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Supplementary Materials for

An epidermis-driven mechanism positions and scales stem cell niches in plants

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This PDF file includes:

Other Supplementary Material for this manuscript includes the following:
(available at advances.sciencemag.org/cgi/content/full/2/1/e1500989/DC1)

Movie S1 (.mp4 format). Primordium growth.

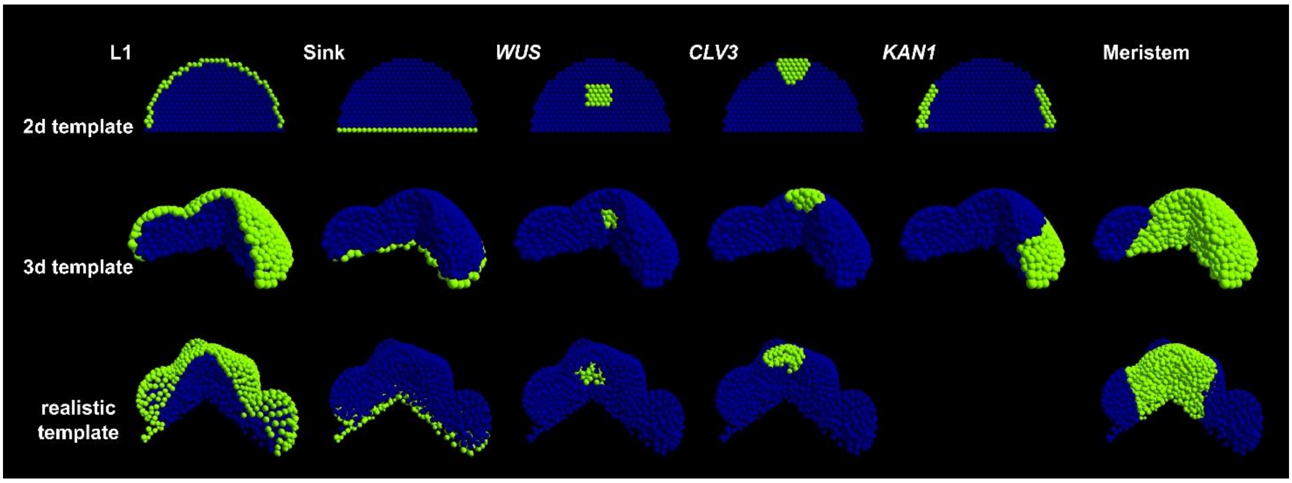

Figure S1 – Templates
The model runs on three different templates, from top to bottom, the lines display: the two-dimensional abstract template, the three-dimensional abstract template and the realistic template. From left to right and in green, are the fixed components used during computations: the boundaries (L1 and Sink), the optimisation targets (*WUS*, *CLV3* and *KAN1*), and the part of the template considered during optimisation of tissues containing primordia.

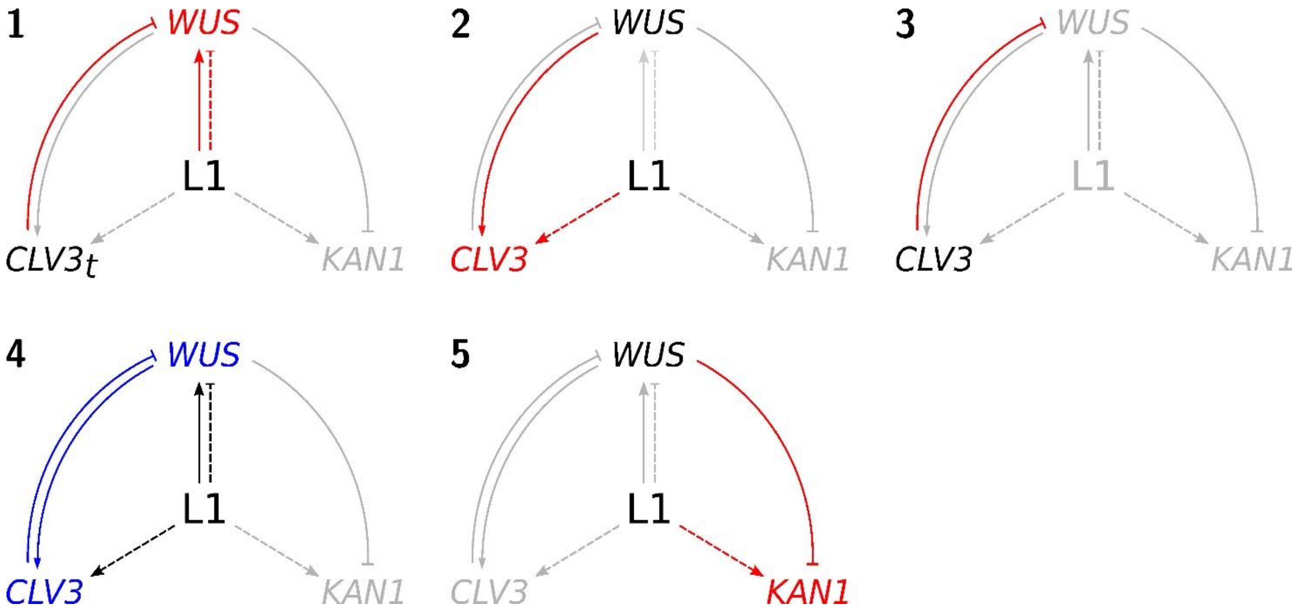

Figure S2 - Optimization strategy
The divide and conquer approach used to optimise the system is summed up in 5 steps. 1) Optimisation of *WUS* using the template defined *CLV3* expression domain. 2) Optimisation of *CLV3*. 3) Re-optimisation of CLV3 peptide gradient. 4) Equilibrium of the core model. 5) Optimisation of *KAN1*. Red: optimised elements, black: fixed element, blue: elements to stabilise, grey: unused elements.

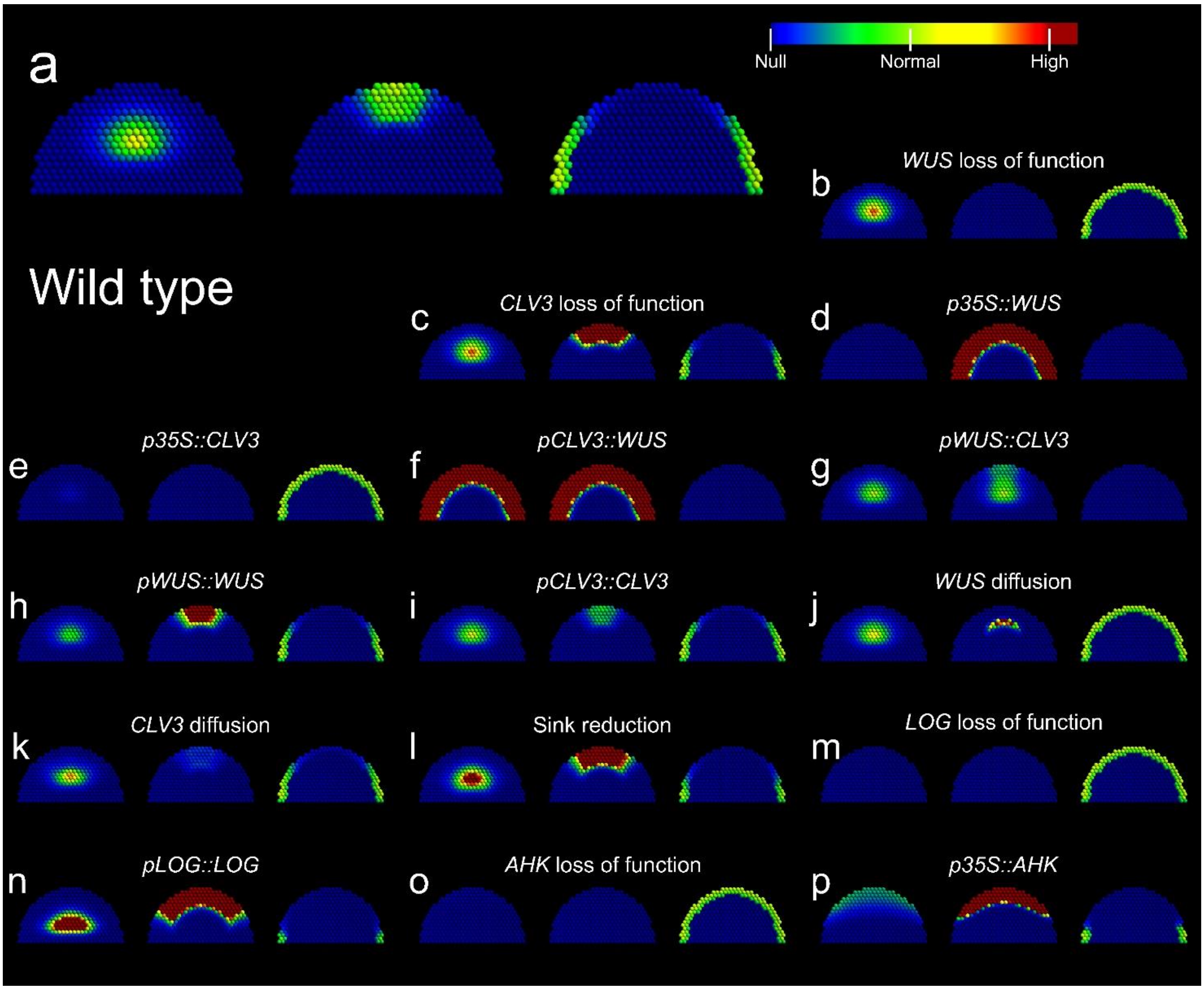

Figure S3 - The model is able to represent a large collection of perturbations
The top panel presents the *wild type* expression patterns obtained after optimisation and is compared to the outcome of various perturbations of the system. Experimentally described mutants are referenced in *(12).*

