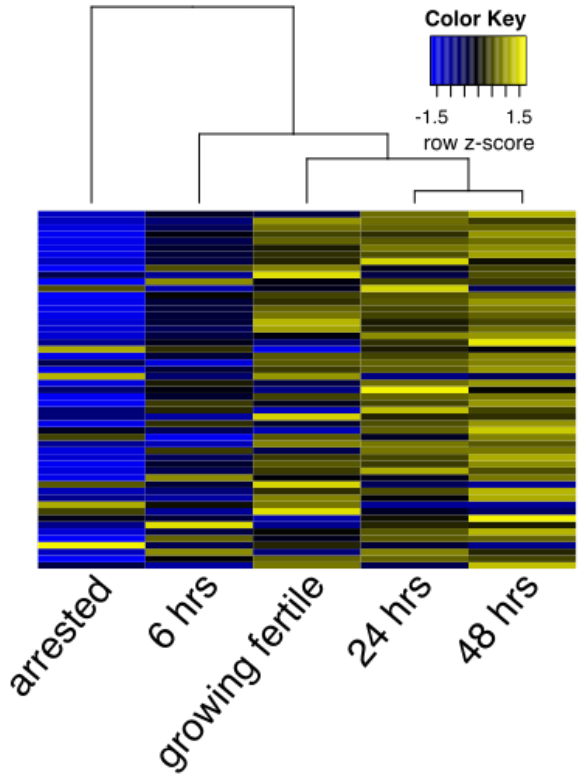
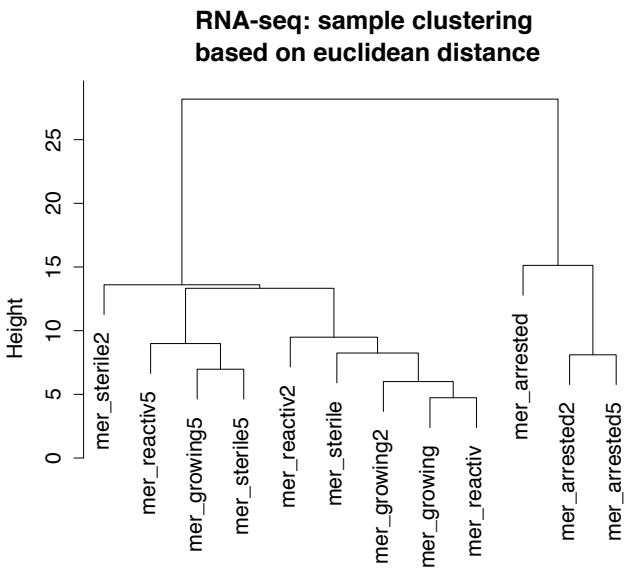
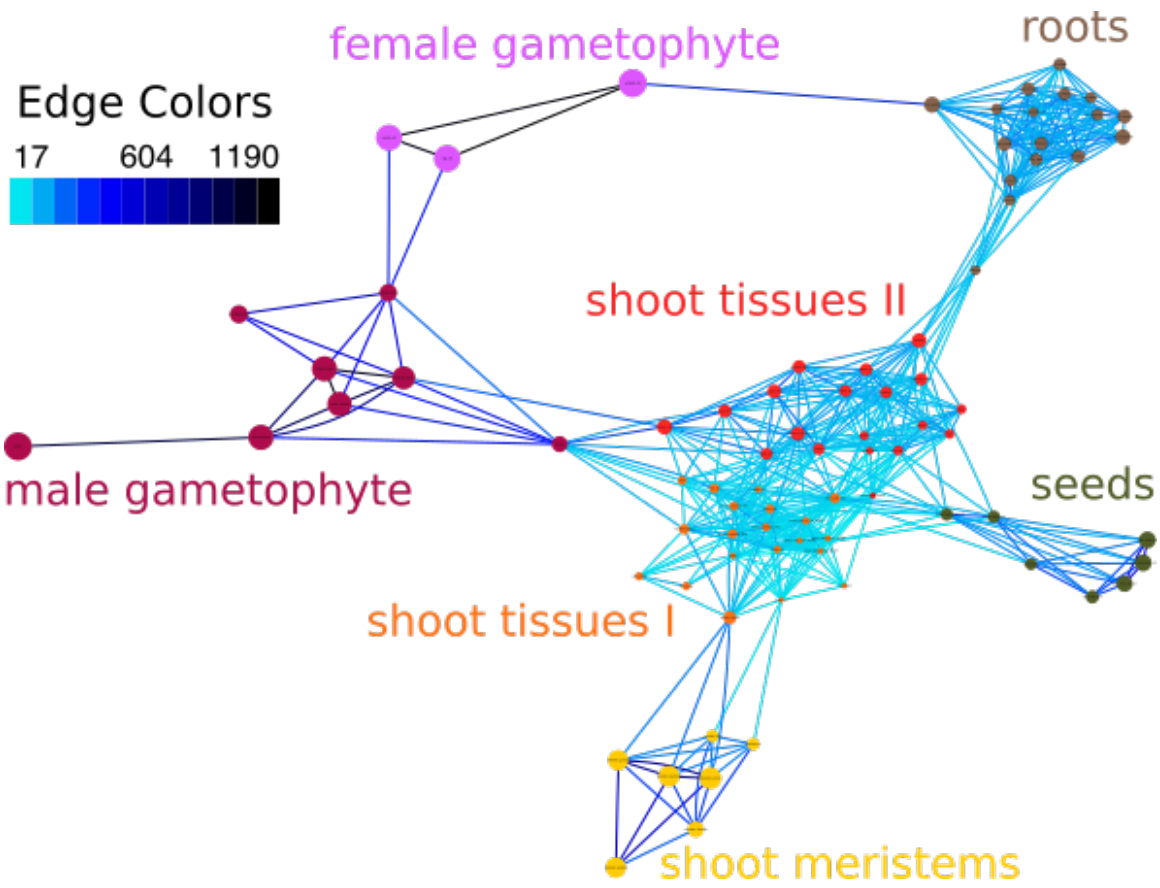
Supplemental Figures and Datasets, Wuest et al. "Correlative controls of seeds over maternal growth and senescence in *Arabidopsis*"



