

Supplemental Information

**A multiscale analysis of early flower development
in *Arabidopsis* provides an integrated view
of molecular regulation and growth control**

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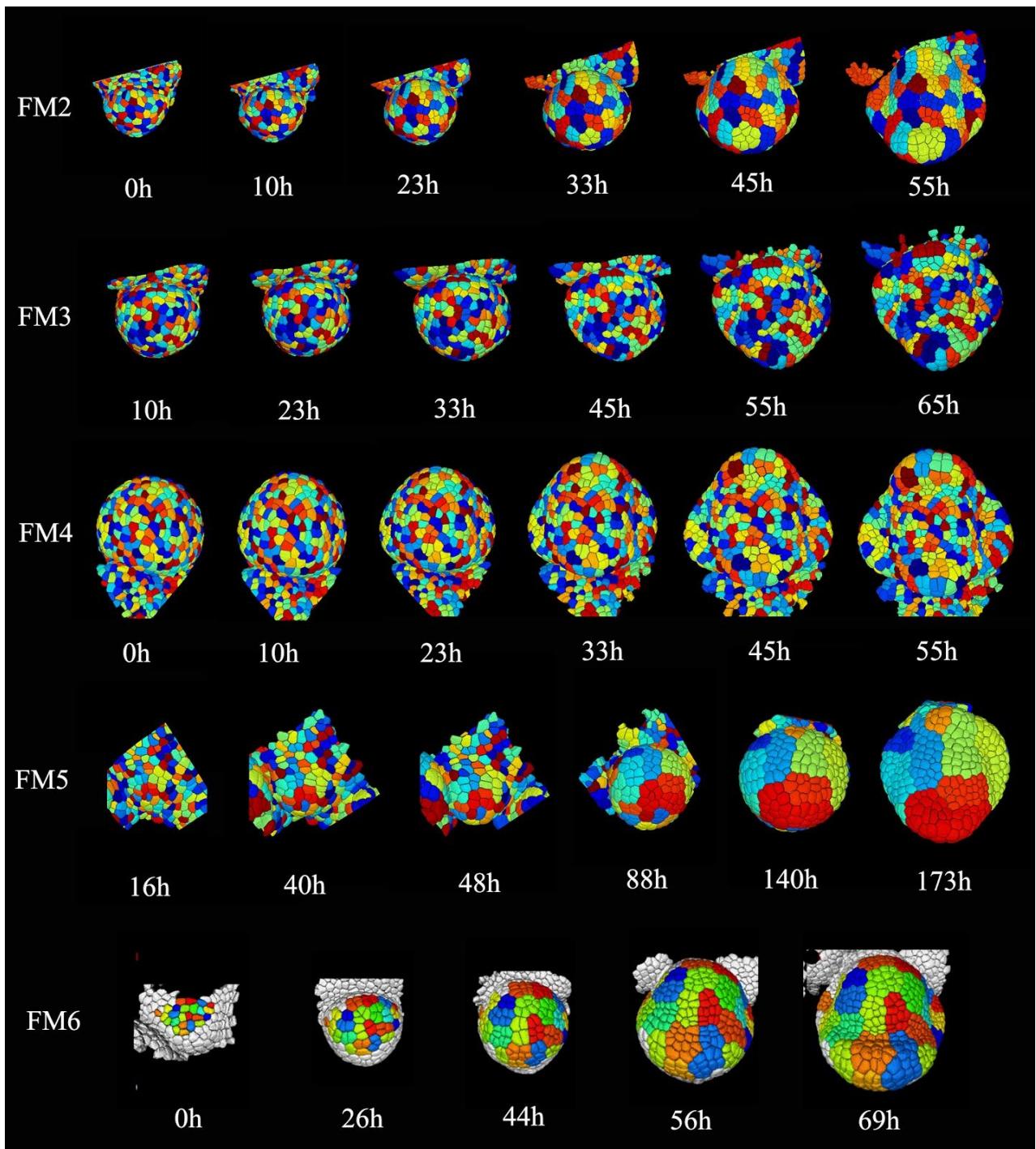


Figure S1 – Surface rendering of segmented images of FM 2-6 time courses (Related to Fig 1A).
 The cells are colored according to computed lineages. The number of hours after first acquisition is indicated below each image.