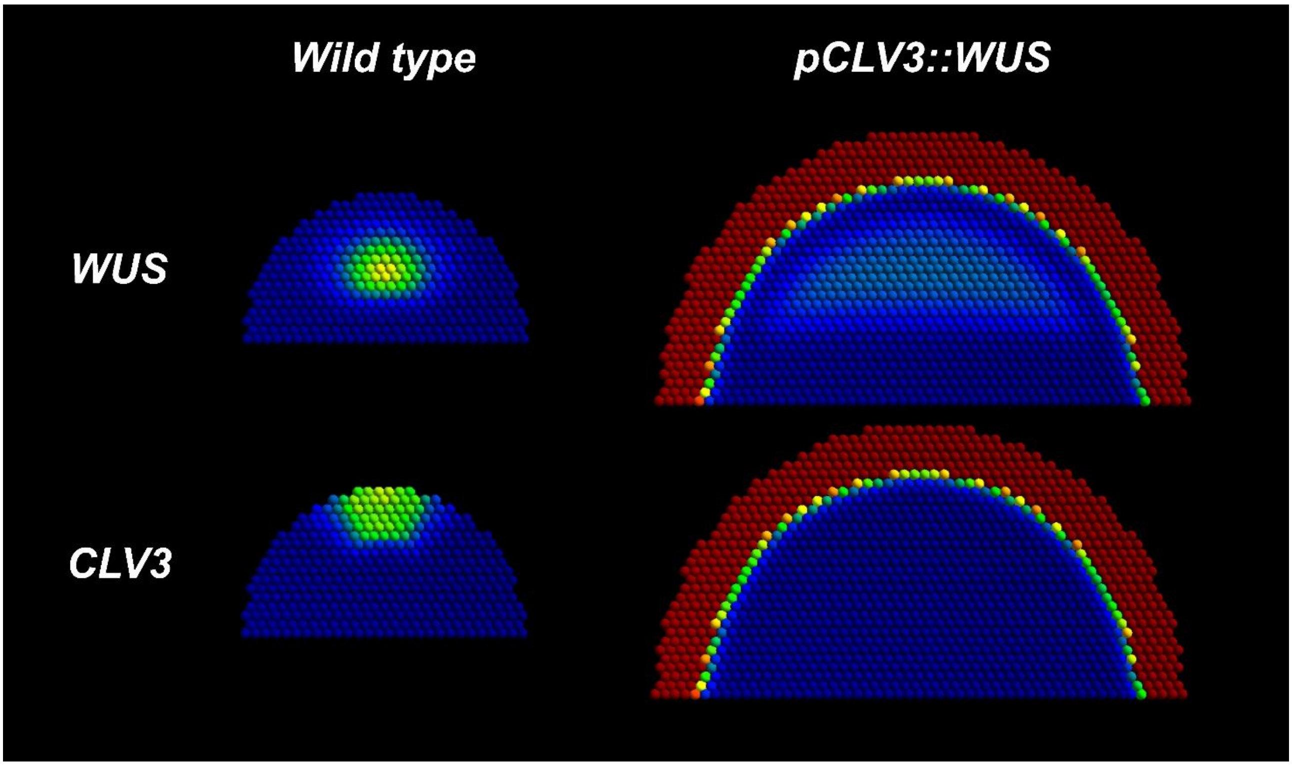

Figure S4 – ***pCLV3::WUS***
Comparison between *wild type* expression domains and a *pCLV3::WUS* mutant applied to a large meristematic tissue

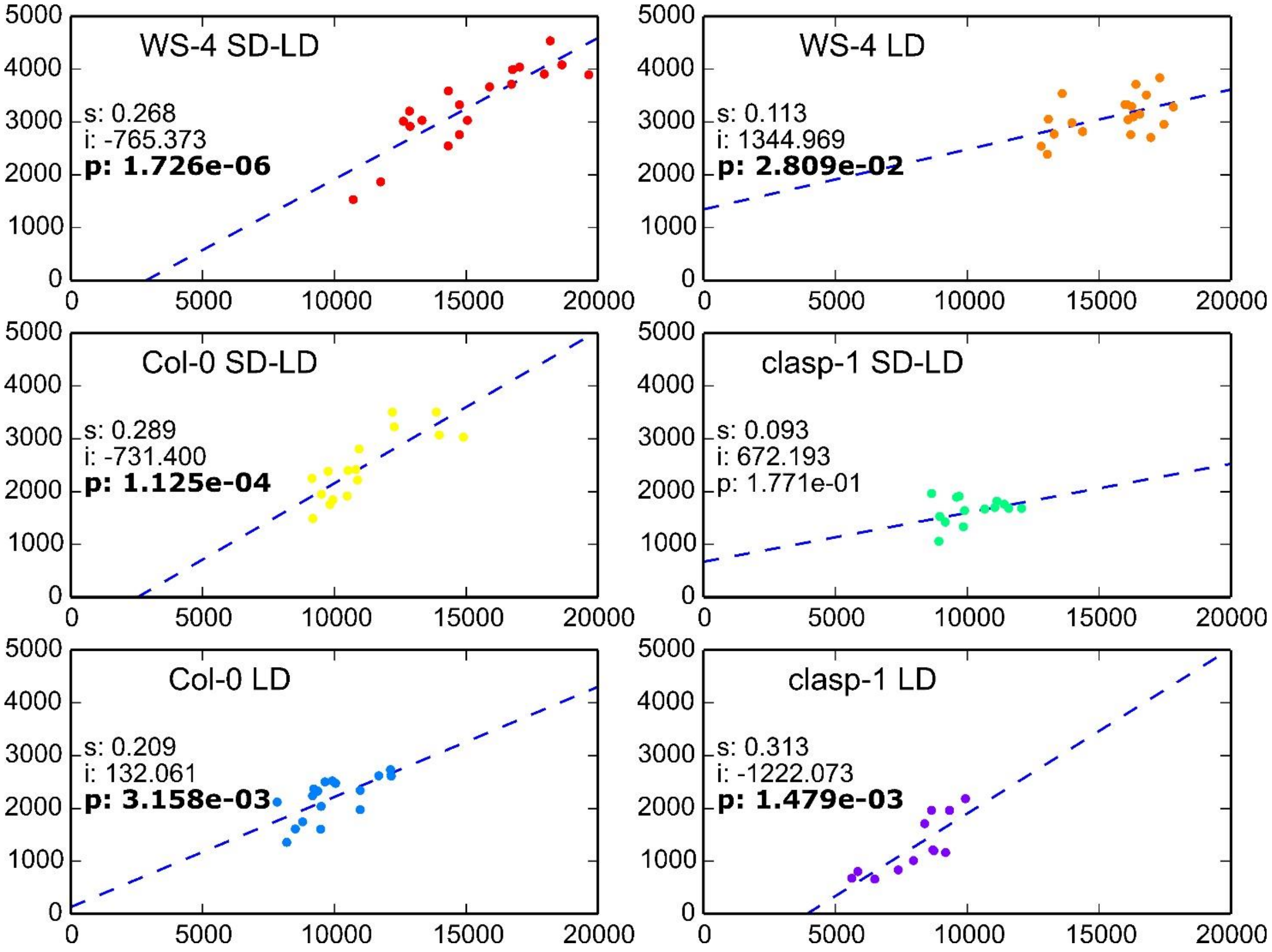

Figure S5 - *WUS* domain size variation

Comparison between size of *WUS* domains and size of SAMs for different growth conditions and genotypes. LD indicates plants grown in long day conditions while SD-LD indicates plants grown in short days followed by long days. A regression line is given with each plot along with its slope, intercept and a p-value testing a null slope.

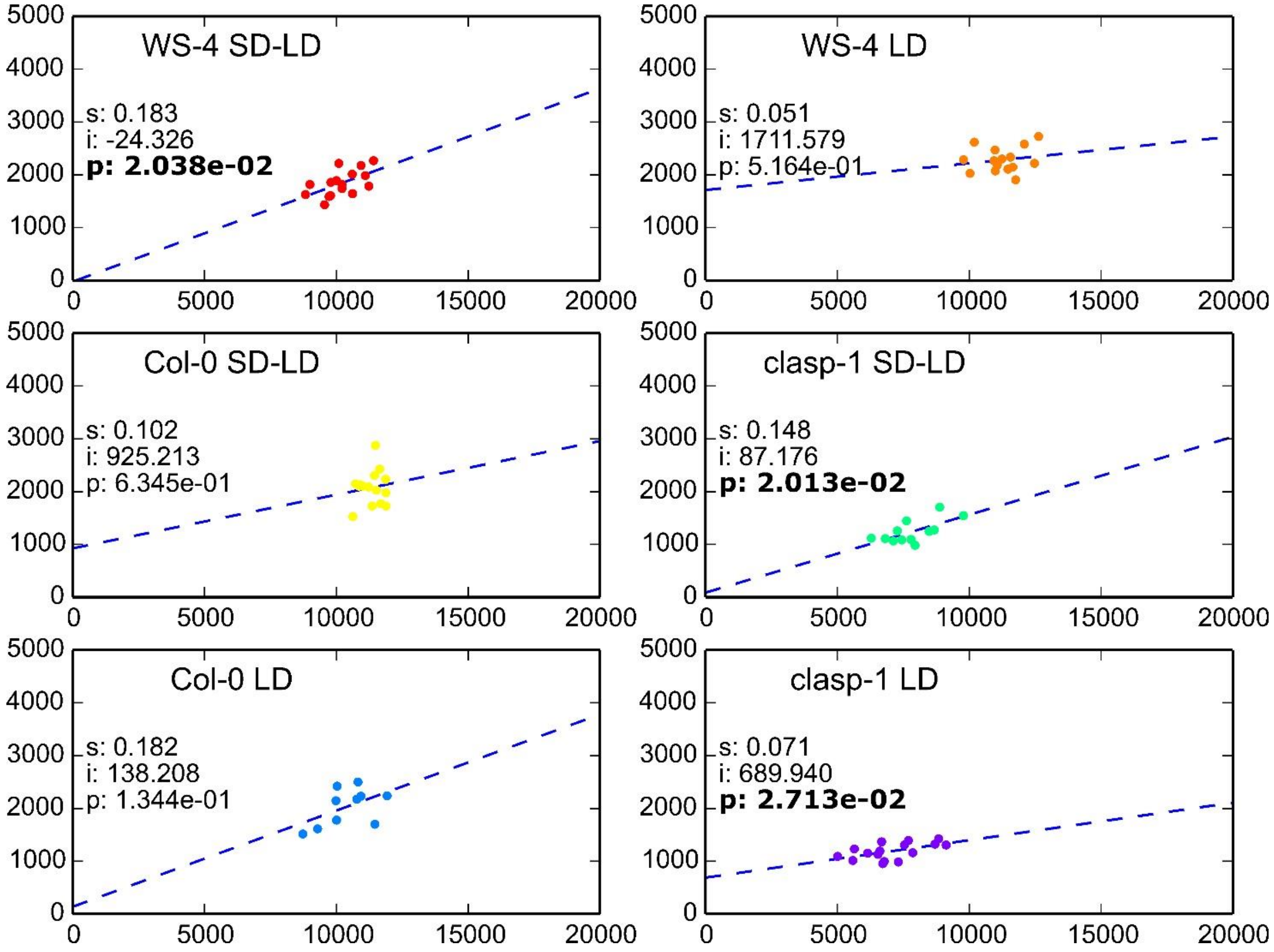

Figure S6 – *CLV3* domain size variation
Comparison between size of *CLV3* domains and size of SAMs for different growth conditions and genotypes. LD indicates plants grown in long day conditions while SD-LD indicates plants grown in short days followed by long days. A regression line is given with each plot along with its slope, intercept and a p-value testing a null slope.