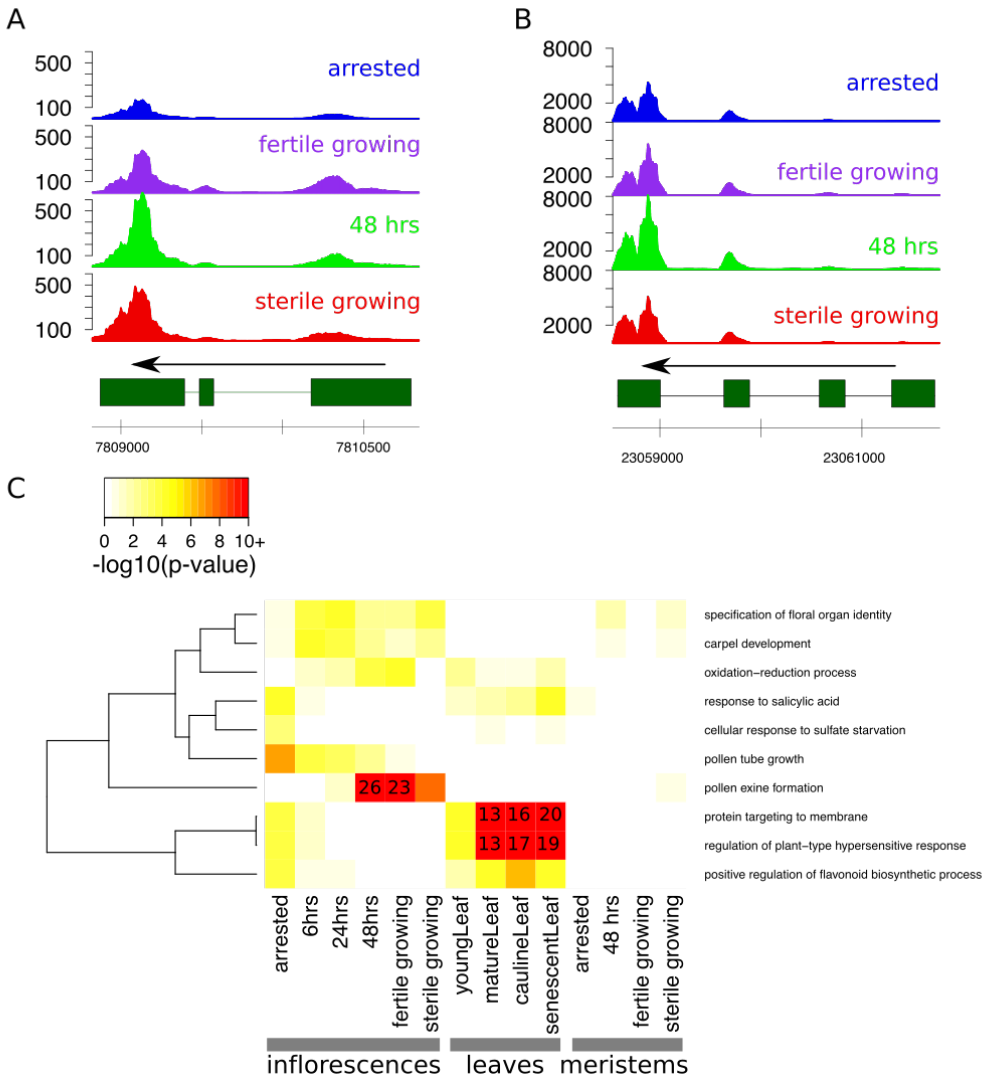
Supplemental Figure 1: Heatmap representing expression of core cell cycle genes in growing whole inflorescences, and in arrested whole inflorescences at 0, 6, 24, and 48 hrs after fruit removal, respectively. Mean expression estimates, scaled across rows are shown, with blue denoting low expression and yellow denoting high expression.