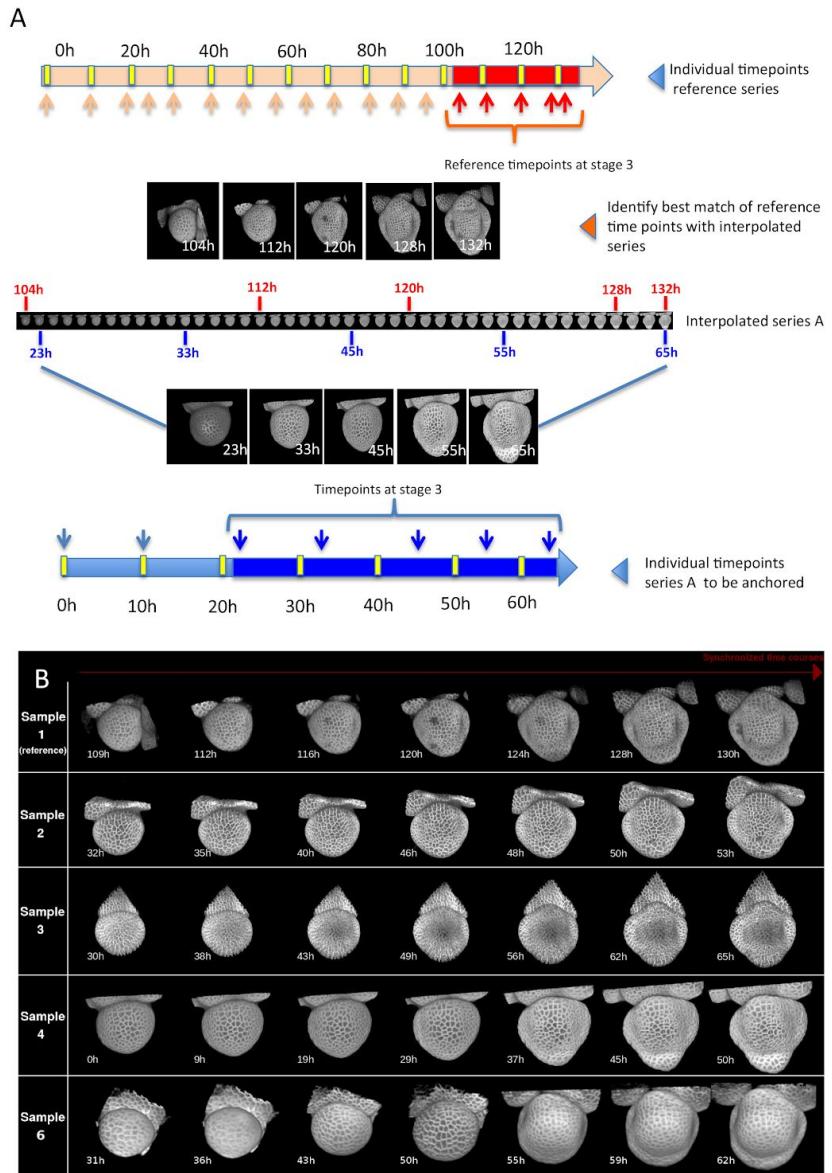


Figure S2 - Approach for comparison of meristems (Related to Fig 2).

(A) Comparison of reference series with 18 time points, from initium until late stage 3 with another series 'A' with 7 time points. Since the changes in shape are most striking during stage 3, this developmental window was chosen for the comparison (dark red zone in the reference series, dark blue in series A). First, a 3D image interpolation is performed to improve temporal resolution to 1h intervals. The 5 timepoints of stage 3 of the reference series are then compared to this interpolated series. The two series are then 'anchored' via shapes that are closest to each other. Note that there is a difference in time scale, as some meristems grow more quickly than others.