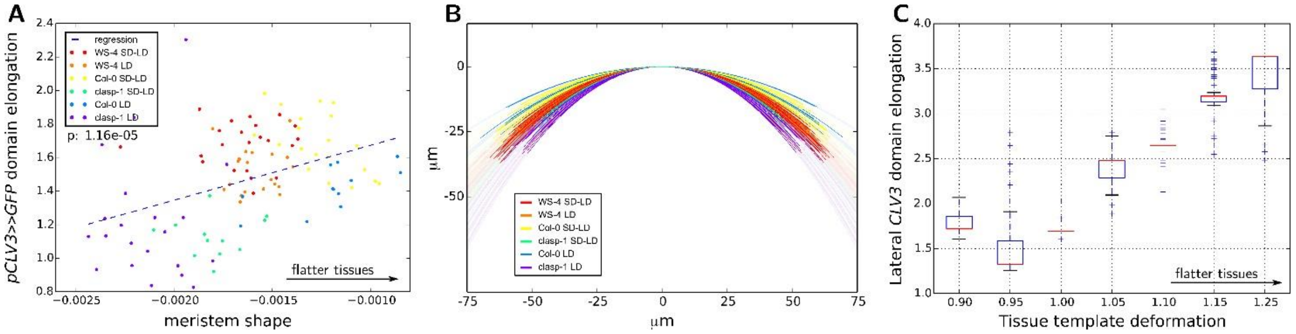

Figure S7 – *pCLV3 >> GFP* meristem shapes and expression domains
A) The x-axis is the value of the *a* parameter of the parabola outlying the meristem, the higher the value, the flatter the meristem. The y-axis is the ratio between the longest vertical axis of *pCLV3>>GFP* expression domain and its longest horizontal axis; the higher the value the more the domain is horizontally elongated. B) Recorded meristem shapes plotted as parabolas. The horizontal span of a plain parabola corresponds to the width of the treated image. C) The x-axis shows the different tissue templates displayed in Figure S20. For the parameter sets optimised for the two dimensional template, the y-axis shows *CLV3* expression domain elongation (longest vertical axis over longest horizontal axis)

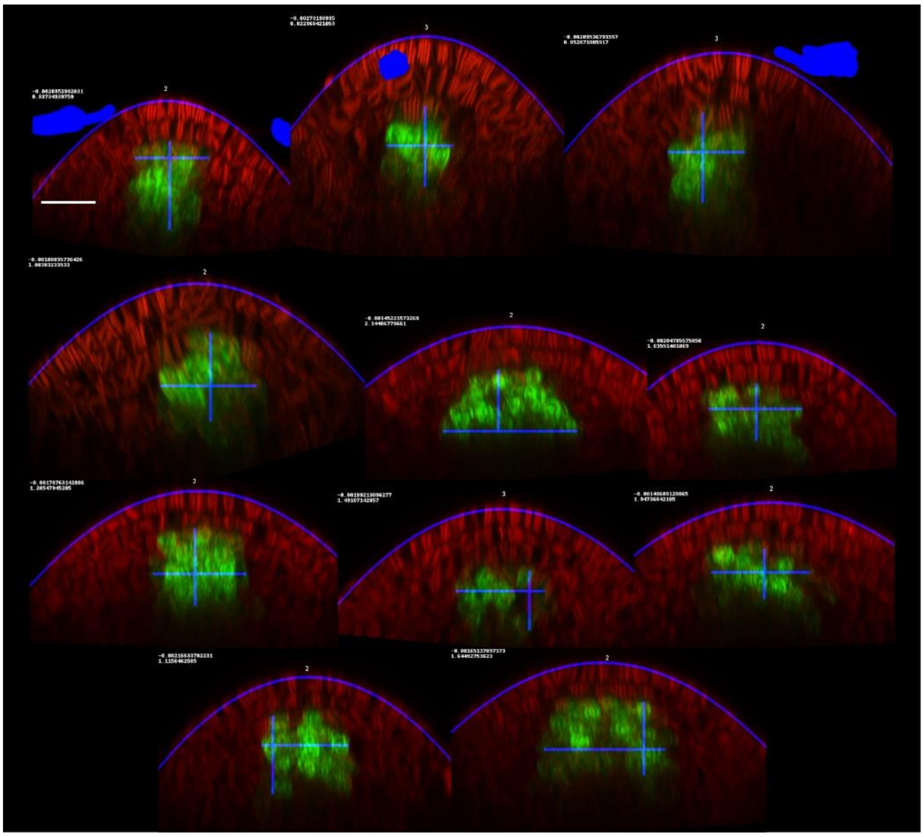

Figure S8 - clasp1 *pWUS* >> *GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. A few images were manually corrected (blue patches) to help the algorithm quantifying the shape of the meristem and expression domain. Scale bar: 20µm.

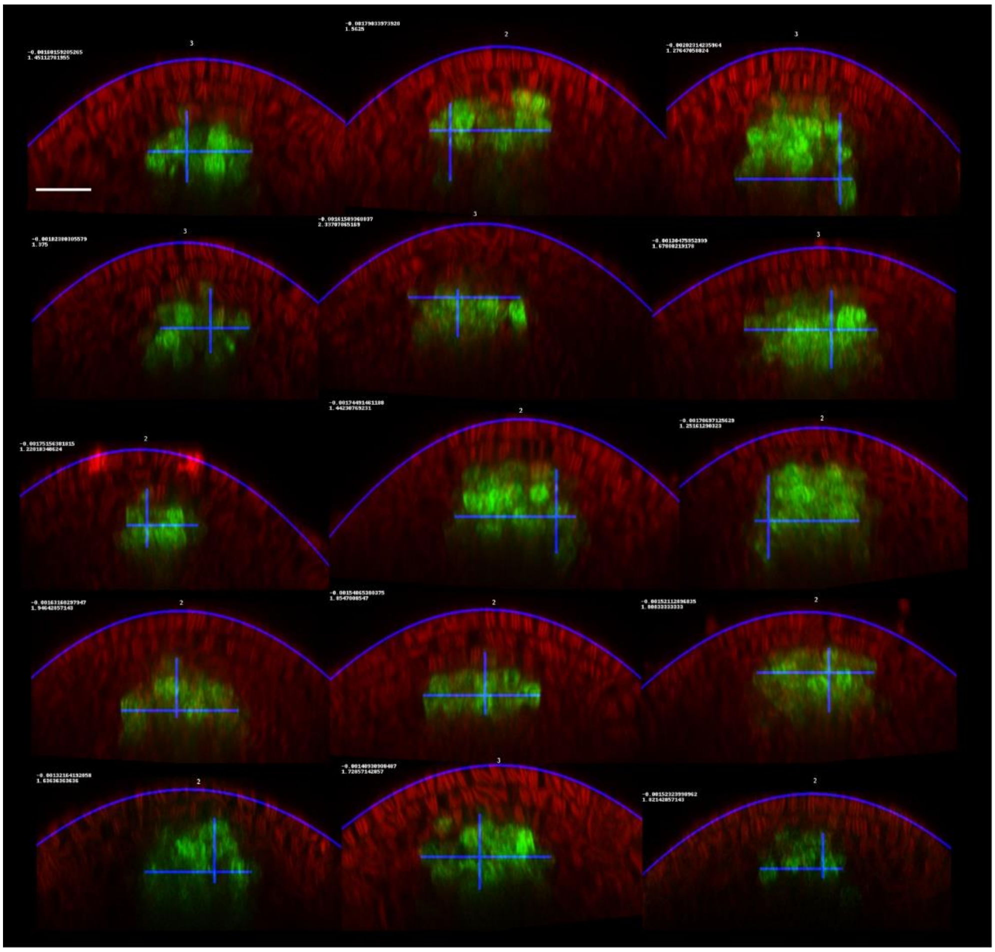

Figure S9 - clasp1 *pWUS >> GFP* meristems, grown in long days followed by short days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. Scale bar: 20µm.

