

## SUPPLEMENTAL FIGURE LEGENDS

**Figure S1. Validation of microarray results using quantitative real time PCR.** Mean  $-\Delta\Delta Ct$  is indicative of the relative amount of product detected by Q-PCR at each stage. Q-PCR data is compared to normalized signal intensities obtained by microarray hybridization.

**Figure S2. Quantitative RT-PCR measurement of transcripts representing combined *35S::AtZFP2* / endogenous *AtZFP2* and *35S::AtZFP2* only in flowers of wild type and *35S::AtZFP2* plants.** (A) Relative expression of combined *35S::AtZFP2* / endogenous *AtZFP2* with wild type level normalized to 1. (B) Relative expression of *35S::AtZFP2* only, with background level normalized to 1. Information on methodology and replications are in Materials and Methods.

**Figure S3. Phenotypes of wildtype and *35S::AtZFP2* floral organs.** Panels 1 and 2; Left to right: flower, sepal, petal, carpel, stamen. Panels 3 and 4; Left to right: flower, green petals on flower, distorted carpels on flower, stamen. Scale bars equal to 500  $\mu\text{m}$ .

**Figure S4. Developmental timing of accumulation of selected *AZ<sub>551</sub>* transcripts.** Entries listed above the dashed line are downregulated at least 2-fold between stages; those listed below the dashed line are upregulated at least two-fold. Maximum negative and positive fold-changes between stages are in bold type. Corresponding quantitative data and additional locus IDs are in Table S2.