Supplemental Experimental Procedures

Zone modeling

The zones are determined by fitting a parametric model to the relation between the sizes of cells and their positions.

The different zones are defined based on the cell elongation rate which is reflected by the cell sizes. They are modeled by a parametric curve, which has three zones – a constant part, a linearly increasing part and another (optional) constant part (depending on the length of the root).

They are connected by smooth transitions. Formally, a continuous function $y = f(x, \theta)$ is fitted to the observed cell positions (x) and sizes (y). It is fully characterized by 6 parameters $\theta = x_1, x_2, y_1, y_2, y_3, y_4$:

$$f(x) = \begin{cases} y_1 + \frac{2B_1}{1+e^{2a(x_1-x)/b_1}} & \text{if } x < x_1 \\ y_2 + a(x-x_1) & \text{if } x_1 \le x \le x_2 \\ y_3 + \frac{2B_2}{1+e^{2a(x_2-x)/b_2}} - b_2 & \text{if } x \ge x_2 \end{cases}$$

$$a = \frac{y_3+y_2}{x_2-x_1}, b_1 = y_2 - y_1, b_2 = y_4 - y_3$$

where the first zone as well as the third zone is modeled as a half of a sigmoid function ($\frac{1}{e^{-x}}$), which models a smooth transition.

The extracted data from cell-wall-stained images can be directly used to fit the above model. The parameter estimation is done by the optimization toolbox in Matlab (using "fminunc" function), i.e. , $min_\theta \sum_i \left\| f(x_i, \theta) - y_i \right\|^2$. 30 optimizations are run with different random initializations, and as the final result the one with the minimal fitting error is selected.

When nuclei-stained data is used for analysis, the cell size cannot directly be measured. The interval between neighboring nuclei in the same cell file is used as an approximate estimation of the cell size.

After obtaining the fitted model, the model is simplified into a continuous piece-wise linear function as:

$$f(x) = \begin{cases} y_1 & \text{if } x < c_1 \\ y_2 + a(x-x_1) & \text{if } c_1 \le x \le c_2 \\ y_4 & \text{if } x \ge c_2 \end{cases}$$

$$c_1 = x_1 + \frac{y_1 - y_2}{a}, b_2 = x_1 + \frac{y_4 - y_2}{a}$$

The assignment of zones is determined by the distance from $f(x)$ to the three line segments above. When the distances to the two closest segments are comparable, the position is considered as a transition between two zones.

Supplemental figures

Supplemental Figure 1: The automatic extraction of the root zonation.

(A-D) Determination of root zonation according to cell length (A, C) or cell volume (B, D) for the cortex of a root growing five days in light (A,B) or darkness (C,D). A continuous function f(x) is fitted (continuous line) to the observed cell position and cell length (A, C) or volume (B,D) (each cell as "+"). This model is then simplified into a piece-wise linear function fl(x) (dotted line). The developmental zones are extracted from this last model. Extracted zone are indicated in colours (meristematic zone MZ, elongation zone EZ, differentiation zone DZ). Grey colour indicates transition between zones (TZ1, TZ2).

Supplemental Figure 2: The influence of the parameter used for meristem length depending of the growth condition.

(A – B) Influence of parameter used on meristem length prediction for root grown for 5 days in light. (C – D) Influence of parameter used on meristem length prediction for root grown for 5 days in darkness. (E – F) Influence of parameter used on meristem length prediction for root grown for 3 days in light and then 1 day in darkness. (G – H) Influence of parameter used on meristem length prediction for root grown for 3 days in light and then 2 day in darkness. (I – J) Influence of parameter used on meristem length prediction for root grown for 3 days in light, then 1 day in darkness and finally 1 day in light. (A, C, E, G and I) Relation between the prediction of meristem length according to cell length and according to cell volume for each cell layer. Curves represent a linear regression fitted to the data. The grey shadow indicates SEM. (B, D, F, H and J) Distribution of meristem length prediction according to cell length and cell volume. Stars indicate significant differences between the two predictions from a Wilcoxon Rank Sum test: * $P<0.05$, ** $P<0.01$, *** $P<0.001$.

Supplemental Figure 3: Cellular geometry of the growing root and its evolution in the meristem.

(A – B) Cell thickness. (C – D) Ratio between cell length and cell thickness. (E – F) Ratio between cell

thickness and cell width. (A, C, E) Average cell dimension according to the layer. Values are the means and error bars SEM. Different letters display significant differences between the layers by a Tukey's test at a 95 percent confidence level. Data extracted from roots marked cell walls (n = 16). (B, D, F) Evolution of cell dimension along the root axis in the meristem. Curves represent a smooth representation of the parameter fitted to the data using generalised additive models. The grey shadow indicates SEM.