(B) Result of temporal alignments of confocal time series of floral meristems. The 3D images of the sample 1 (reference sequence) are paired to their best match in shape and size in the samples 2, 3, 4 and 6. This was not possible for series 5 (see text for details).

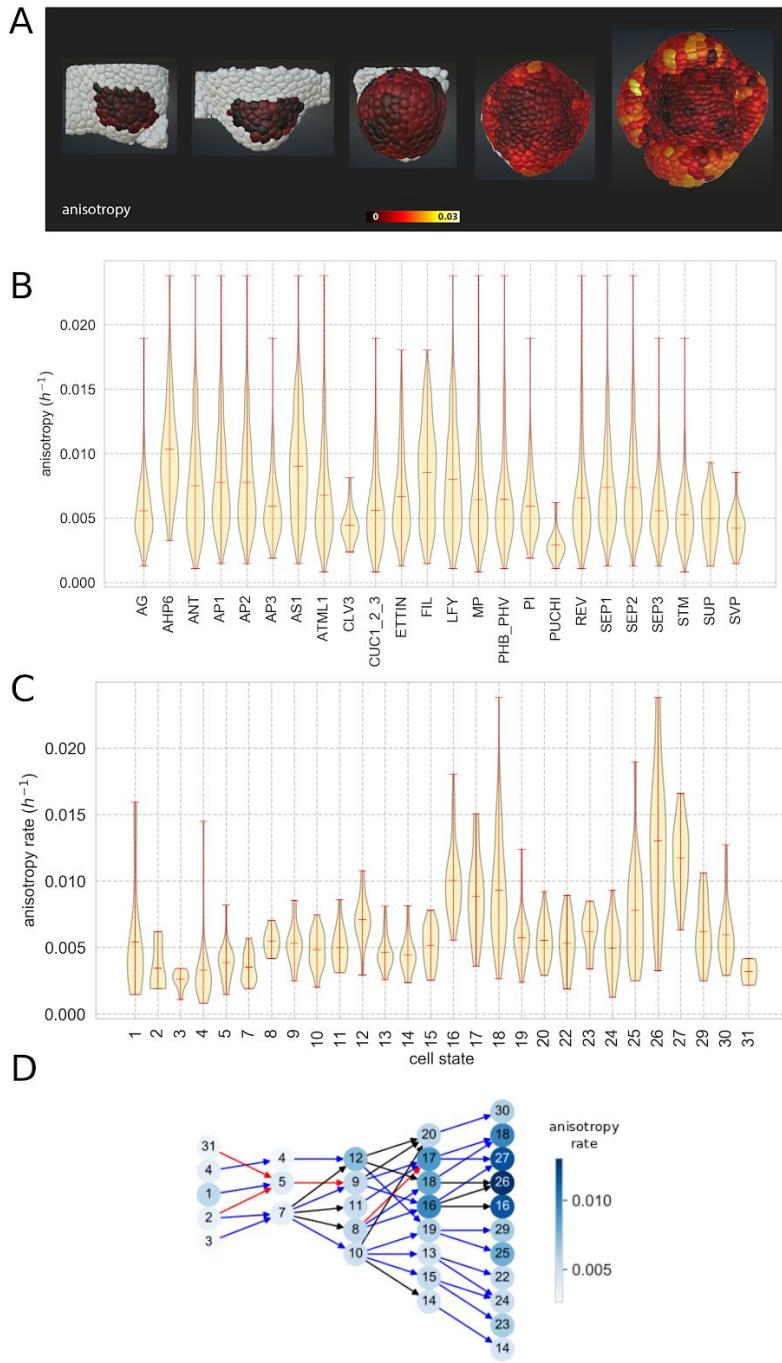


Figure S3 - Anisotropy rates (related to Fig 5). **(A)** Growth anisotropy of L1 cells. Color scale indicates degree of anisotropy per hour (see methods). Light grey cells are not taken into account. **(B)** 3D growth anisotropy rate of expression domains of individual genes. **(C)** Growth anisotropy/hour in combinatorial patterns or cell states (numbering as in fig 2 and 3). Note that the values were calculated from one point to the next point (forward), only the values of the cell states of the last time point are calculated backwards. **(D)** Growth anisotropy on the pattern transition graph calculated as the average of the backward and forward anisotropy rate (except initium stage, only forward and stage 4 only backward)

