predictions (orange lines) from a displacement field with the additional constraint to have uniform growth in space (but not time), such that the relative increase in cell area is uniform, also matches well with the real data (black lines). It matches almost as well as the unconstrained displacement field (R^2 and RMSE). For the real imaging data we show additional walls, which did not exist in the reference time point or were not considered there (black dashed lines). **(C, F)** Graph of the average relative growth rate relative to the cell area at the reference time shows that the real data (blue dots) and the spatially averaged data (red squares) vary greatly around the uniform relative growth rate (green crosses) used in the prediction for Flowers C **(C)** and D **(F)**.

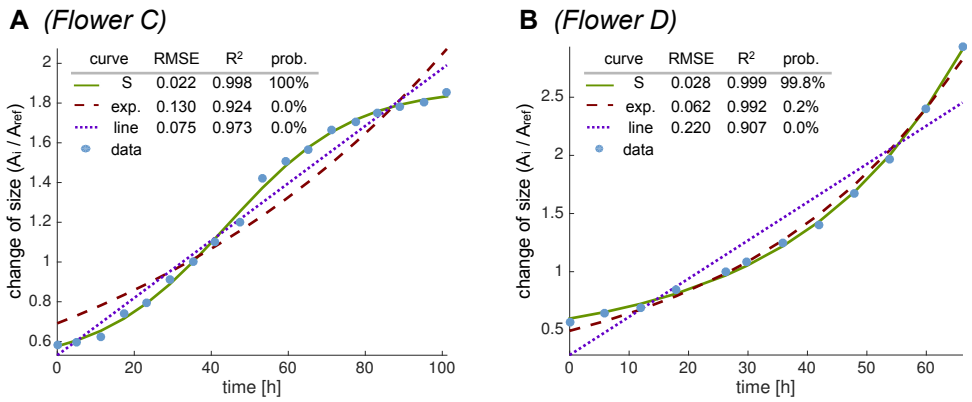

Fig. S7. Tissue growth curves fit sigmoid shapes. We compare the tissue growth (blue dots) with fits to linear (blue dotted line), exponential (red dashed line) and sigmoid (green solid line) curves for Flowers C **(A)** and D **(B)**. In all cases, the sigmoid (S) curve fits very well (low RMSE values and R^2 values close to 1). Probabilities computed with the Akaike information criterion clearly show that the S curve is the most likely fit to the data. We define the growth curves as tissue area (A_i) at time t_i divided by tissue area (A_{ref}) at the reference time point t_{ref} plotted against time.

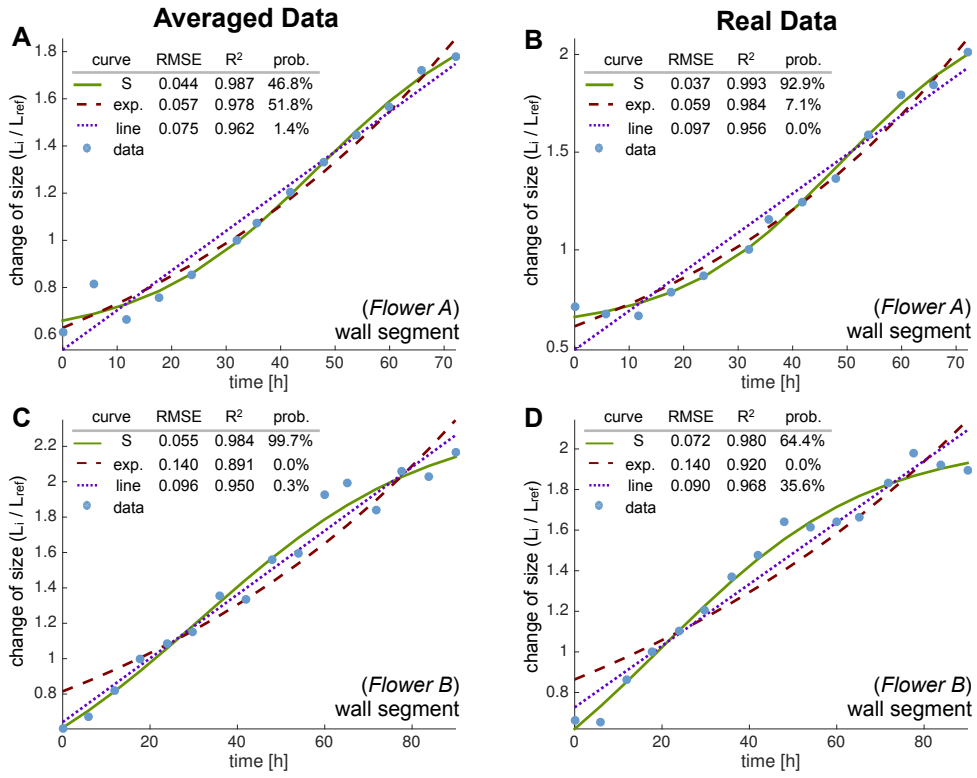

Fig. S8. Individual wall segment growth curves fit sigmoid shapes. We show growth (blue dots) for individual wall segments of Flowers A **(A-B)** and B **(C-D)** using the spatially averaged **(A, C)** and the real **(B, D)** data. We compare fits to linear (blue dotted line), exponential (red dashed line) and sigmoid (green solid line) curves. We chose growth curves with as many data points as possible to reduce errors from the fit. In all cases, the sigmoid (S) curve fits best (lowest RMSE and R^2 values). Probabilities computed with the Akaike information criterion show that the sigmoid curve is the most likely fit to the data in most cases. We define the growth curves as wall segment length (L_i) at time t_i divided by the length (L_{ref}) at the reference time point t_{ref} plotted against time.