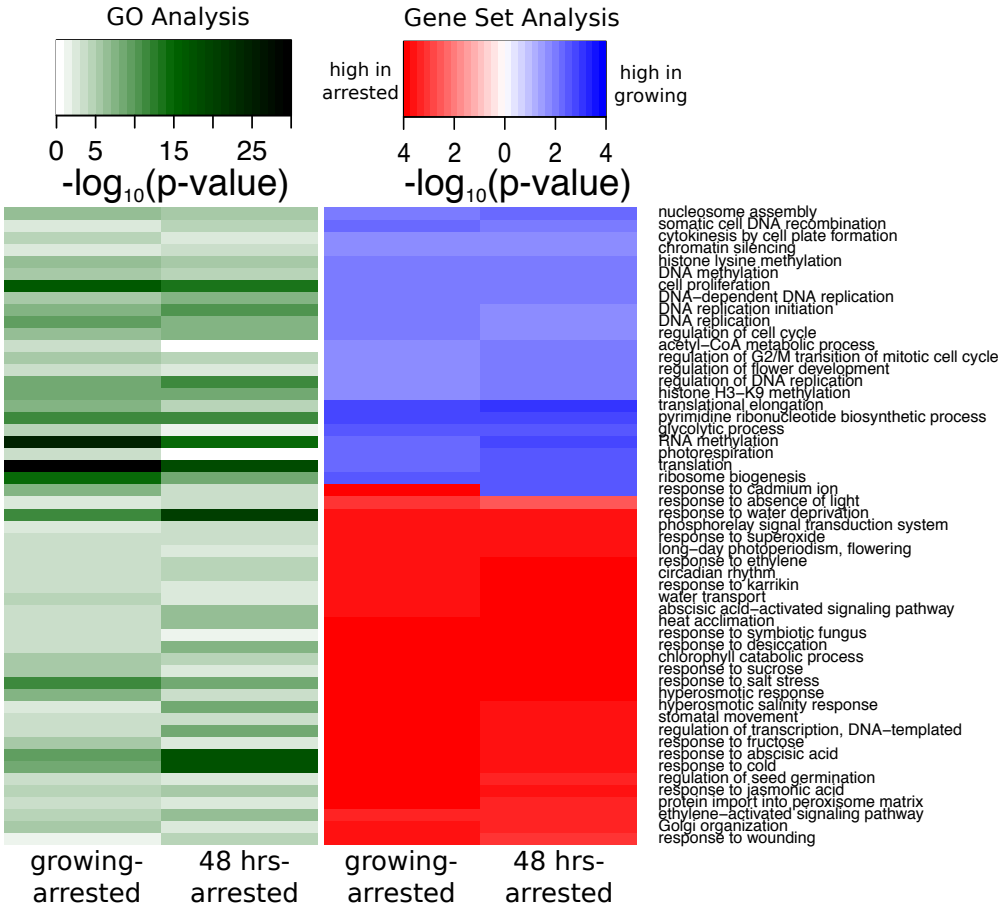
Supplemental Figure 2: Sample clustering of RNA-Seq dataset, based on top 1000 most variable genes, log-transformed counts per million. Arrested meristems and growing meristems form two clearly distinct clusters.