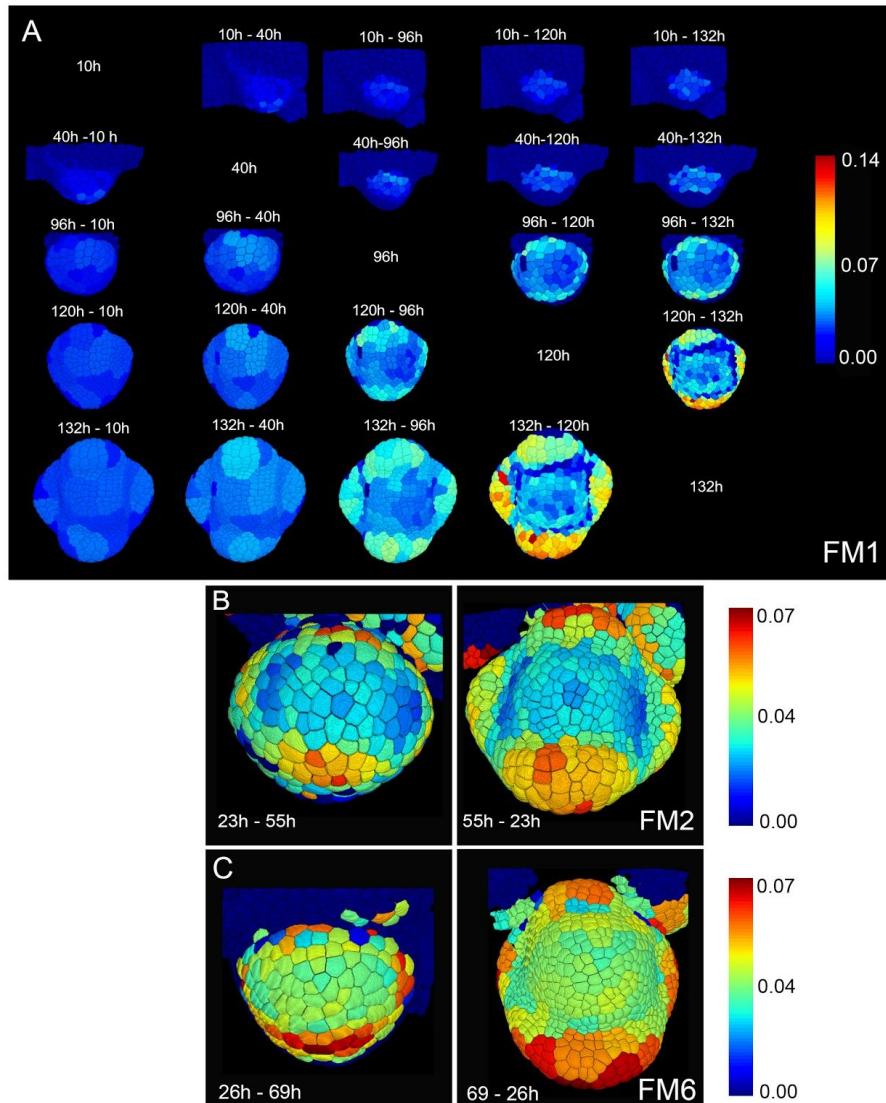


Figure S4 - Growth rates between time points reveal predetermined patterns at stage 2 (related to Fig 5).