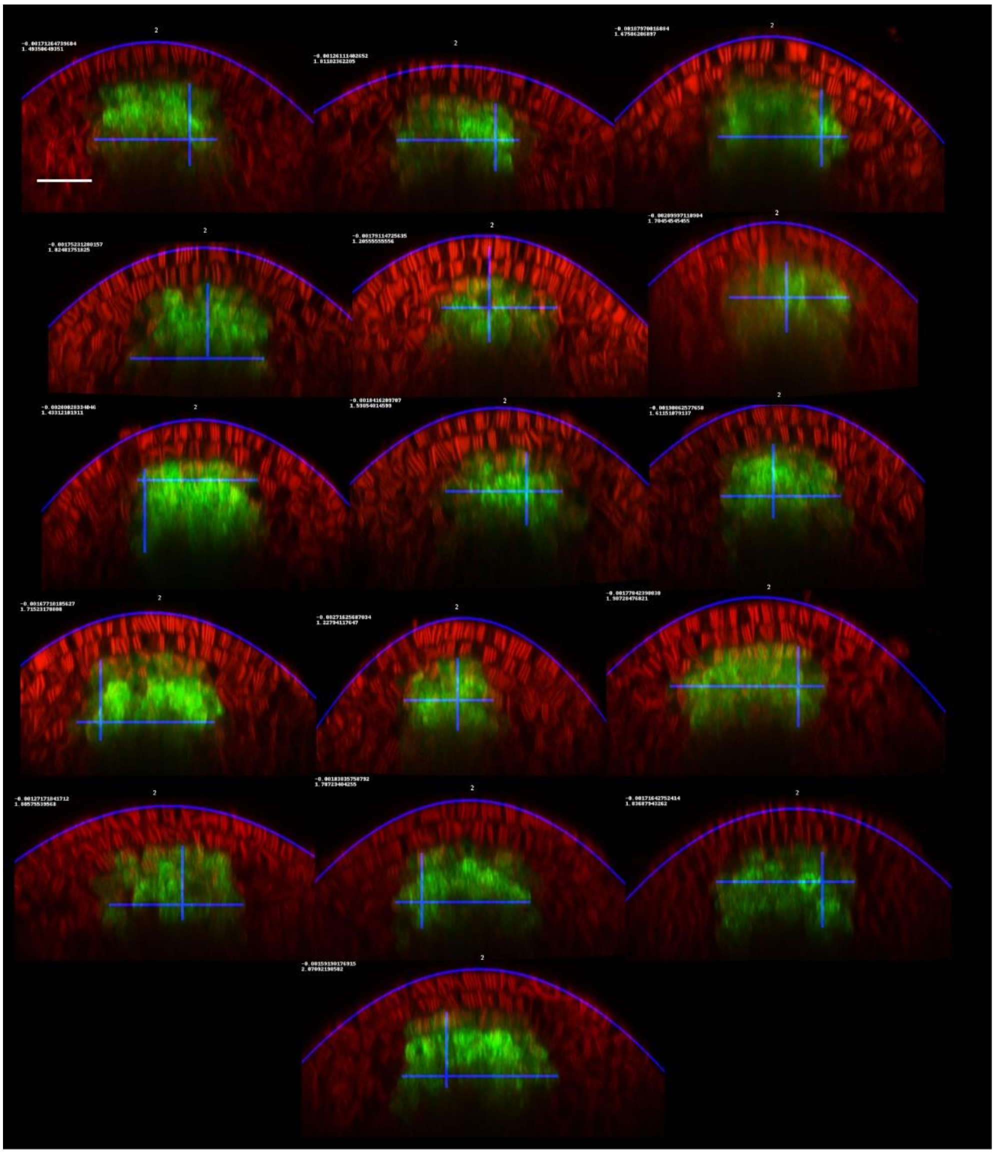

Figure S10 – Col.0 *pWUS* >> *GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. Scale bar: 20μm.

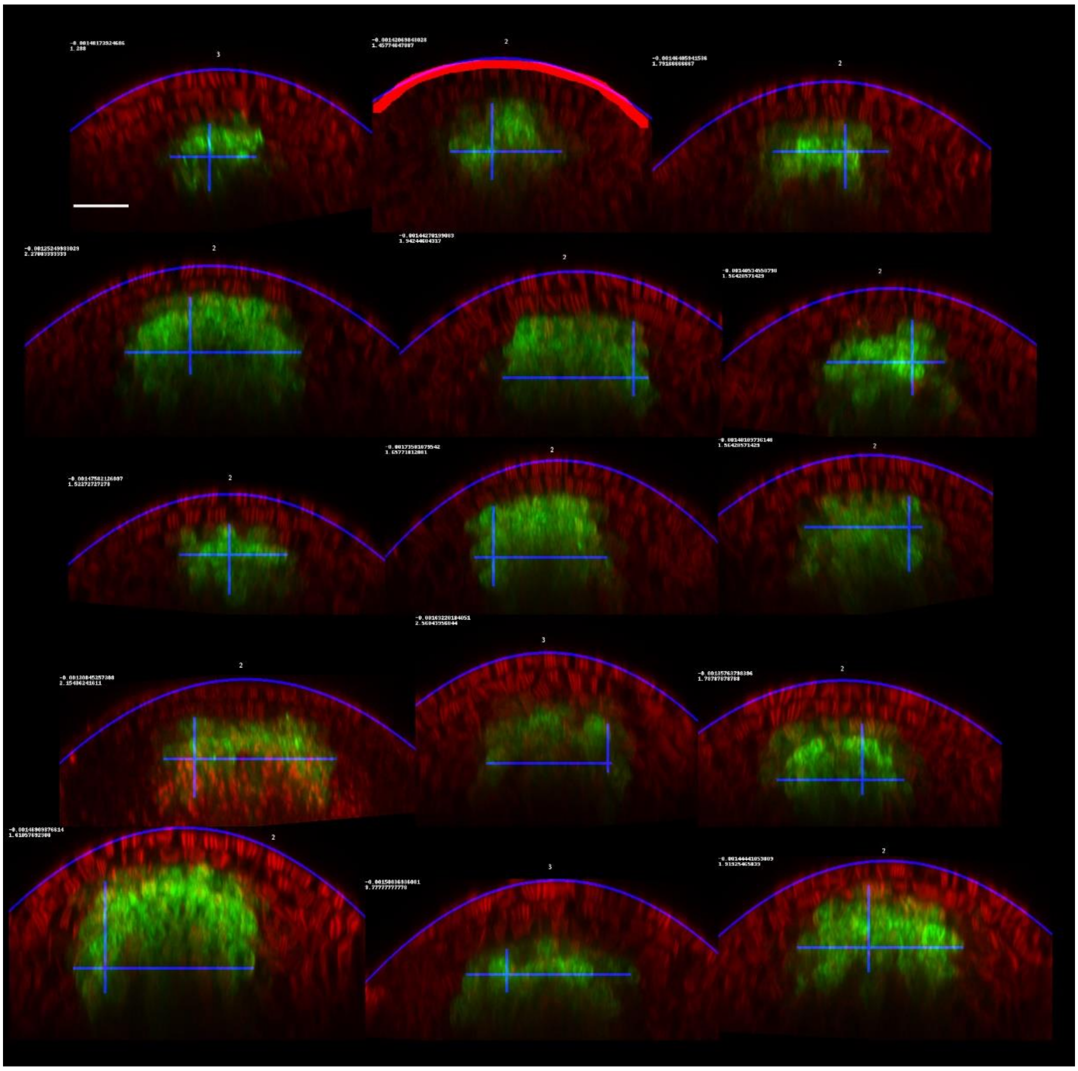

Figure S11 – Col.0 *pWUS >> GFP* meristems, grown in long days followed by short days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. In one image, the outline of the meristem was manually traced (red line) to help the algorithm quantifying the shape. Scale bar: 20μm.

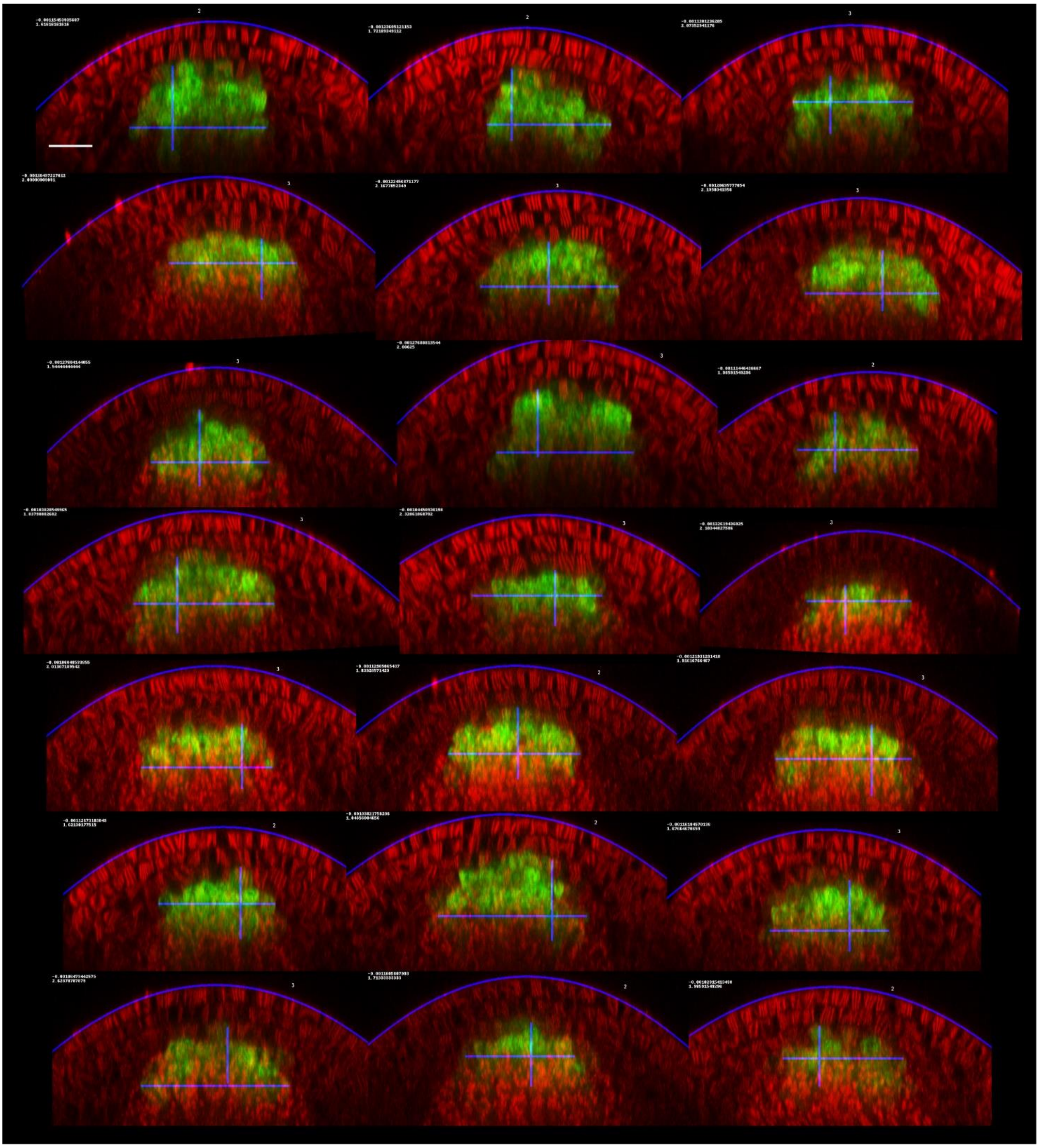

Figure S12 – WS-4 *pWUS >> GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. Scale bar: 20µm.

