Supplementary figures

Figure S1



Figure S1. Arabidopsis *cdkd* and *smg7-6* mutants. Approximately 6-weks old plants are shown. Longer inflorescence bolt in the *smg7-6* mutant is caused by reduced fertility.

Figure S2



Figure S2. Mapping mutations associated with the rescued fertility in *EMS58-1* by whole genome sequencing. The causative mutation is recessive and is, therefore, expected to fully associate with the rescued phenotype. The charts indicate positions of *de novo* mutations on individual Arabidopsis chromosomes (x axis) and their frequency in population of B2 plants exhibiting increased fertility. Colored diamonds on chromosome 1 mark *de novo* mutations with the highest association. This region is zoomed in the lower left graph with indicated AGI codes for the mutated genes.





Figure S3. Genetic complementation of *EMS58-1* plants with the *CDKD;3* genic construct causes infertility in transformed T1 plants. The chart shows average silique length in individual T1 transformants (error bars indicate SD; n= 25). Data for *smg7-6* are shown in red, for EMS58-1 in gray, for complemented T1 transformants in blue and for non-complemented transformants in green.

Figure S4



Figure S4. Fertility of *cdkd;3-3* mutants. (a) Quantification of silique length along the main inflorescence bolt in wild type (n = 10) and cdkd;3-3 (n = 5). The trend lines of the data were plotted by LOESS smooth function (colored line; shaded area represents 95% confidence intervals). (b) Anthers from wild type and *cdkd;3-3* plants after Alexander staining. (c) Violin plots showing viable pollen per anther. Significance of the difference is indicated (two tailed t-test; wild type n = 20; *cdkd;3-3* = 5). (d) Tetrads in anther lobes stained with DAPI.





Figure S5. Approximately six weeks old mutant plants.

Figure S6



Figure S6. Time-lapse series of *smg7-6* and EMS58-1 meiotic nuclei undergoing meiosis II and meiosis III. Nuclei derived from the same PMC are encircled with identical color. Note that chromatid tends to spread over larger area during anaphase III in *smg7-6* mutants. Chromatin is visualized with HTA10:TagRFP marker. Scale bar = 5 μ m.