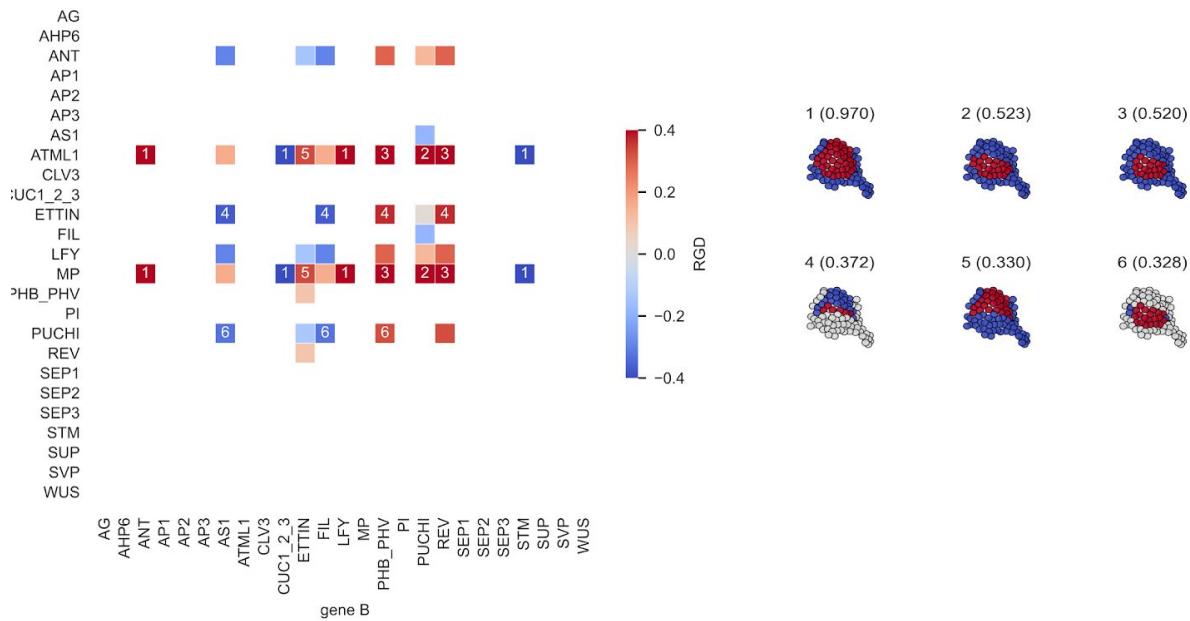
(A) Backward (how much cells have grown, below diagonal) and forward (how much cells will grow, above diagonal) growth rates as μm^3 per hour between time points (Flower Meristem 1), illustrating that the increased growth rate in the sepal is determined from 96h (stage 2) onwards, when the bud has still a globular shape. Bar indicates color code for growth rates (μm^3 per hour). The untracked cells (not generating the cells at 132h) are marked as having now growth (dark blue).

(B) Forward (23h to 55h) and backward growth rate (55h - 23h) of cells in flower meristem 2 (FM2), also showing predetermined growth rates from stage 2 onward.

(C) Forward and backward growth rates in flower meristem 6 (FM6) also showing predetermined growth from stage 2 stage onwards. Color codes in (B) and (C) as in (A).

The color bar is truncated at 0.