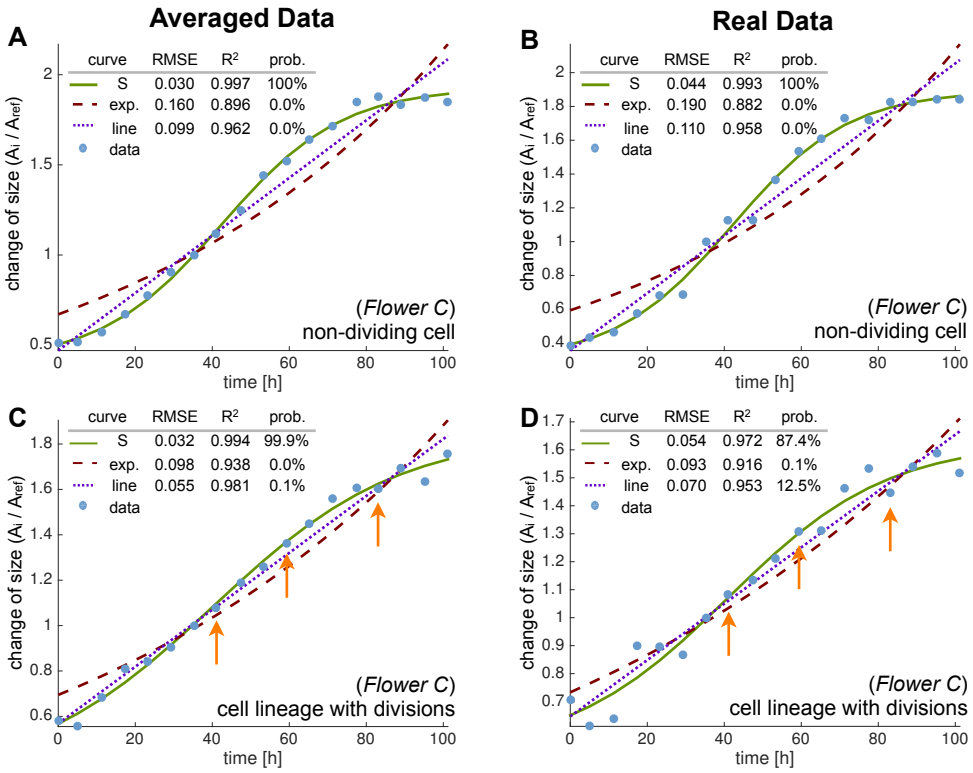

Fig. S9. Individual cell lineage growth curves fit sigmoid shapes. We show growth (blue dots) for individual cell lineages of Flower C using the spatially averaged **(A, C)** and the real **(B, D)** data. We do not consider Flower D because it contained too few data points. We compare fits to linear (blue dotted line), exponential (red dashed line) and sigmoid (green solid line) curves. We chose growth curves with as many data points as possible to reduce errors from the fit. In all cases, the sigmoid (S) curve fits very well (RMSE and R^2 values). Probabilities computed with the Akaike information criterion show that the sigmoid curve is the most likely fit to the data in most cases. We consider non-dividing (**A-B**) and dividing (**C-D**) cells. Cell divisions are marked with orange arrows but did not have a major effect on the lineage growth curves. We define the growth curves as cell lineage area (A_i) at time t_i divided by cell area (A_{ref}) at the reference time point t_{ref} plotted against time.