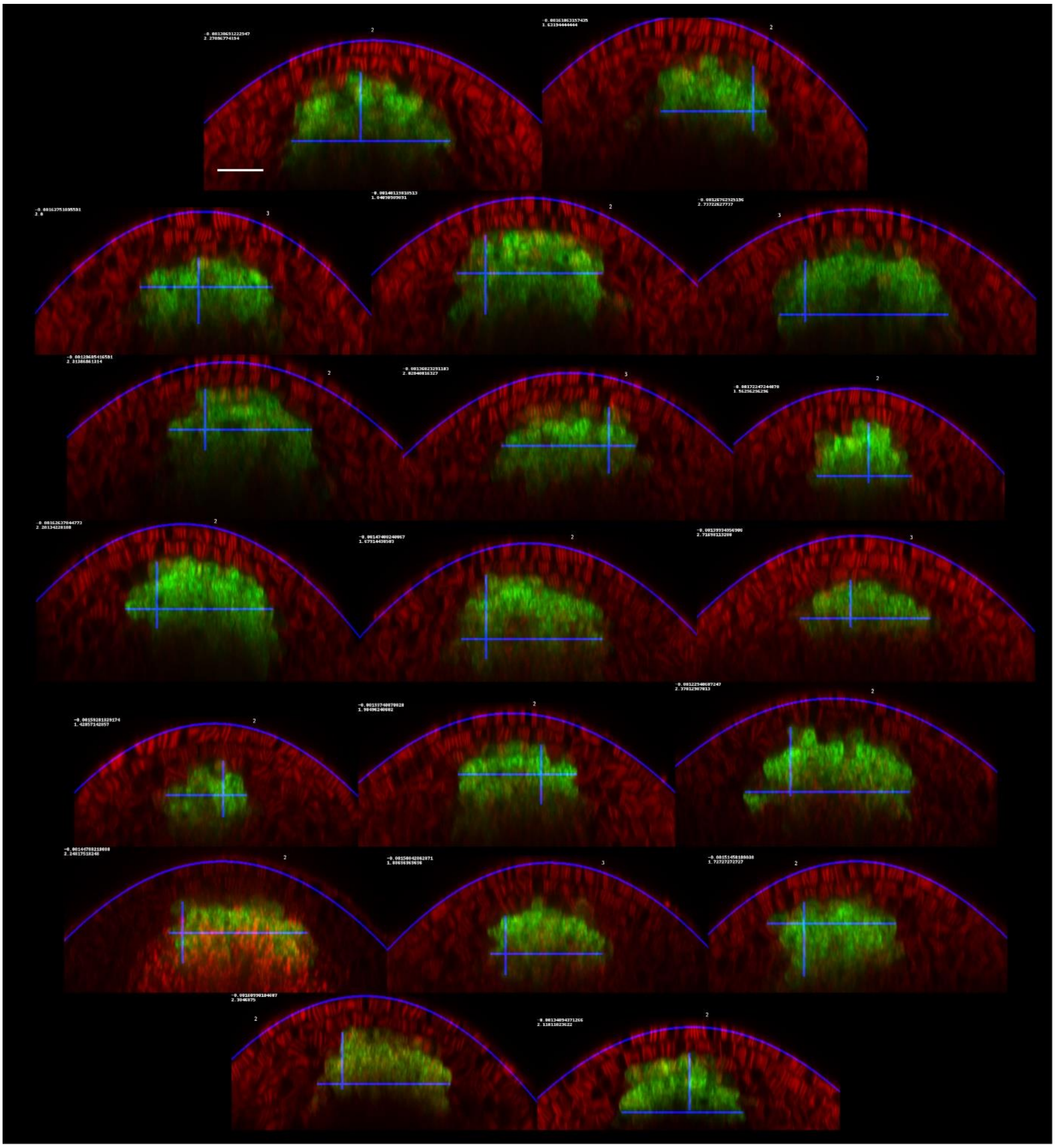

Figure S13 – WS-4 *pWUS* >> *GFP* meristems, grown in long days followed by short days The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. The number above each meristem is a visual count of the amount of cell layers between the tip of the meristem and the top of *WUS* expression domain. Scale bar: 20µm.

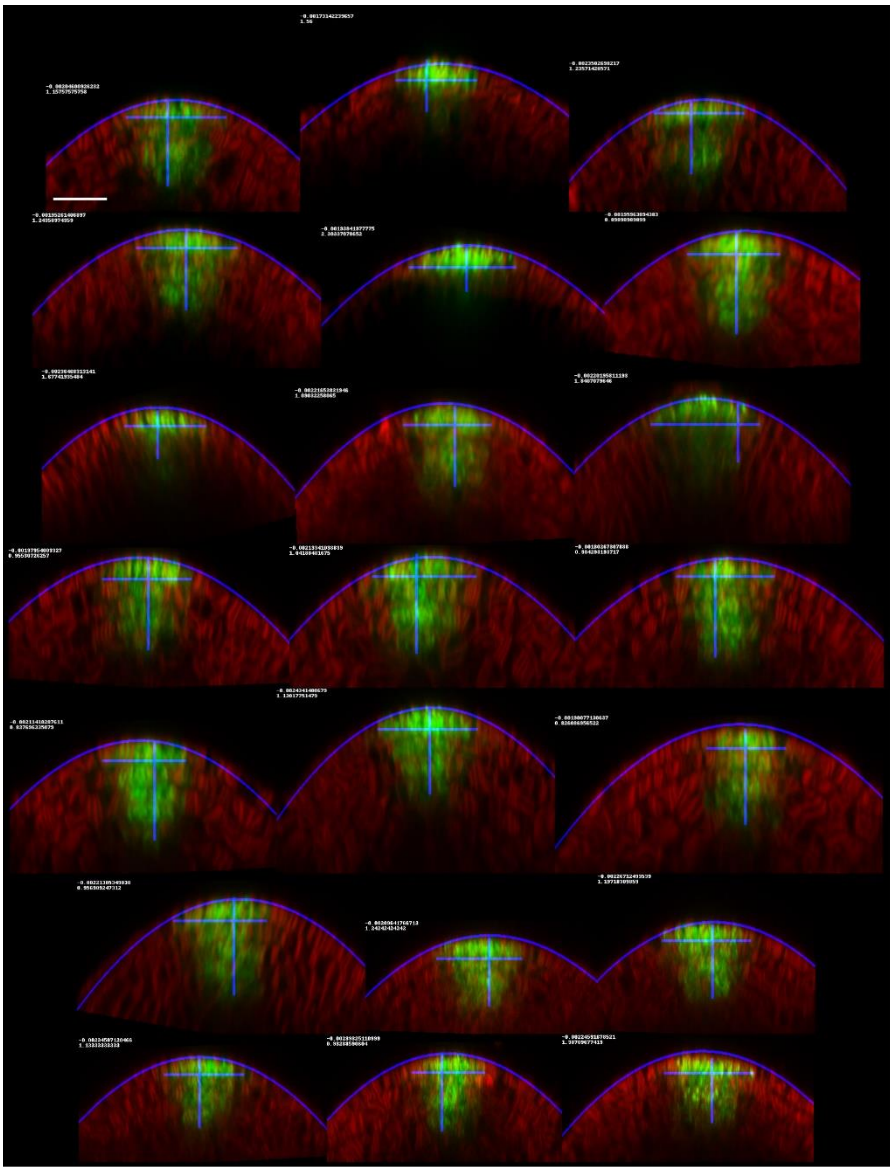

Figure S14 - clasp1 *pCLV3 >> GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

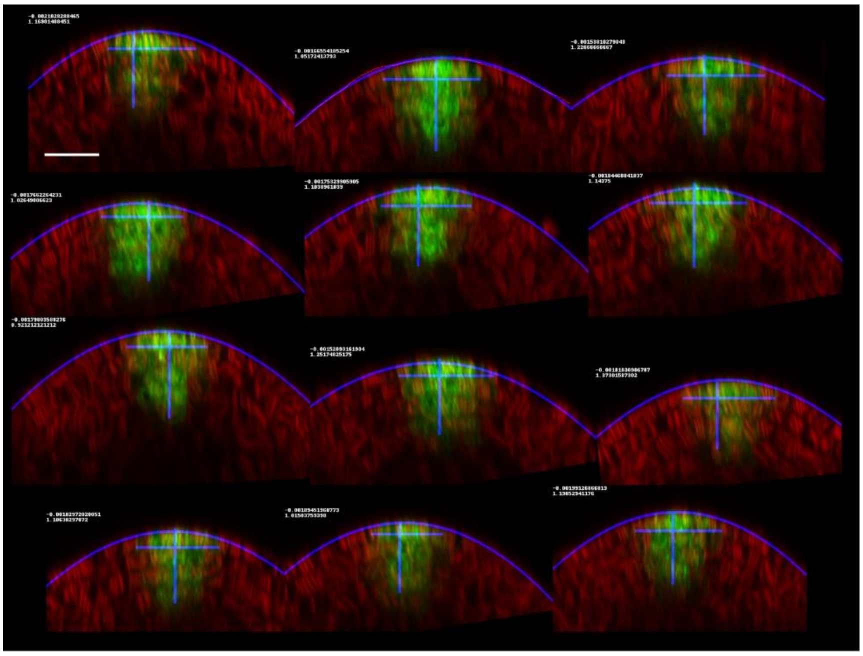

Figure S15 - clasp1 ***pCLV3 >> GFP*** **meristems, grown in long days followed by short days**
The automatically defined parabolas and expression domain axes are displayed in blue. The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

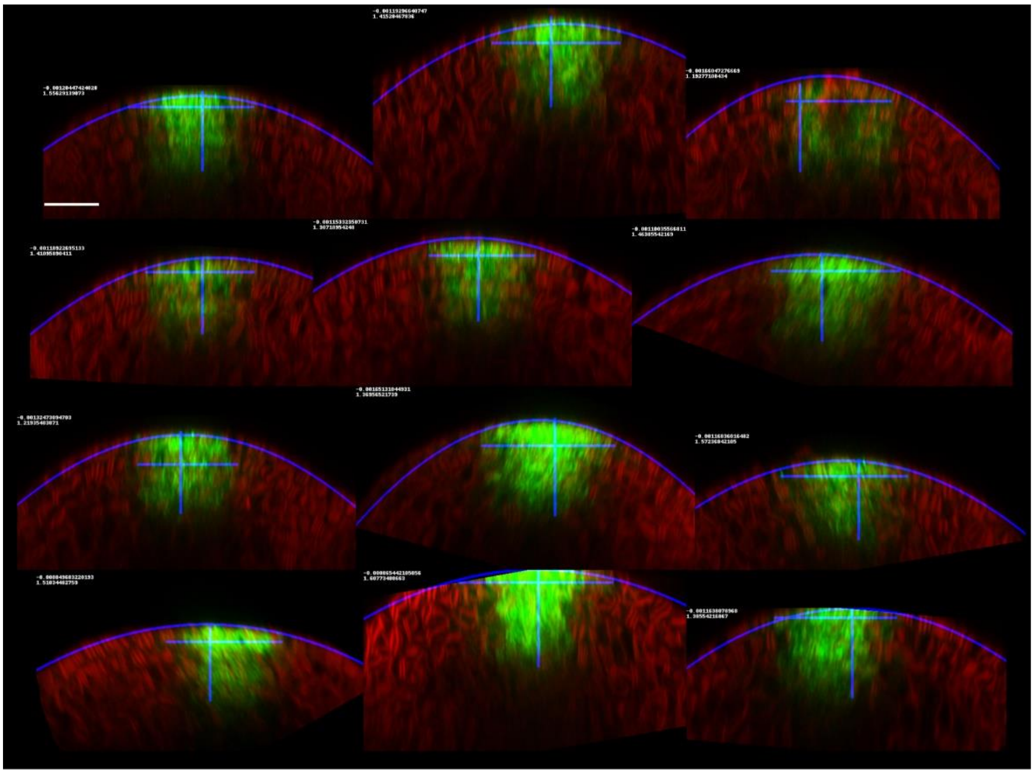

Figure S16 - Col.0 *pCLV3 >> GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