stage 0



stage 1

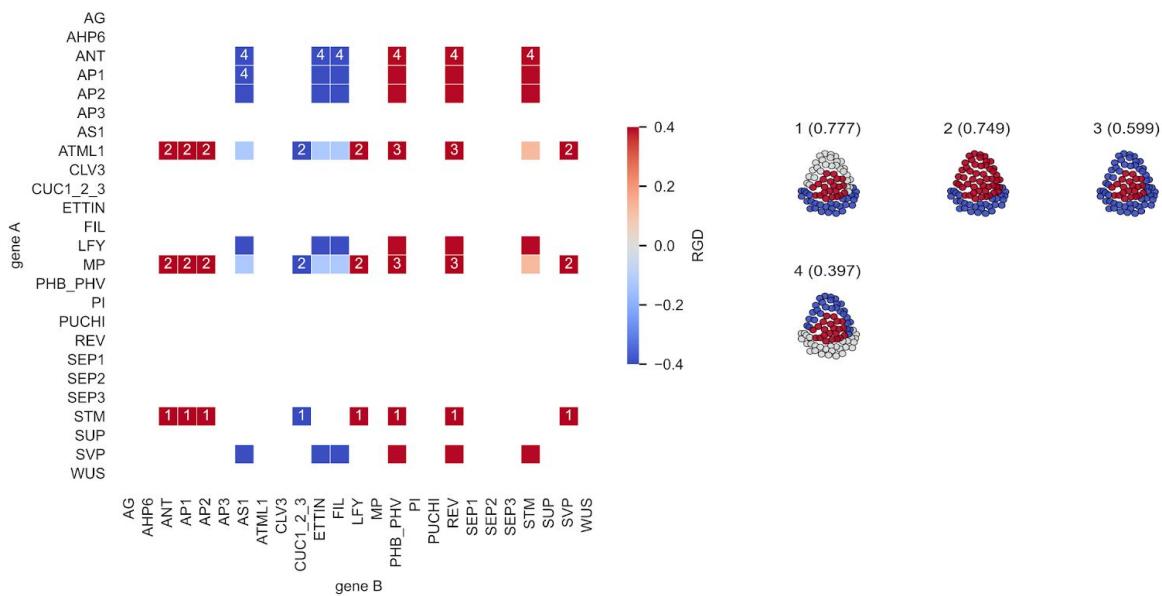
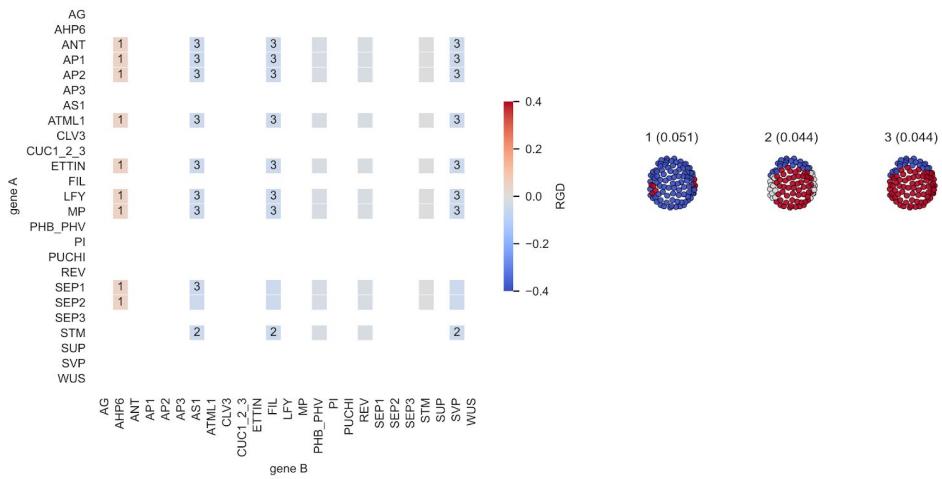


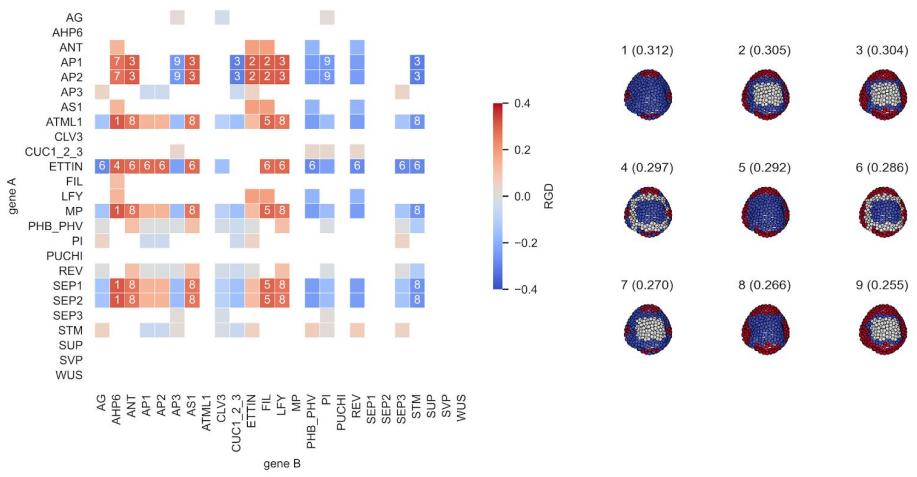
Figure S5 - Relative Growth Differences (RGDs) (related to Fig 6). RGDs between gene pairs (left) and the regions they define (right) for stages 0 and 1. For each pair of genes the colour on the heatmap refers to the RGD between the mean growth rate of the population of cells co-expressing gene A and B versus the mean growth rate of the population of cells expressing *only* gene A. The color bars are truncated to the range -0.4 to 0.4. The RGD for pairs of genes where either population is empty (i.e. completely overlapping or not overlapping at all) is not reported (blank cells).