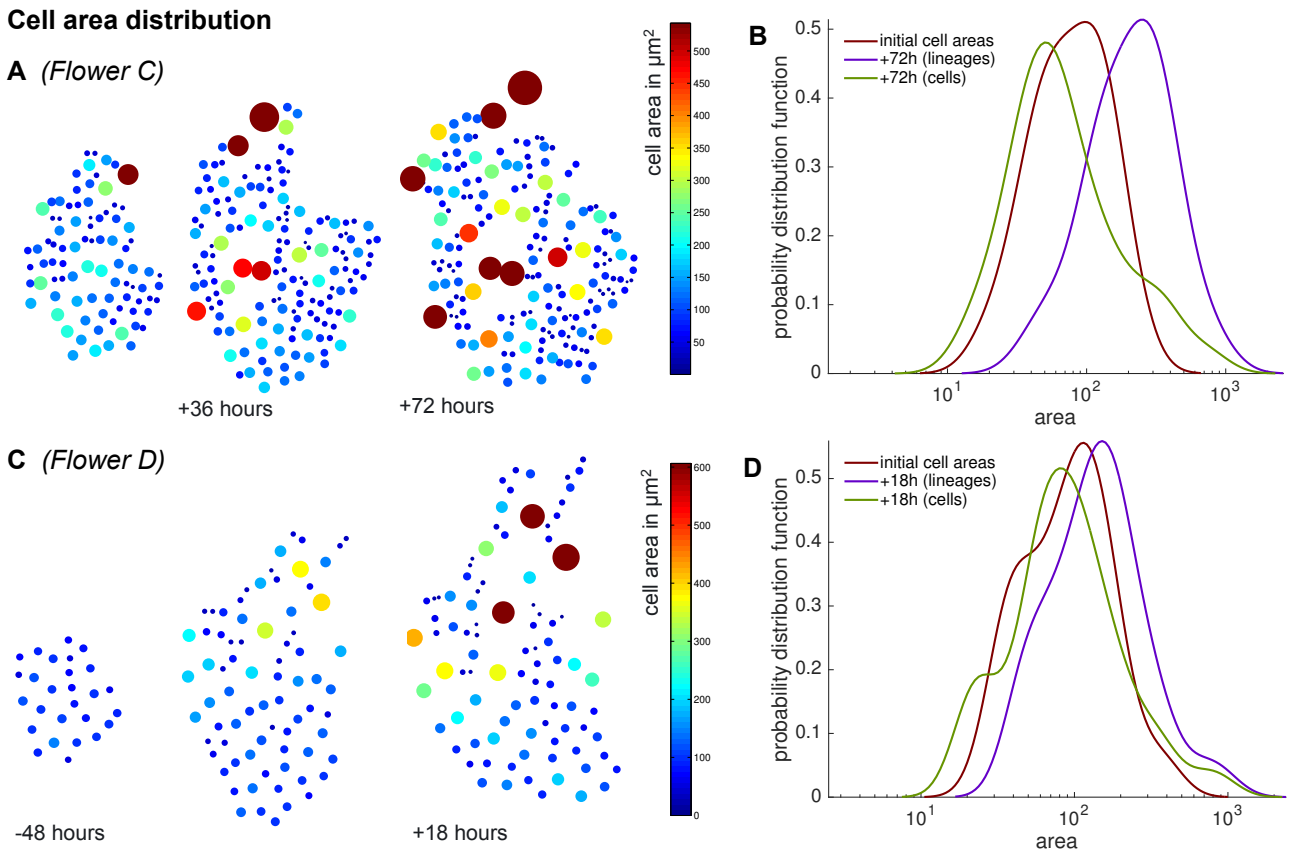

Fig. S10. Cell size variability increases in time. (A, C) The variability in cell areas increases in time for Flowers C **(A)** and D **(C)**. Each cell is represented as a dot whose size and color (colormap) is scaled according to the cell area. Each dot is positioned at the cell center; note that there is no obvious spatial pattern in the distribution of large and small cells. The sepal and the cell centers of each cell are flattened to two dimensions for visualization purposes. **(B, D)** The cell area distribution curves from an initial time point (red) become broader at the final time point (green, 72 hours later for Flower C, 18 hours later for Flower D) when cell division is taken into account for Flowers C **(B)** and D **(D)**. In contrast, when cell lineages are considered without cell division (blue), the curve shape is maintained and the curve is shifted to the right due to growth.

(Flower C)

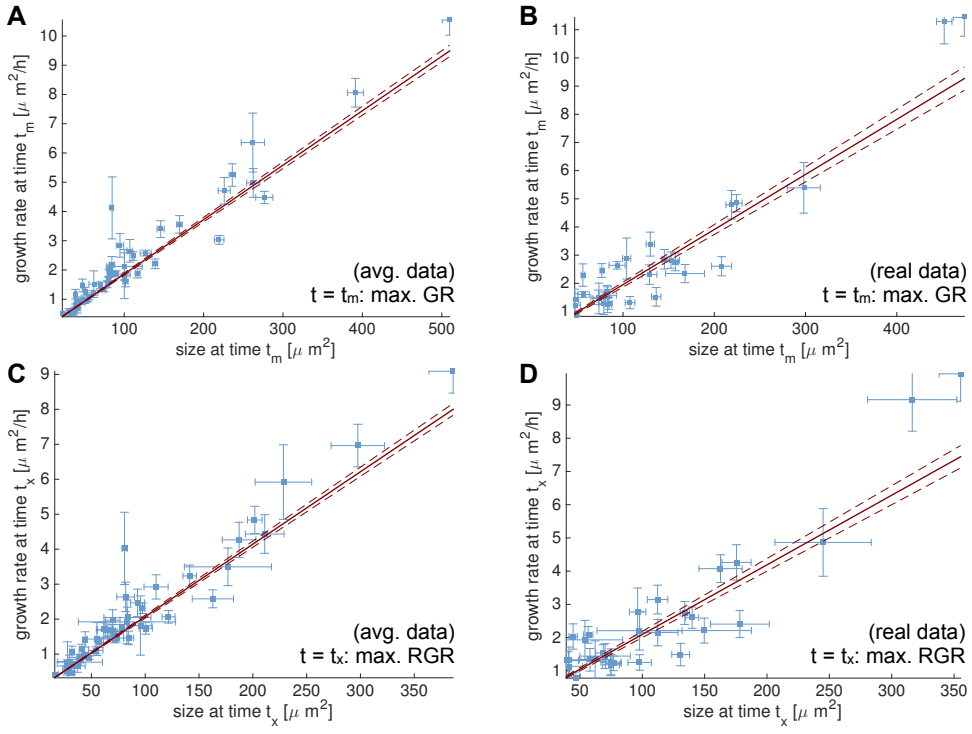

Fig. S11. Growth rate and size are linearly correlated at times t_m and t_x. We analyze growth curves for Flower C using both the spatially averaged **(A, C)** and the real **(B, D)** data. We do not consider Flower D because it contained too few data points. We consider the time point t_m **(A-B)**, when the growth rate GR is maximal, and the time point t_x **(C-D)**, when the relative growth rate RGR(t) = GR(t) / Area(t) is maximal. In all cases, we observe a linear correlation between growth rate and size, which suggests that RGR(t_m) is the same for all cell lineages in the sepal. Likewise, this suggests that RGR(t_x) is the same for all cell lineages in the sepal. Both the growth rate (GR(t_m) and GR(t_x)) and the size (Area(t_m) and Area(t_x)) are estimated from the fit of the data to a sigmoid curve. We only consider data with a meaningful fit. The uncertainty from the fit is propagated into a standard deviation for GR and Area, which is shown in the plots as error bars. We fit constants for RGR(t_m) and RGR(t_x) and show them as red solid lines with its 95% confidence bounds as dotted lines.