Supplemental Figure 4: The influence of light on cell division in the root tip.

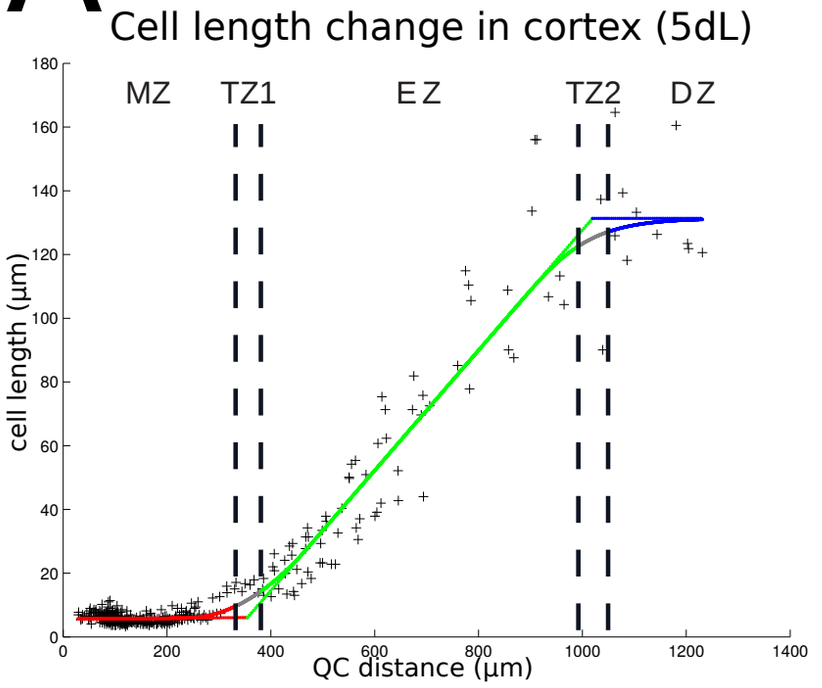
Mitotic index according to cell layer and light regime. Values are mean values and error bars are SEM. Different letters display significant differences between the growth conditions by Tukey's test at 95 percent confidence level (n = 19 for 5dL, n = 14 for 3dL1dD, n = 16 for 3dL2dD and n = 16 for 3dL1dD1dL).

Supplemental Figure 5: The influence of growth speed on the cellular geometry of the MZ.

The evolution of the cell dimensions along the root axis: (A) cell length, (B) cell volume, (C) cell thickness, (D) length to thickness ratio and (M) thickness to width ratio. Curves are fitting curve using generalized additive models based on Gaussian distributions. The grey shadow indicates standard error. Data extracted from roots with marked cell walls (n = 16 for 5dL, n = 16 roots for 3dL1dD, n = 17 for 3dL2dD and n = 15 for 3dL1dD1dL).

Supplemental Figure 1

A



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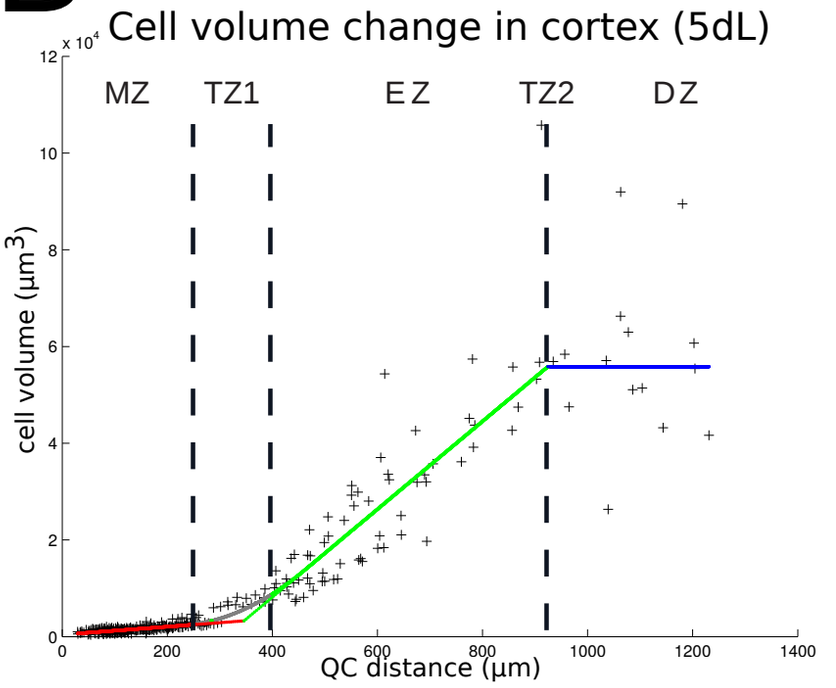