The numbered annotations refer to the regions (A +B or -B) implied by the gene pairs as shown at the right. The regions are shown along with their real (untruncated) RGD in parentheses on the tissue geometry sorted by RGD where the region with the higher mean growth rate of the two is shown in red and the region with the lower growth rate is shown in blue.

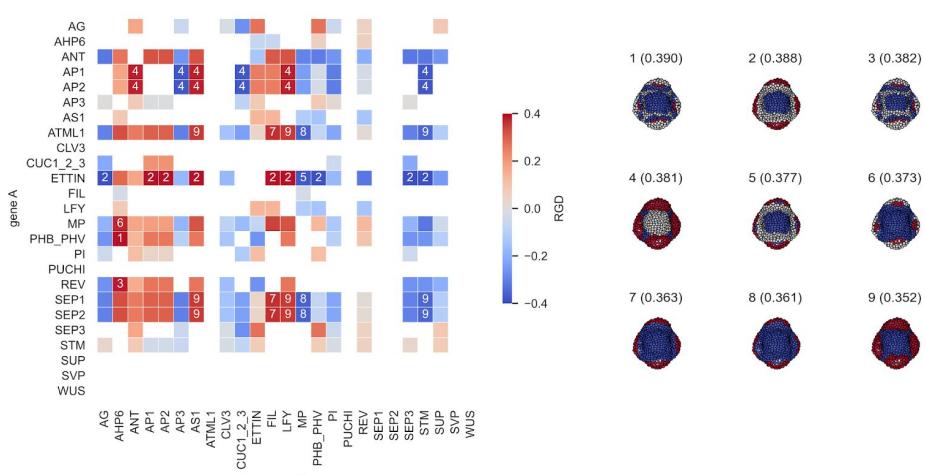
stage 2



stage 3



stage 4



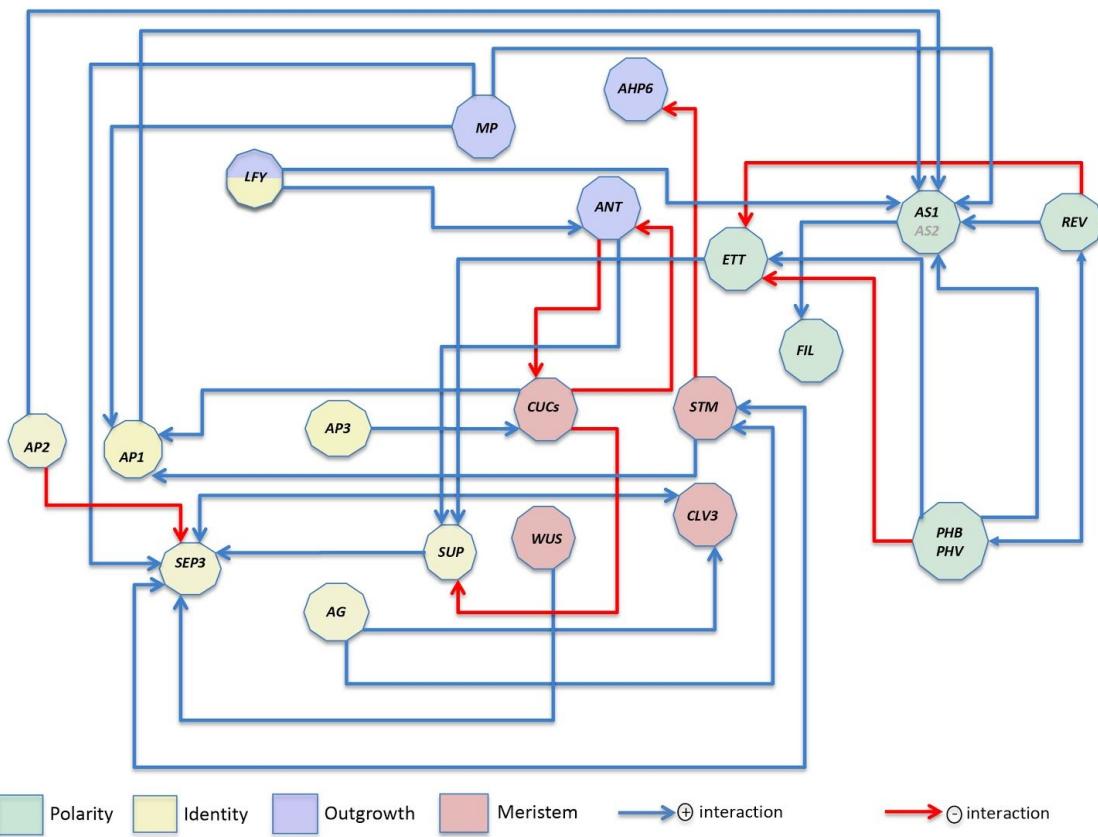


Figure S7 - Hypotheses resulting from network analysis (related to Fig 1; tables S1, S3 and S4).
 Selection of 32 (single) hypotheses for gene interactions not retrieved from the literature search , that improve the predicted expression patterns at more than one floral stage (see table S4). Red and blue connections represent negative and positive regulations respectively. Color code indicates function in floral meristem development, floral organ identity (sepals, petals, stamens and carpels) and abaxial/adaxial organ polarity as described in the litterature.

Supplemental Table S2 (related to figure 2B and 3) : List of cell states and clusters with the description of their identity.

Domain	Detailed description	General description	Organ identity
2	Abaxial floral meristem	Floral meristem	Undifferentiated
3	Floral meristem initium stage		
6	Floral meristem stage 1(L2)		