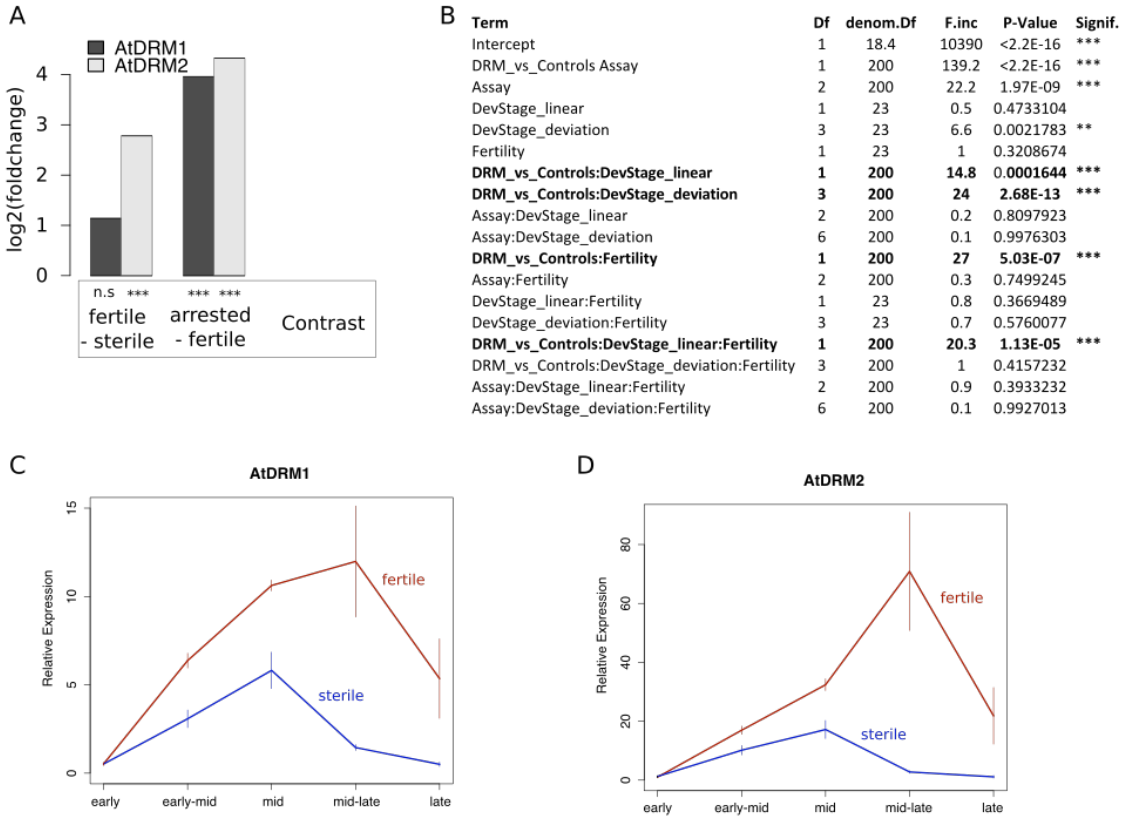
Supplemental Figure 3: Gene-sharing network of all tissues considered in this study. Node colors denote the seven different communities (i.e. subgroups of nodes within the network that are strongly interconnected) identified by a random walk algorithm. Edge colors denote the number of genes shared between two different nodes. Note: The connection between female gametophyte and root communities occurs through a "synergid"-"root xylem precursor" edge, maybe because these cell types share similar eventual fate of undergoing programmed cell death.