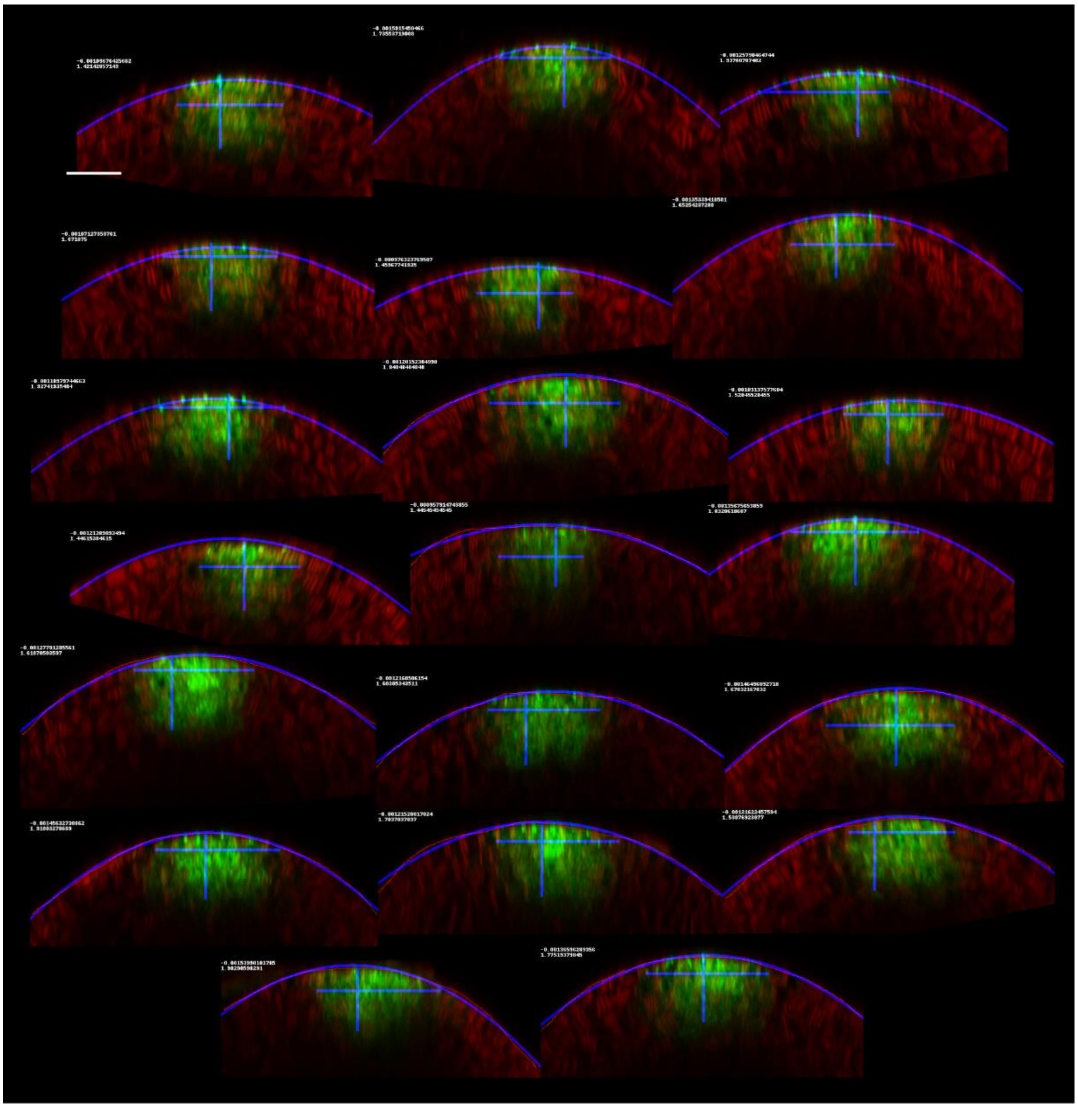

Figure S17 - Col.0 *pCLV3 >> GFP* meristems, grown in long days followed by short days The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

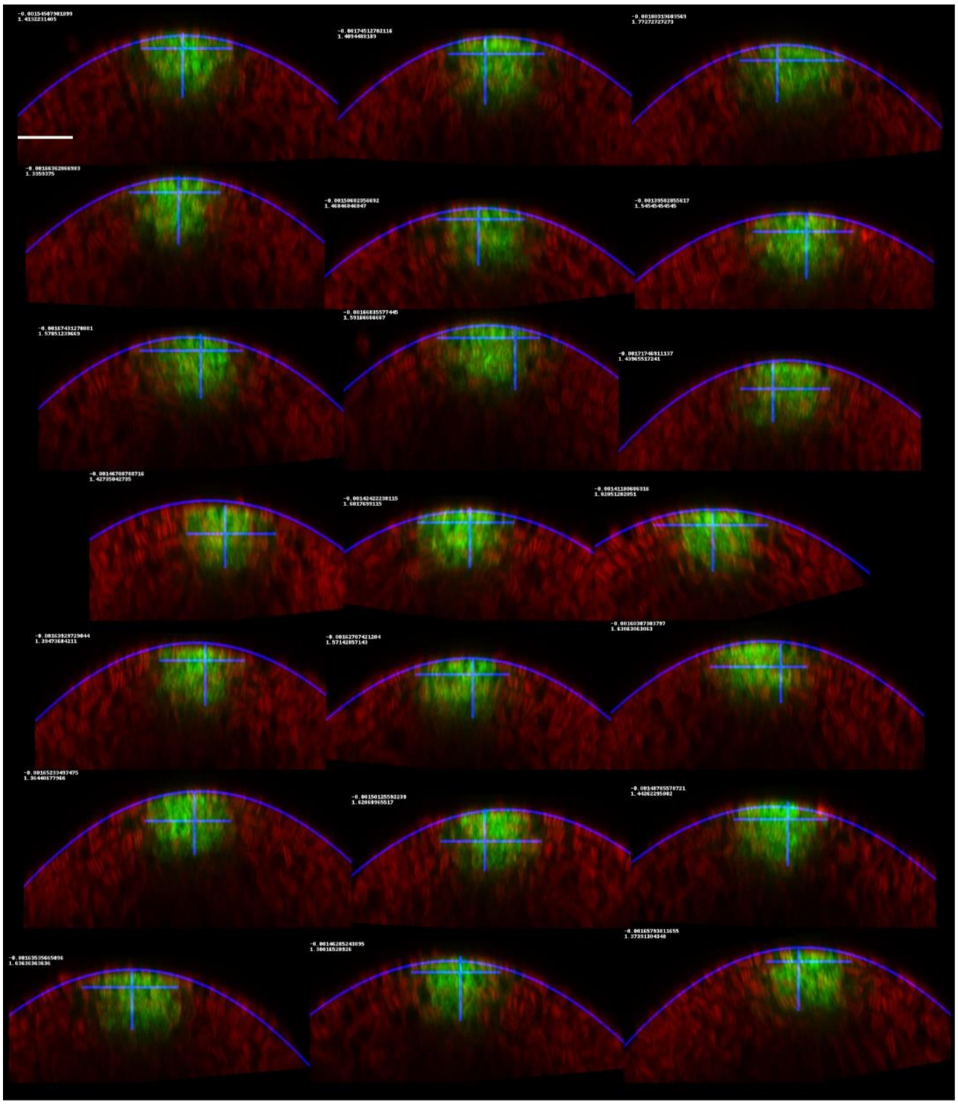

Figure S18 - WS-4 *pCLV3* >> *GFP* meristems, grown in long days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