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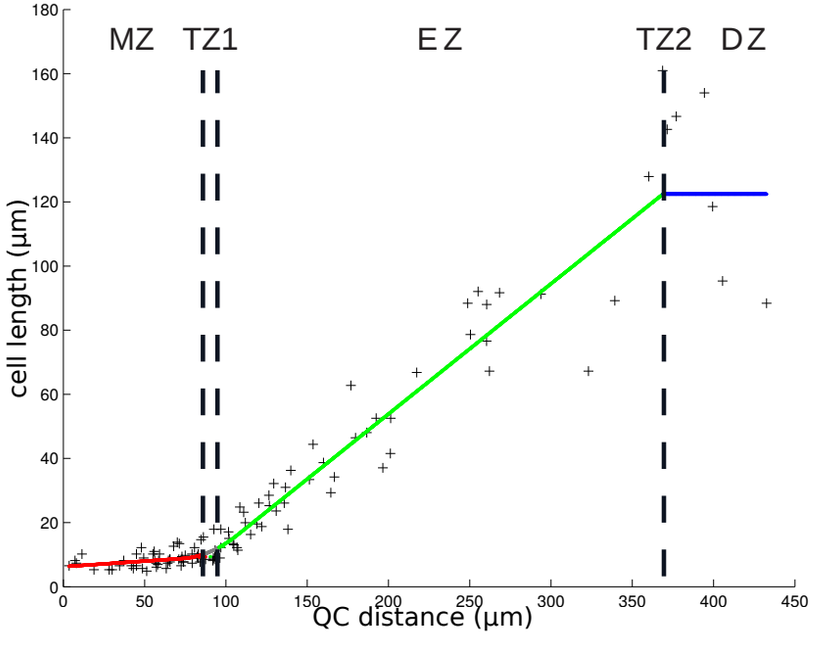