(Flower C)

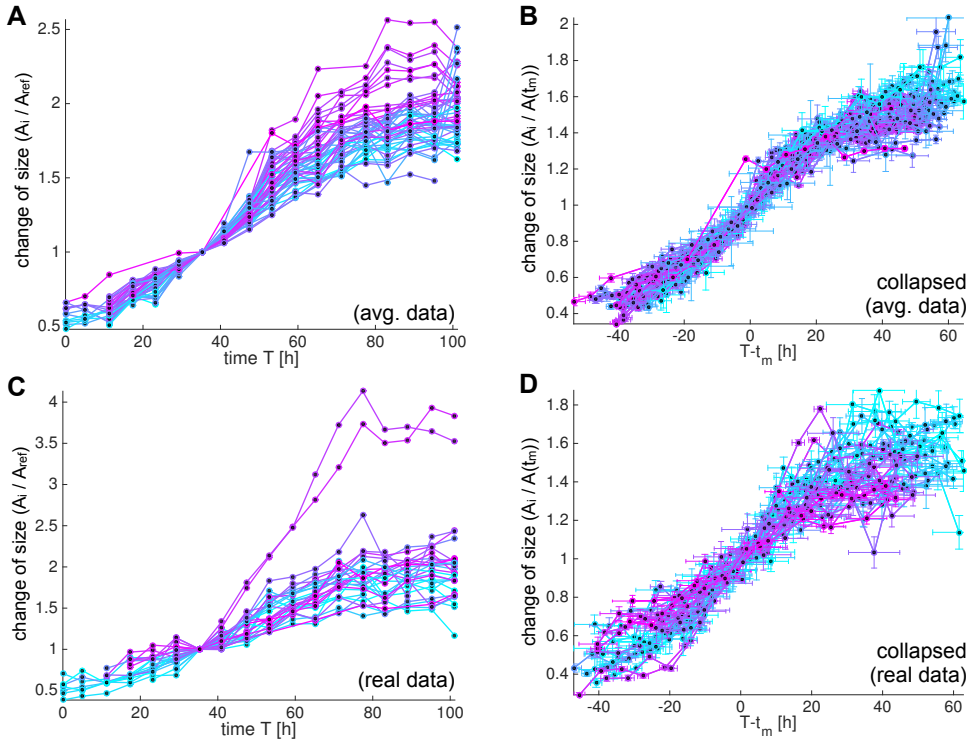

Fig. S12. Individual growth curves can be collapsed to similar sigmoid curves. We analyze growth curves for Flower C using both the spatially averaged **(A-B)** and the real **(C-D)** data. We do not consider Flower D because it contained too few data points. The growth curves are colored according to t_m (early (cyan) to late (purple)). **(A, C)** The individual growth curves f(T) show the change in each cell lineage area in time compared to the reference time. The curve f(T) is only defined at discrete time points $T = t_i$ marked with dots ($f(t_i) = A_i/A_{ref}$). We only consider data with a meaningful fit to a sigmoid curve. **(B, D)** We collapse the growth curves onto more similar curves by aligning them according to the nearly constant $RGR(t_m)$. We align them in time by removing the dependency of t_m and we scale the curves according to their size at time t_m such that their slope corresponds to $RGR(t_m)$. We therefore compute $f_c(t) = f(t + t_m)/f(t_m)$ and plot $f_c(t)$ against $t = T – t_m$. Both t_m and $f(t_m)$ were estimated from the best fitting sigmoid curve, while we evaluate $f(t + t_m)$ at discrete time points $t = t_i – t_m$ from the actual data ($f_c(t_i-t_m) = A_i/A(t_m)$). Note that since f still depends on three of the four parameters defining the sigmoid curve, it is not obvious for the curves to collapse to a single curve. The fact that the transformed growth curves $f_c(t)$ line up well confirms that the relative growth rates at times t_m and t_x are the same for each cell lineage.