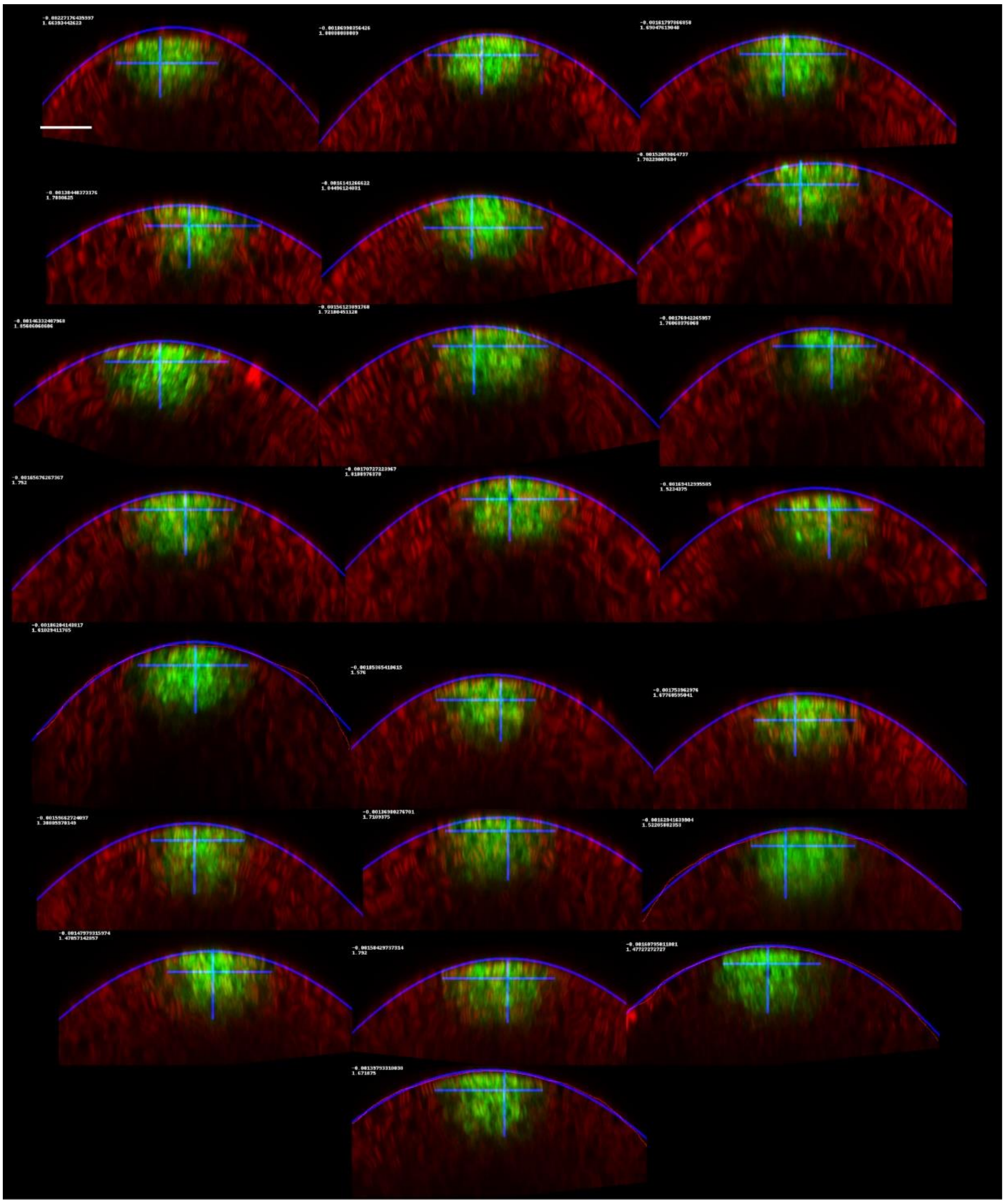

Figure S19 - WS-4 *pCLV3 >> GFP* meristems, grown in long days followed by short days
The top left number in each panel is the *a* parameter describing the blue parabola outlying the meristem shape, the second number is the ratio of the two blue axis describing the expression domain of *WUS*. Scale bar: 20µm.

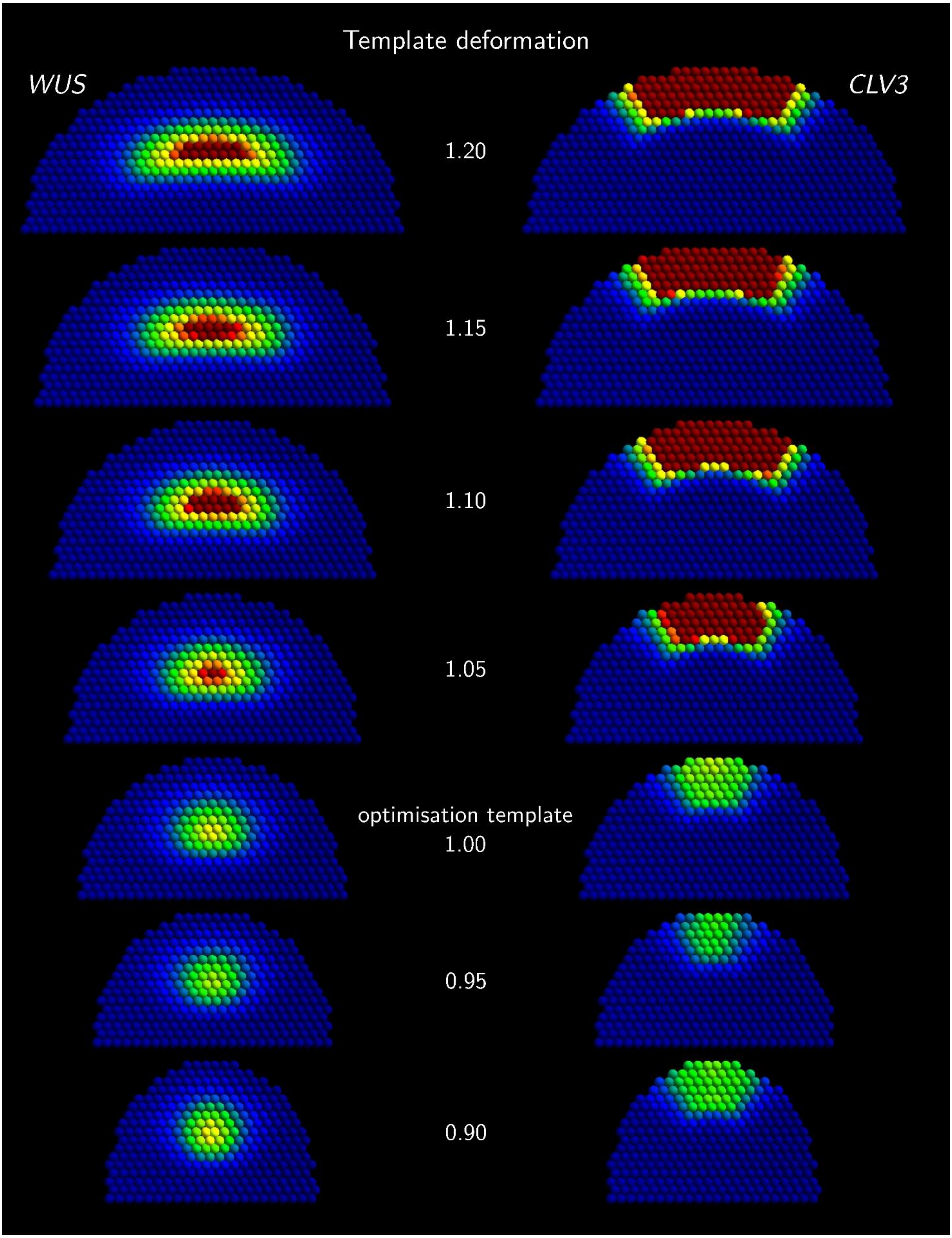

Figure S20 - Example of expression domain variations upon tissue shape changes
From top to bottom, meristems templates are organised from larger and flatter to smaller and narrower. The left row of meristems displays the expression domain of *WUS* and the right row the expression of *CLV3*.

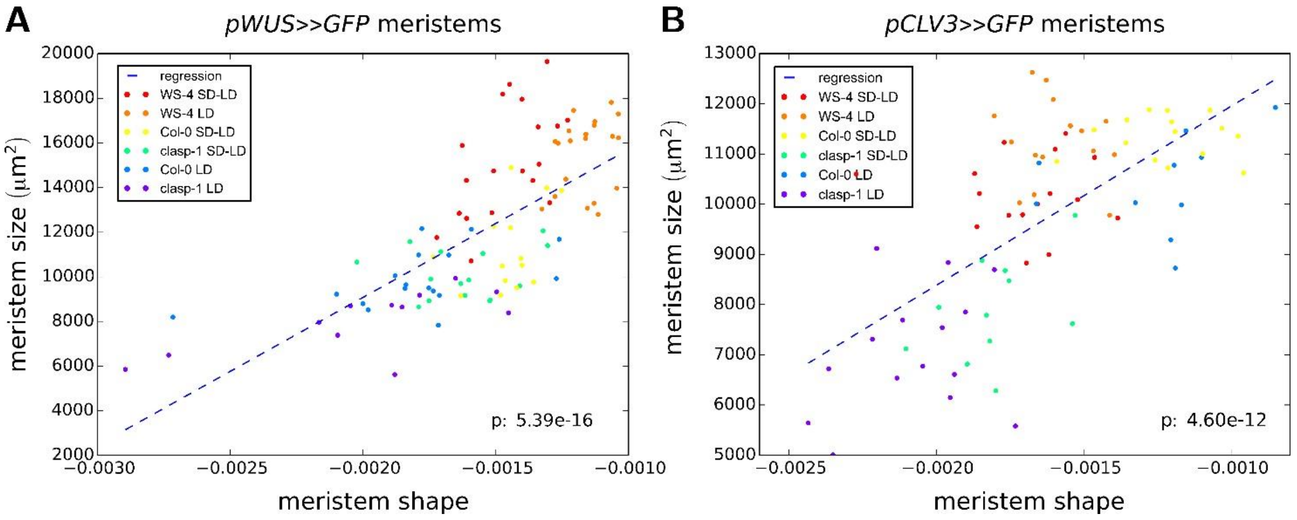

Figure S21 - Meristem size measure versus shape measure
For both panels, the x-axis is the shape of the recorded parabolas (*a* parameter) for the measured meristems. The y-axis is the measured meristem size (Figure 2, main text). In each panel, the linear regression of the data is plotted and the resulting p-value indicated. A) *pWUS>>GFP* meristems. B) *pCLV3>>GFP* meristems.

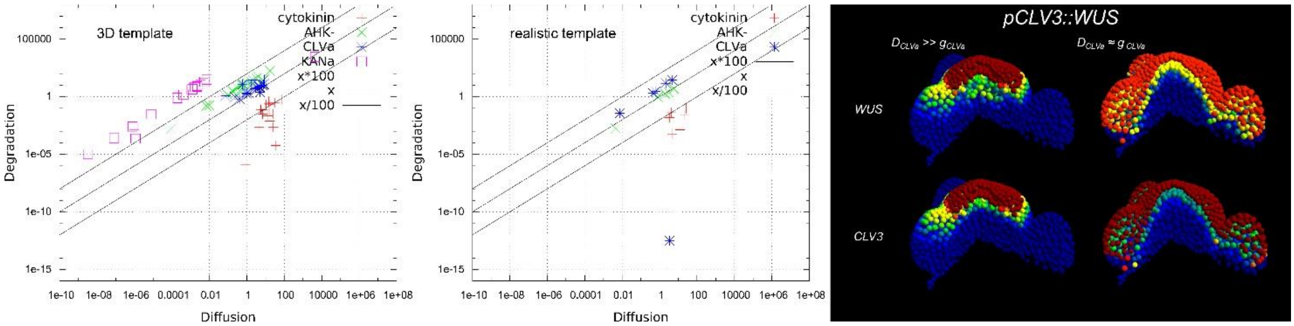

Figure S22 - Long-range and short-range signals
The two first panels plot the optimised diffusion rates against the optimised degradation rates obtained for the three dimensional abstract (left) and realistic (right) templates. The top two dashed lines represent the short-range signals exemplified in Figure 5 (main text), the bottom one is the long-range signal. The right panel explains the outlier point of the realistic template panel (blue point at the bottom) where CLV3a has a long-range type of signal. The simulation presents the outcome of a *pCLV3::WUS* mutant in the case of the outlier and in another example. The outlier can be rejected as it does not display the correct overlap of both *WUS* and *CLV3* domains in the outer cell layers.