7	Floral meristem stage 1 (L1)		
10	Floral meristem stage 2		
18	Sepal, adaxial domain	Adaxial domain organ	Sepal
26	Sepal tip, adaxial domain		
21	Basal boundary between sepals stage 3 (L2)	Boundary	Boundary
12	Adaxial domain flower primordium	Primordium	Flower
8	Centre future lateral sepal	Lateral initium	Sepal
11	Periphery future lateral sepal		
28	Sepal abaxial domain stage 3 (L2)	Abaxial domain organ	
27	Sepal abaxial domain stage 4 (L1)		
16	Sepal tip, abaxial domain		
17	Sepal, abaxial domain stage 3		
9	Abaxial domain flower primordium	Flower primordium	Primordium
1	Bract initium stage	bract	Bract
31	Lateral domain bract initium stage		
5	Bract stage 1		
4	Boundary young flower primordium	Boundary	Boundary
20	Boundary between sepals stage 3		
30	Boundary between sepals 4		
29	Petal precursors, sepal boundary	Organ precursors, boundary	Petal/
19	Petal and Stamen precursors, boundary	Organ precursors and boundaries	Petal/stamen
25	Stamen precursor stage 4, sepal boundary		Stamen

13	Stamen precursor stage 1, sepal boundary		
22	Stamen precursor stage 4, meristem	Organ precursors/meristem	
24	Boundary between stamen and carpel, meristem	Boundary	Boundary
15	Carpel precursor stage 3, periphery meristem	Organ precursors and meristem	Carpel
23	Carpel precursor stage 4, meristem		
14	Carpel precursor stage 4, central meristem,		