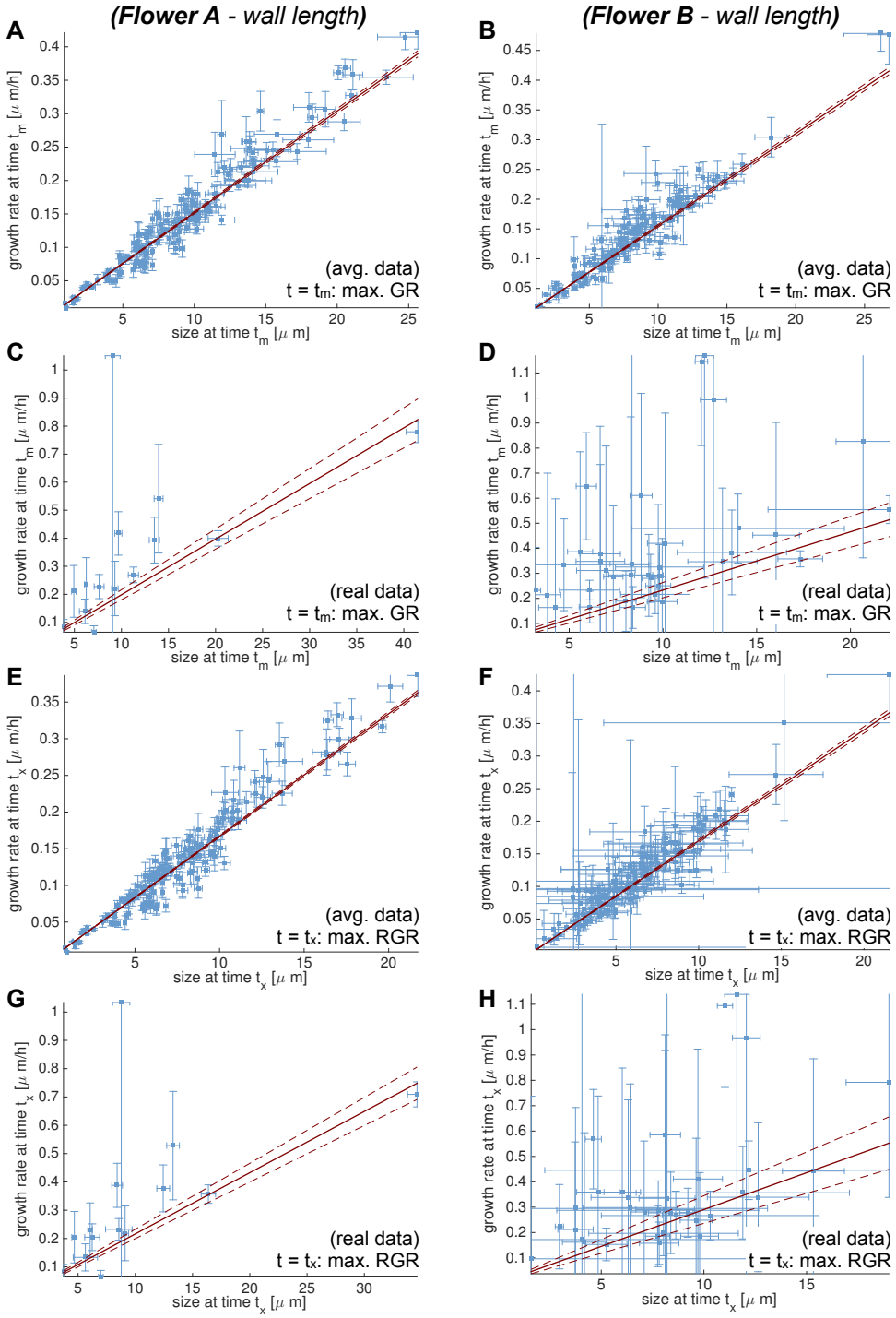

Fig. S13. Growth rate and size of wall segments are linearly correlated at times t_m and t_x. We analyze growth curves for Flowers A **(A, C, E, G)** and B **(B, D, F, H)** using both the spatially averaged **(A-B, E-F)** and the real **(C-D, G-H)** data. We consider the time point t_m **(A-D)**, when the growth rate GR is maximal, and the time point t_x **(E-H)**, when the relative growth rate RGR(t) = GR(t) / Length(t) is maximal. In all cases, we observe a linear correlation between growth rate and size, which suggests that RGR(t_m) is the same for all wall segments in the sepal. Likewise, this suggests that RGR(t_x) is the same for all wall segments in the sepal. Both the growth rate (GR(t_m) and GR(t_x)) and the size (Length(t_m) and Length(t_x)) are estimated from the fit of the data to a sigmoid curve. We only consider data with a meaningful fit. The uncertainty from the fit is propagated into a standard deviation for GR and Length, which is shown in the plots as error bars. We fit constants for RGR(t_m) and RGR(t_x) and show them as red solid lines with its 95% confidence bounds as dotted lines.