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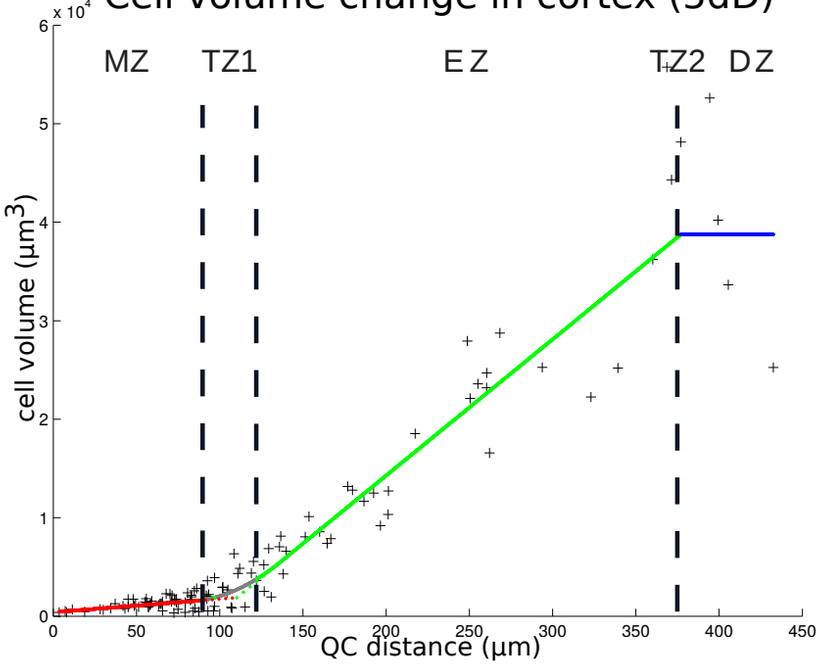
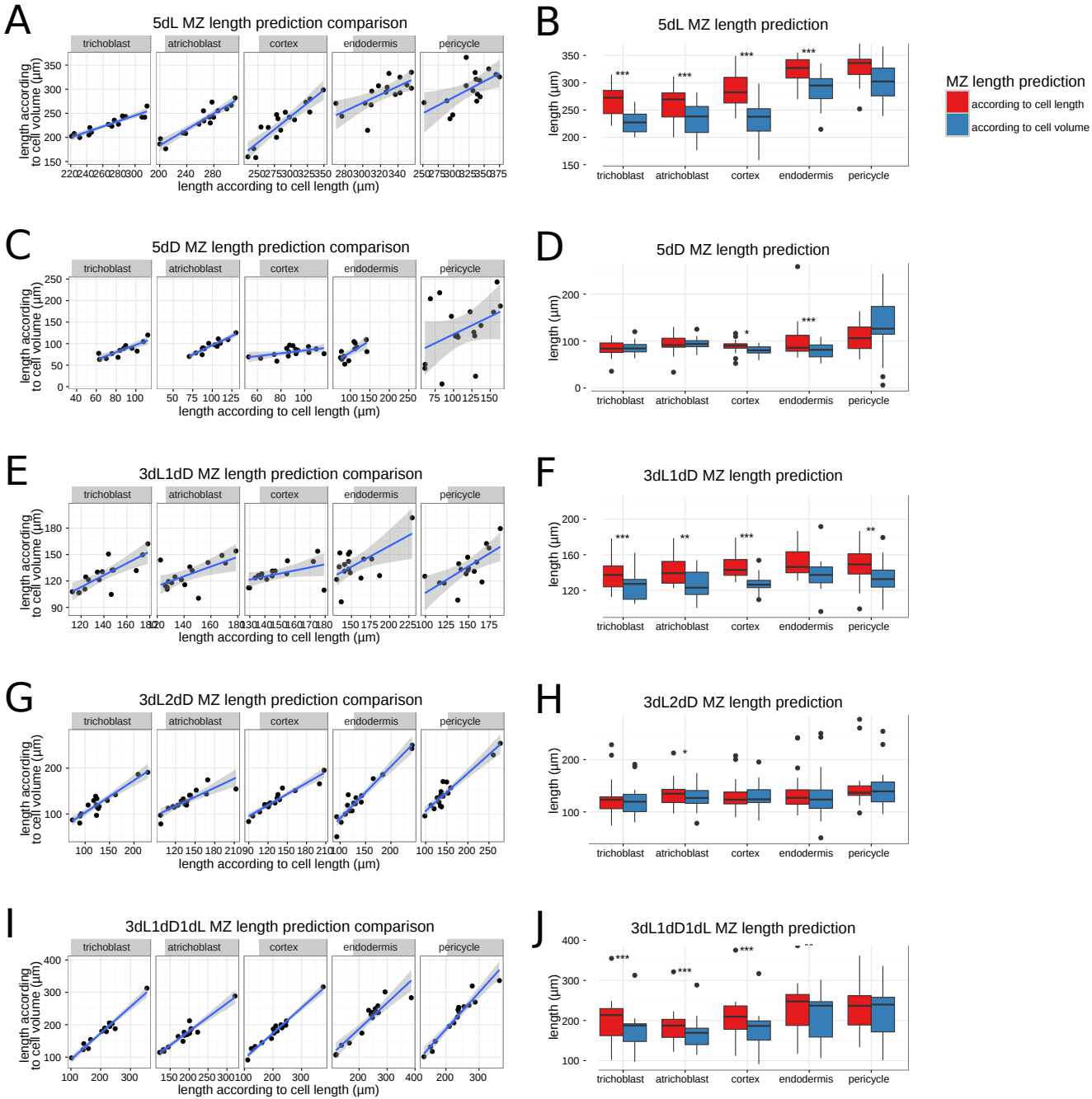
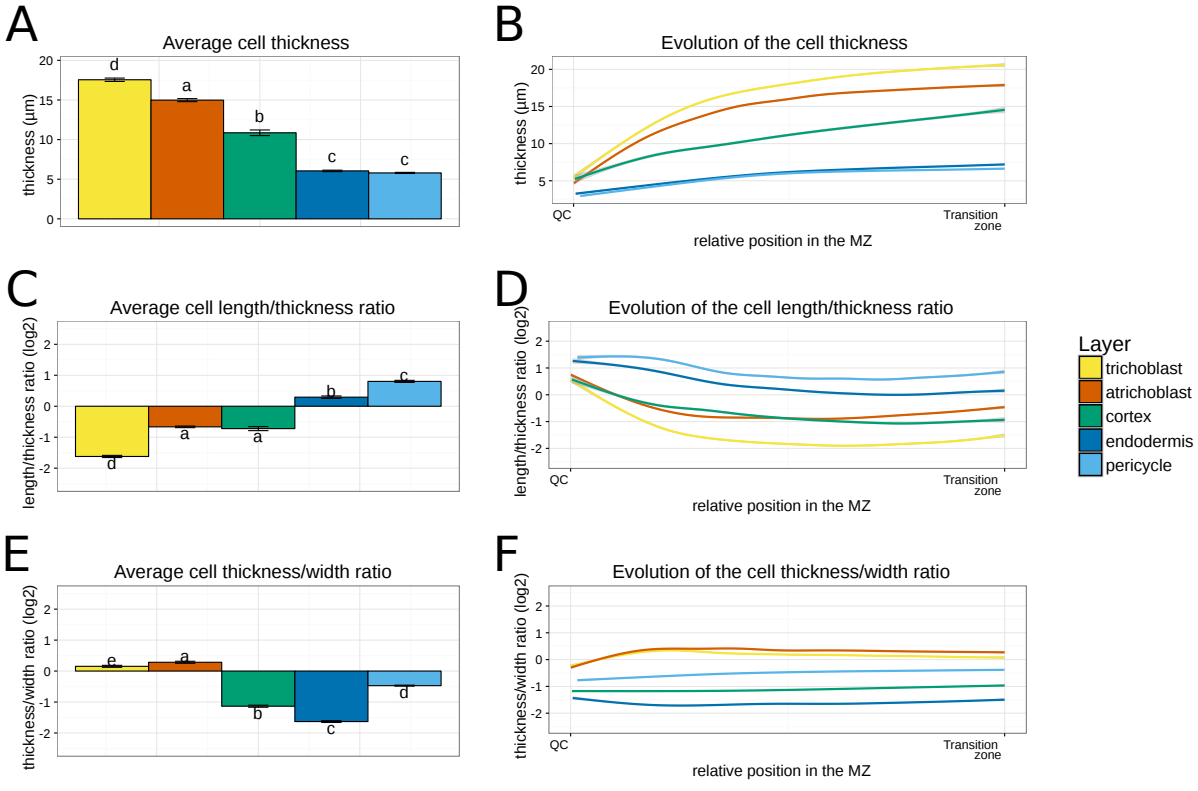