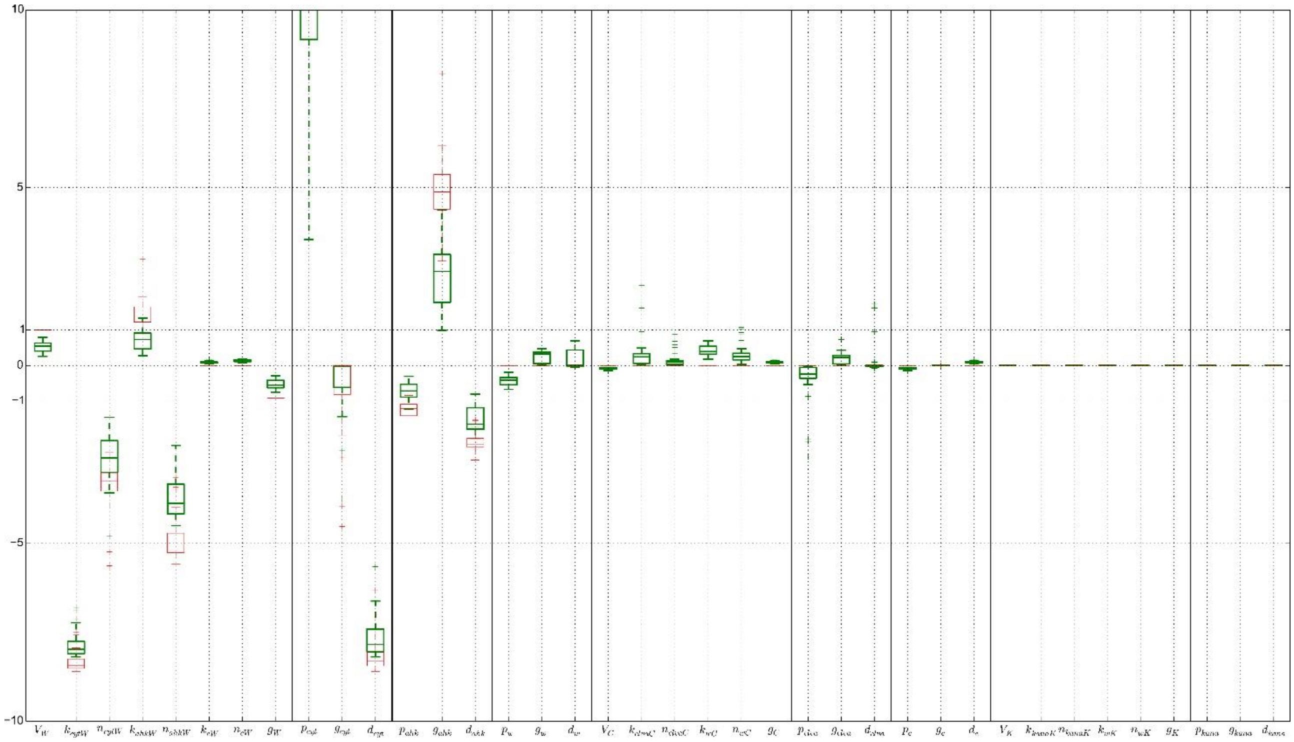

Figure S23 – *WUS* sensitivity analysis
The data is computed for the 255 parameter sets resulting of the optimisations of the two-dimensional abstract template. The x-axis shows the parameters and the y-axis the sensitivity of the *WUS* domain to variations of the considered parameter following: $\frac{\Delta m}{\Delta p} \times \frac{p}{m}$ (see text). Green: *wild type*. Red: *clavata* phenotype. Inclusion of the *CLV3*/*WUS* feedback increases robustness.

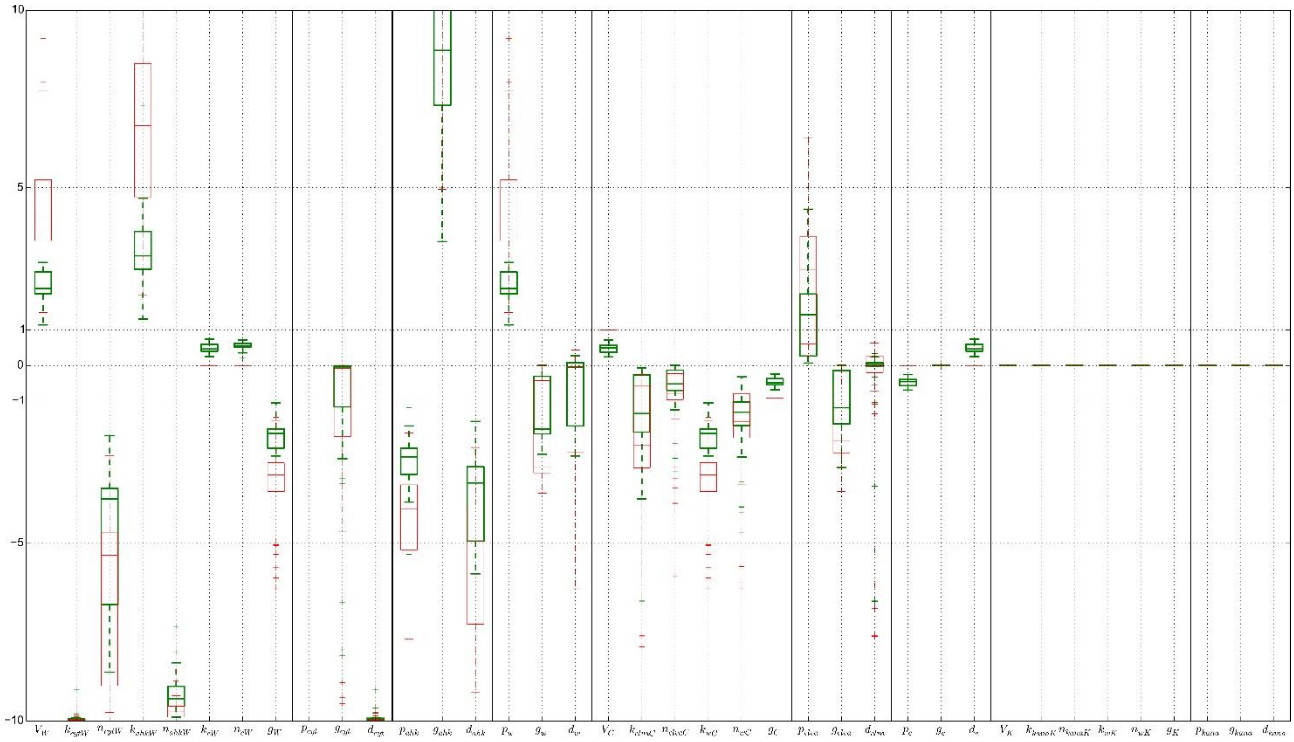

Figure S24 – *CLV3* sensitivity analysis
The data is computed for the 255 parameter sets resulting of the optimisations of the two-dimensional abstract template. The x-axis shows the parameters and the y-axis the sensitivity of the *CLV3* domain to variations of the considered parameter following: $\frac{\Delta m}{\Delta p} \times \frac{p}{m}$ (see text). Green: *wild type*. Red: *clavata* phenotype. Inclusion of the *CLV3*/*WUS* feedback increases robustness.

parameter	2D	3D	Real	parameter	2D	3D	Real
V_W	8.42e+00	1.84e+01	1.51e+01	k_{L_cW}	1.13e+01	8.20e+00	1.79e+01
n_{L_cW}	1.04e+01	2.09e+01	7.26e+00	k_{L_aW}	2.19e+01	1.00e-04	7.99e+00
n_{L_aW}	1.62e+00	1.34e+00	1.99e+00	k_{cW}	1.24e+01	6.67e+00	5.07e-02
n_{cW}	1.00e+00	1.00e+00	6.66e+00	g_W	6.05e-03	2.39e-04	2.29e-03
p_w	1.68e+01	1.03e+01	1.50e+00	g_w	1.49e+00	1.37e+01	2.10e-13
D_w	1.21e+01	2.07e+01	4.37e+00	V_C	3.84e+01	1.24e+01	1.80e+01
k_{L_CC}	1.36e+00	6.10e+00	3.08e+00	n_{L_CC}	1.77e+00	1.51e+01	9.20e+00
k_{wC}	2.97e+00	8.21e-02	3.94e+00	n_{wC}	9.52e+00	3.63e+00	5.36e+00
g_C	1.69e-02	5.59e-02	3.76e+00	p_c	4.39e+00	2.27e+00	3.97e+00
g_c	7.61E-02	3.46e-15	1.02e+01	D_c	2.71e+00	4.63e+00	3.45e-12
V_K	7.74e+00	2.00e+00		k_{L_KK}	1.76e+01	5.85e-01	
n_{L_KK}	1.33+00	1.43e+00		k_{wK}	5.39e-01	9.63e-03	
n_{wK}	4.47e+00	4.10e+00		g_K	6.78e+00	1.97e+00	
p_{L_c}	1.10e+00	2.21e+01	3.28e+00	g_{L_c}	2.63e-06	8.38e-02	5.97e-04
D_{L_c}	1.04e+00	1.57e+01	4.90e+00	p_{L_a}	1.45e+00	2.41e+00	5.76e+00
g_{L_a}	3.45e-05	2.70e-01	1.80e-03	D_{L_a}	3.00e-05	2.45e-02	4.51e-03
p_{L_C}	1.37e+01	5.23e+00	4.65e-01	g_{L_C}	2.83e+00	1.00e-04	3.11e-13
D_{L_C}	1.10e+00	7.57e+00	3.43e+00	p_{L_K}	1.14e+01	2.61e+01	
g_{L_K}	1.76e-04	3.48e-02		D_{L_K}	5.07e-08	1.00e-04	

Table S1 - Example parameter sets
2D, 3D and real refer to the templates the parameter sets were optimised for (two-dimensional abstract, three dimensional abstract and realistic).

Movie S1 - Primordium growth

Simulation showing the result of the growth of a primordium like domain on the side of the three-dimensional abstract template. The colour scale for gene expression domains is the same as in Figure 1. The colour scale for diffusing molecules is relative to the concentration of the considered molecule across the whole simulation (red: maximum, blue: minimum).