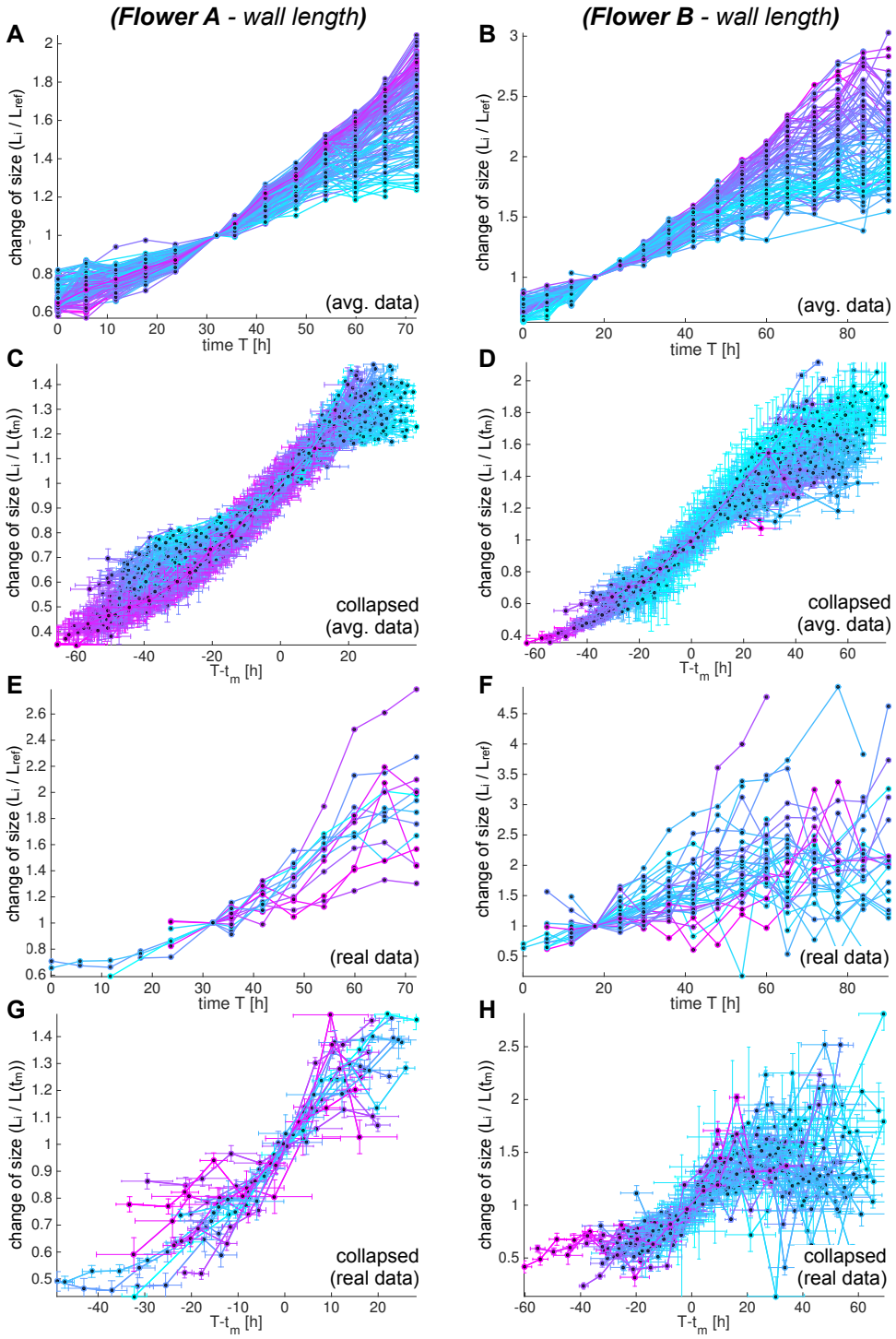

Fig. S14. Individual growth curves of wall segments can be collapsed to similar sigmoid curves. We analyze growth curves for Flowers A **(A, C, E, G)** and B **(B, D, F, H)** using both the spatially averaged **(A-D)** and the real **(E-H)** data. The growth curves are colored according to t_m (early (cyan) to late (purple)). **(A-B, E-F)** The individual growth curves f(T) show the change in each wall segment length in time compared to the reference time. The curve f(T) is only defined at discrete time points $T = t_i$ marked with dots ($f(t_i) = L_i/L_{ref}$). We only consider data with a meaningful fit to a sigmoid curve. **(C-D, G-H)** We collapse the growth curves onto more similar curves by aligning them according to the nearly constant $RGR(t_m)$. We align them in time by removing the dependency of t_m and we scale the curves according to their size at time t_m such that their slope corresponds to $RGR(t_m)$. We therefore compute $f_c(t) = f(t + t_m)/f(t_m)$ and plot $f_c(t)$ against $t = T – t_m$. Both t_m and $f(t_m)$ were estimated from the best fitting sigmoid curve, while we evaluate $f(t + t_m)$ at discrete time points $t = t_i – t_m$ from the actual data ($f_c(t_i-t_m) = L_i/L(t_m)$). Note that since f still depends on three of the four parameters defining the sigmoid curve, it is not obvious for the curves to collapse to a single curve. The fact that the transformed growth curves $f_c(t)$ line up well confirms that the relative growth rates at times t_m and t_x are the same for each wall segment.

