FIGURE LEGENDS, SUPPLEMENT

Table S1. Segregation of double mutants

Segregation *of mp pin1, mp pid* and *pid pin1* double mutants stemming from doubly heterozygous parental plants. Double mutant populations were identified first by screening for *mp* seedling phenotypes and *pin1* inflorescence phenotypes. In double mutant populations, seedlings with *mp* phenotypes were transferred to new petridishes and kept in short day conditions for observation of possible segregation of *mp* single and double mutant phenotypes in the vegetative meristem. Plants were scored for parental phenotypes (*mp, pin1, pid*), and for phenotypes different from parental phenotypes (novel; see figure 1 for description). Absolute numbers are followed by percentage of total number, given in brackets. Expected number is based on a 9:3:3:1 segregation of two unlinked loci. Statistical analysis of segregation ratios using Chi-square analysis resulted in no statistical difference between expected and observed numbers of individuals with novel phenotypes in the segregating population; *mp pin1* double mutant $p = 0.75$, *mp pid* double mutants $p = 0.69$, *pin1 pid* double mutants $p = 0.88$.

Figure S1. Time series of *AS1* expression in leafless domes.

Whole mount in situ hybridization illustrating the switch of *AS1* expression which is initially expressed in a collar of cells surrounding the meristem at 3 and 4 DAG to simultaneous expression in the meristem at 6 DAG and is exclusive expression in the enlarging meristem from 9 DAG onwards. (A) 3 DAG, (B) 4 DAG, (C) 6 DAG, (D) 9 DAG, (E) 21 DAG, a = apex of meristem, scale bars are 50μm.

Figure S2. Quantification of central zone and meristem areas.

Material grown on medium supplemented with 10μM NPA indicated as "+ NPA". Representative images of Pro_{CLV3}*:GFP:ER* and Pro_{STM}*:GUS* expression at 3, 10 and 21 DAG in *WT*, *mp*, *WT* +NPA, and *mp*+NPA meristems. Size bars are 50μm.