Supplemental Figure 4: Meristems retain identity throughout state transitions and respond differentially than whole inflorescences to GPA. **(A)** Normalized read coverage across the *WUSCHEL* genic region in our RNA-Seq meristem dataset. **(B)** Normalized read coverage across the *SHOOTMERISTEMLESS* genic region in our RNA-Seq meristem dataset. **(C)** Heatmap showing terms with most variable results of a GO-term enrichment analysis in our whole inflorescence nodes. Values were truncated to 10 (in cases the adjusted p-values were lower than 1e-10), and cells with higher values are indicated.



Supplemental Figure 5: GO- and Gene Set Enrichment Analysis on gene differentially expressed in growing and arrested meristems. Results from analyses from two different contrasts are shown, i.e. the contrast of fertile growing vs. arrested meristems and the contrast of meristems at 48 hours after fruit removal vs. arrested meristems.



Term	Df	denom.Df	F.inc	P-Value	Signif.
Intercept	1	18.4	10390	<2.2E-16	***
DRM_vs_Controls Assay	1	200	139.2	<2.2E-16	***
Assay	2	200	22.2	1.97E-09	***
DevStage_linear	1	23	0.5	0.4733104	
DevStage_deviation	3	23	6.6	0.0021783	**
Fertility	1	23	1	0.3208674	
DRM_vs_Controls:DevStage_linear	**1**	**200**	**14.8**	**0.0001644**	***
DRM_vs_Controls:DevStage_deviation	**3**	**200**	**24**	**2.68E-13**	***
Assay:DevStage_linear	2	200	0.2	0.8097923	
Assay:DevStage_deviation	6	200	0.1	0.9976303	
DRM_vs_Controls:Fertility	**1**	**200**	**27**	**5.03E-07**	***
Assay:Fertility	2	200	0.3	0.7499245	
DevStage_linear:Fertility	1	23	0.8	0.3669489	
DevStage_deviation:Fertility	3	23	0.7	0.5760077	
DRM_vs_Controls:DevStage_linear:Fertility	**1**	**200**	**20.3**	**1.13E-05**	***
DRM_vs_Controls:DevStage_deviation:Fertility	3	200	1	0.4157232	
Assay:DevStage_linear:Fertility	2	200	0.9	0.3933232	
Assay:DevStage_deviation:Fertility	6	200	0.1	0.9927013	

Supplemental Figure 6: Expression of the AtDRM1/2 genes upon the production of fruits and proliferative arrest.

(A) Estimated log2-foldchanges of *AtDRM1* and *AtDRM2* gene expression in either the fertile-sterile growing plant meristems contrast (left) or the arrested-sterile growing plant meristems contrast (right). n.s. not significant; *** p-value <0.01. **(B)** ANOVA table from a mixed-model analysis of the qRT-PCR dataset using ASREML-R. The threshold cycles (CT) are modelled as a function of the assays (AtDRM1, AtDRM2, AT4G34270, AT2G28390), the reproductive status (*ms1-1* homozygous and sterile vs. wild-type segregants from the same family) and developmental stage (i.e. early fruit development up to proliferative arrest) as fixed terms, and technical replicate (i.e. two independent cDNA synthesis and qPCR replicates) as well as individual tissue samples as random terms. For the fixed terms "Assay" and "Developmental Stage", we included contrasts of interest with a single degree of freedom each, i.e. i) contrasting the two AtDRM vs. the two reference assays, and ii) a linear contrast (1=early stage of fruiting, 2=early-mid stage of fruiting, …, 5=proliferative arrest) versus the deviation at individual stages from the linear contrast, respectively. **(C)** Relative expression of AtDRM1 in fertile and sterile

plants at the different developmental stages described in Figure 6. Error bars: s.e.m. with n=3. **(D)** Relative expression of AtDRM2 (as in C).

Supplemental Dataset 1: Results of the GO-enrichment analysis in selected nodes of the gene sharing network

Supplemental Dataset 2: RNA-seq analysis of laser-dissected meristem samples using the edgeR package