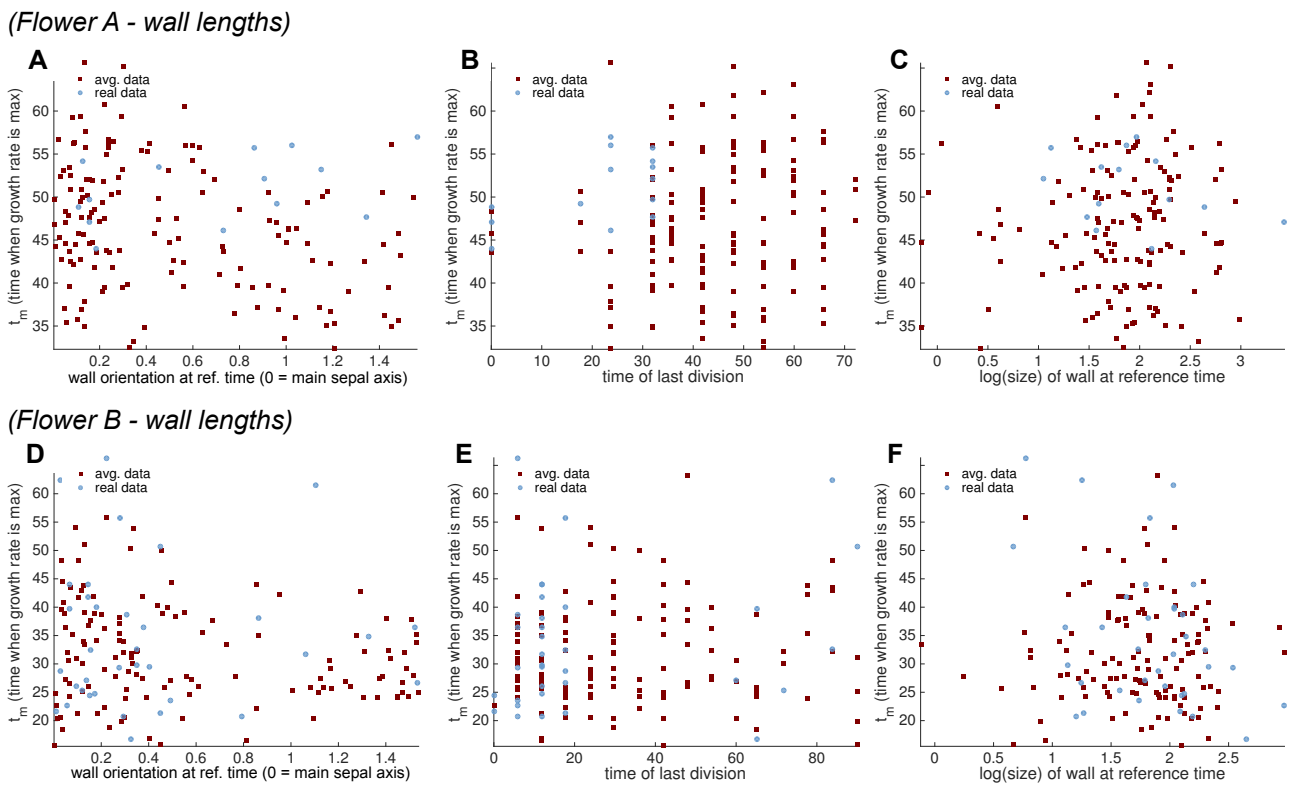

Fig. S15. T_m of wall segments does not correlate with wall orientation, time of last division, or length. We looked for correlations between t_m and wall orientation **(A,D)**, time of last division **(B,E)** and ln(length) **(C,F)** for real (blue) and spatially averaged (red) wall segments of Flowers A **(A-C)** and B **(E-H)**. The wall orientation is measured as the angle (radians) between the main sepal axis and the main axis of each wall segment. The time of last division refers to divisions of the neighboring cells. We take the logarithm of the wall length to avoid spreading out. Both the length and the angle are measured at the reference time point.

(Flower C)

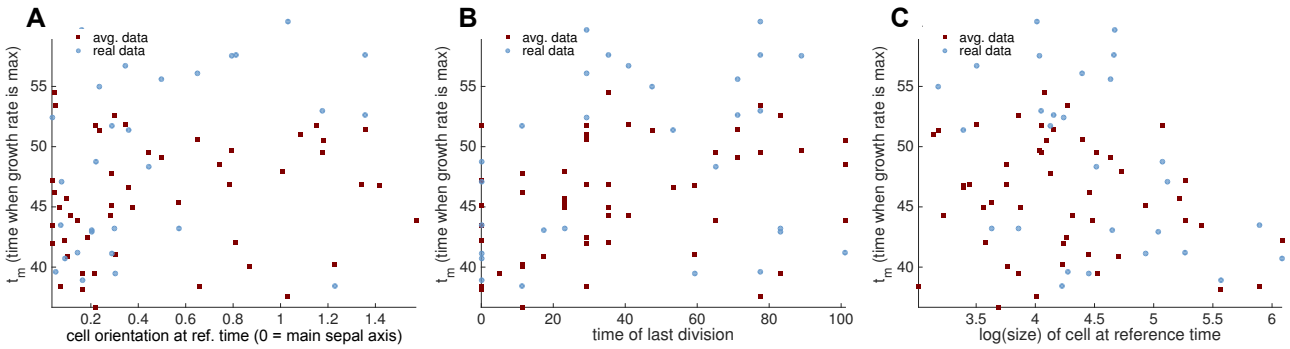

Fig. S16. T_m does not correlate with cell orientation, time of last division, or area. We looked for correlations between t_m and cell orientation **(A)**, time of last division **(B)** and ln(area) **(C)** for real (blue) and spatially averaged (red) cell lineages of Flower C. We do not consider Flower D because it contained too few data points. The cell orientation is measured as the angle (radians) between the main sepal axis and the main axis of each cell. The time of last division is indicative of whether the cell lineage is actively dividing (late time of last division) or endoreduplicating (early time of last division). We take the logarithm of the cell area to avoid spreading out. Both the area and the angle are measured at the reference time point.