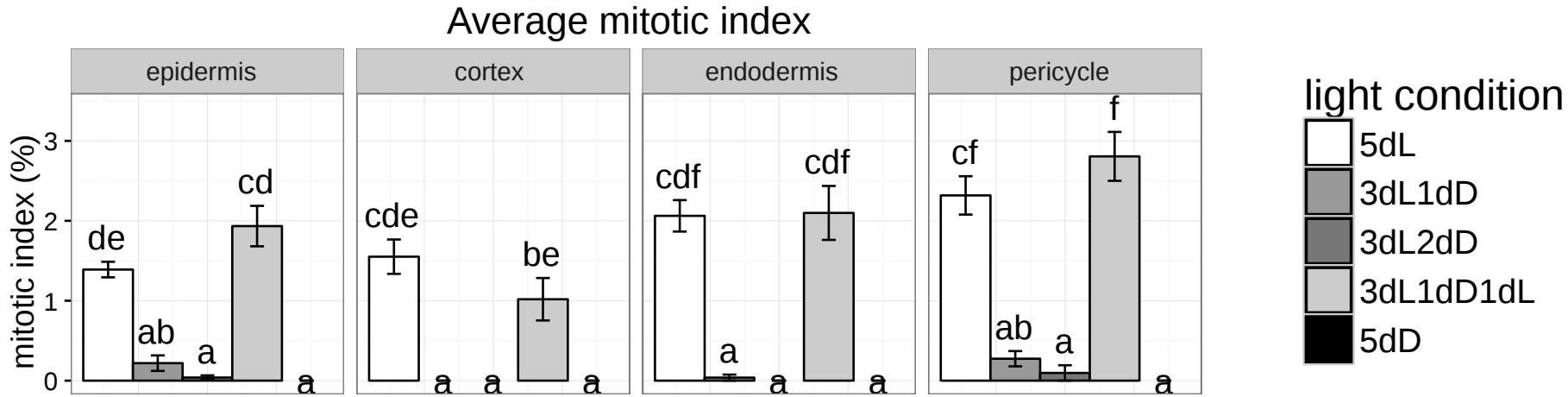
Supplemental Figure 2



Supplemental Figure 3



Supplemental Figure 4



Supplemental Figure 5