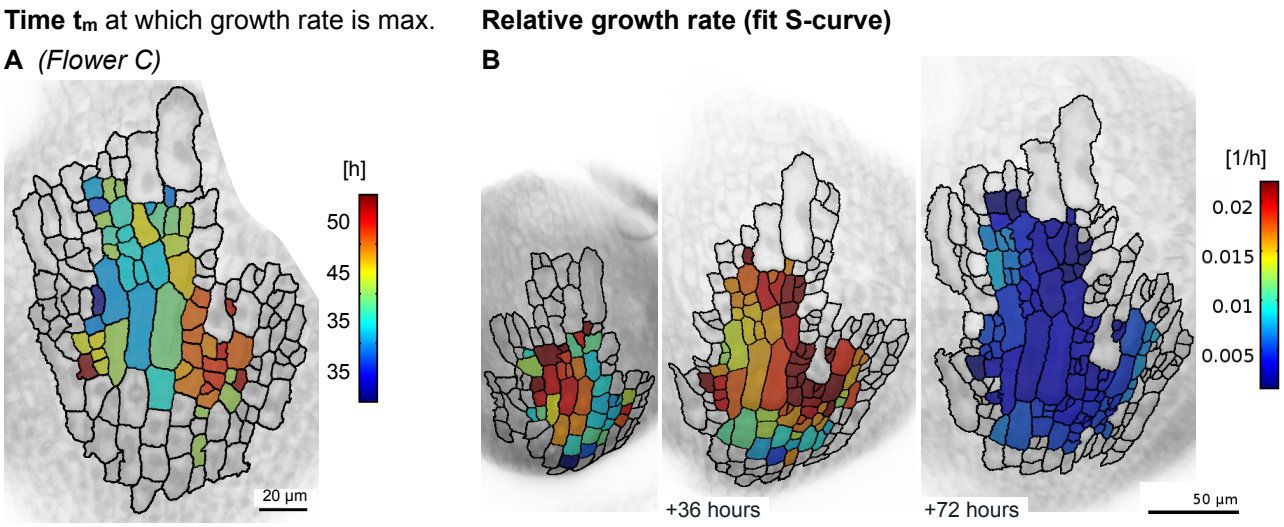

Fig. S17. We observe spatial trends for the relative growth rate and the time of maximum growth. (A) Spatial distribution of t_m appears smooth, with a trend from the top to the bottom of the sepal for Flower C. We only consider data with a meaningful fit to a sigmoid function. We do not consider Flower D because it contained too few data points. The data is shown on the mesh at $t = t_r$. Scale: 20 µm. **(B)** The relative growth rate RGR(t) of Flower C at an initial time point, 36, and 72 hours later. We show RGR(t) based on the fit to a sigmoid curve. Note that while individual neighbors can have different relative growth rates, there is a peak of faster growth that starts at the tip of the sepal and moves downward as the sepal develops. Scale: 50 µm.

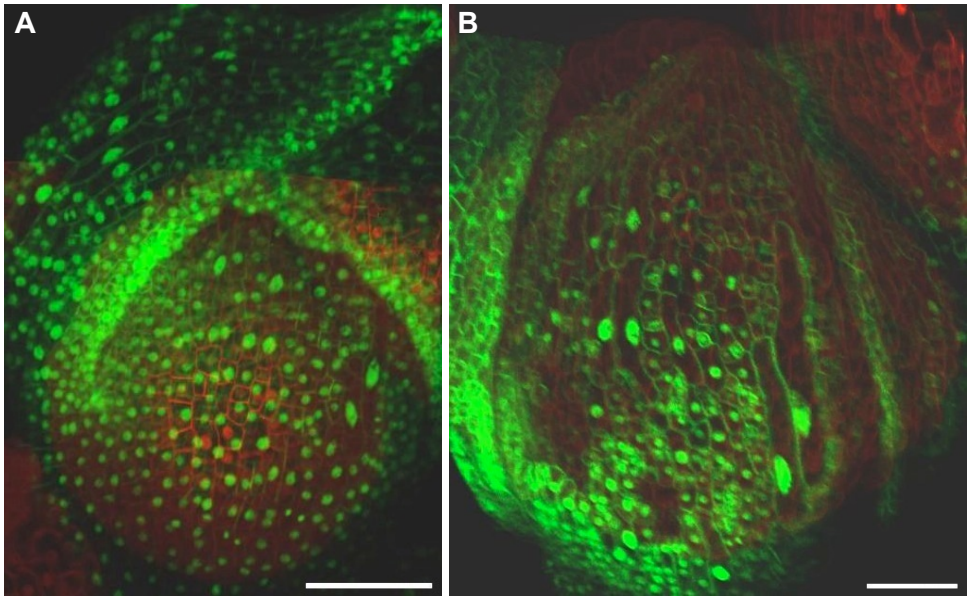

Fig. S18. Comparison of sepals. We compare sepals of Flowers A (green) and B (red) at an initial time point **(A)** and 72 hours later **(B)**. The flowers look similar in size and shape initially. 72 hours later they are similar in length, but Flower B grew larger. Scale: 50 μm.

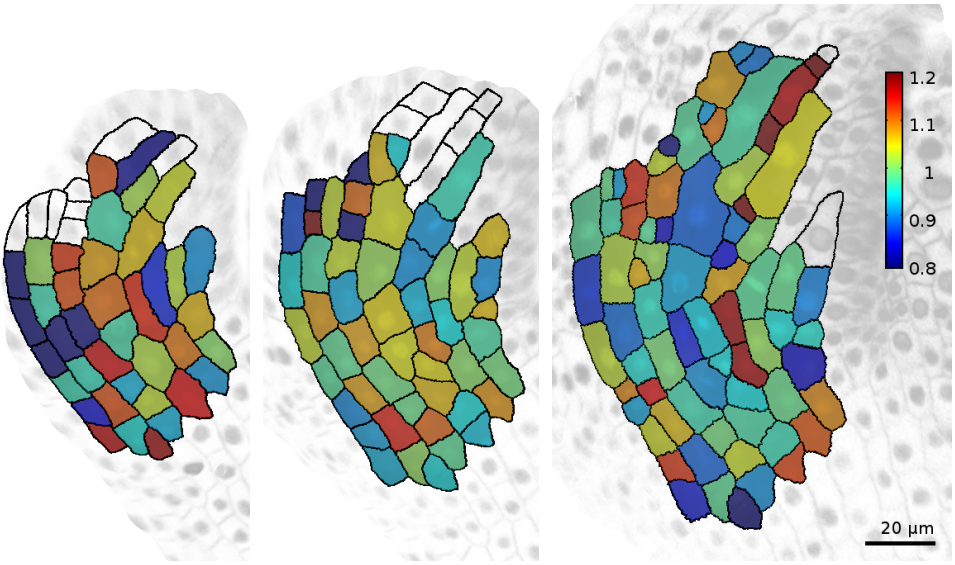

Fig. S19. Estimation of segmentation error. Three time points of Flower D were re-analyzed independently and compared with the original segmentation. The colormap displays the ratio of the cell areas of the two segmentations. We observe that cell areas can vary by 20% between independent segmentation and we assume that segmentation errors are in that order.