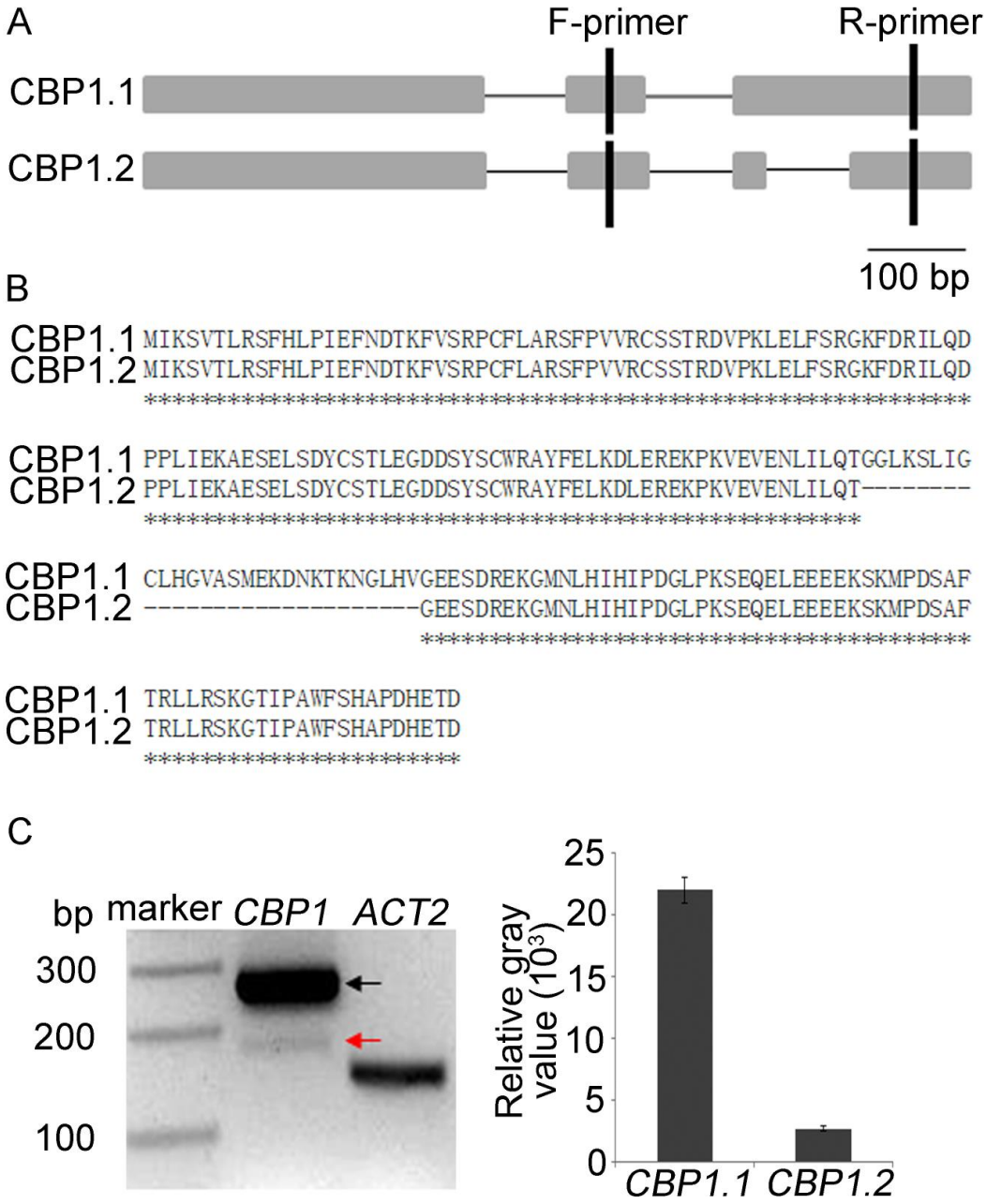
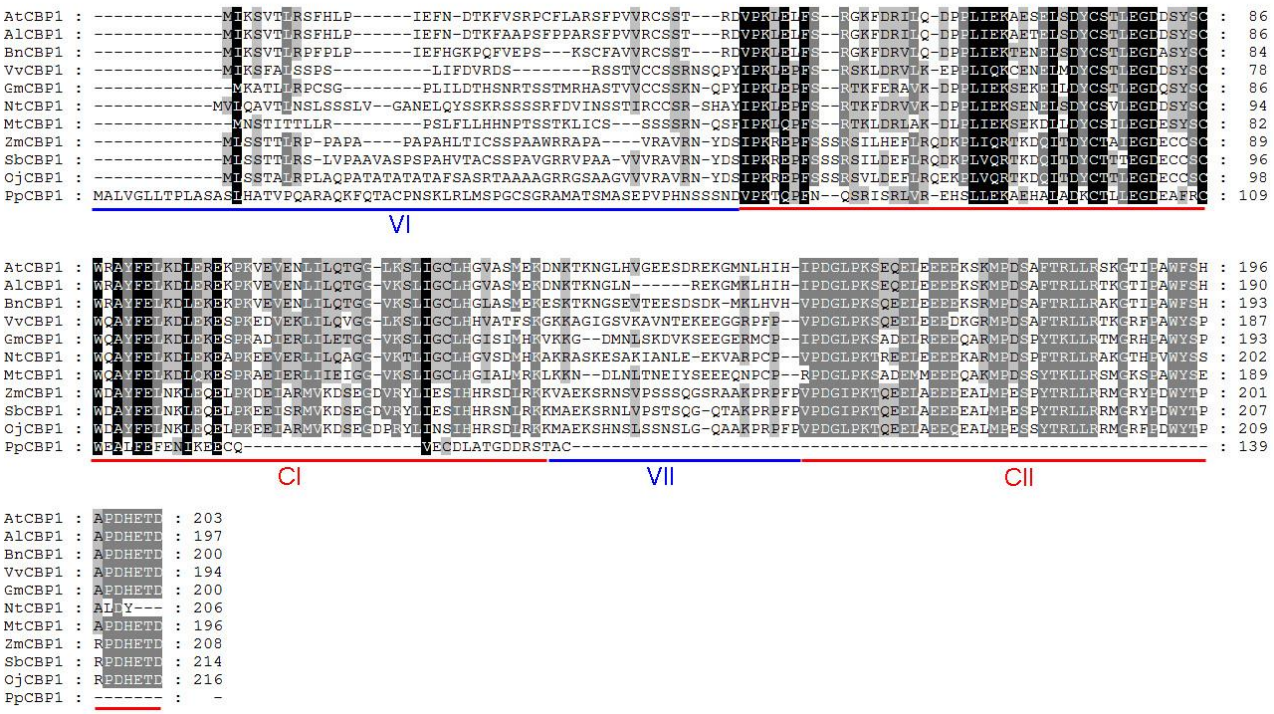
Supplemental Figure 1



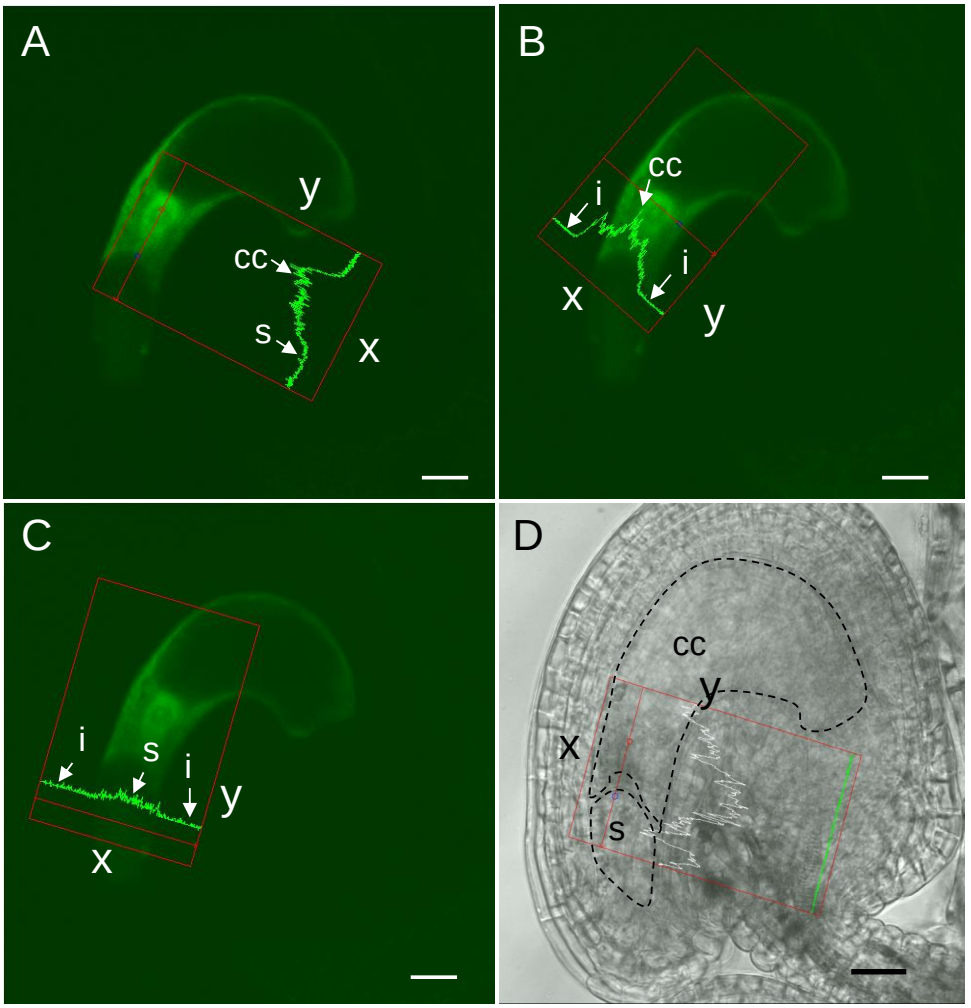
Supplemental Figure 1. Two splicing forms of *CBP1*. A. Schematic structure of *CBP1.1* and *CBP1.2*. *CBP1.2* contains an extra intron causing a 28 amino acid deletion relative to *CBP1.1*. Grey boxes indicate the exons and lines indicate the introns. B. Alignment of the full-length amino acid sequence of CBP1.1 and CBP1.2. Asterisks indicate the same amino acids. C. RT-PCR result showing two splicing forms of *CBP1* amplified with the primers indicated in (A), the black arrow indicates *CBP1.1* and red arrow indicates *CBP1.2*; right panel indicates the relative quantity of the two *CBP1* transcripts in the left panel by quantifying the gray value.

Supplemental Figure 2



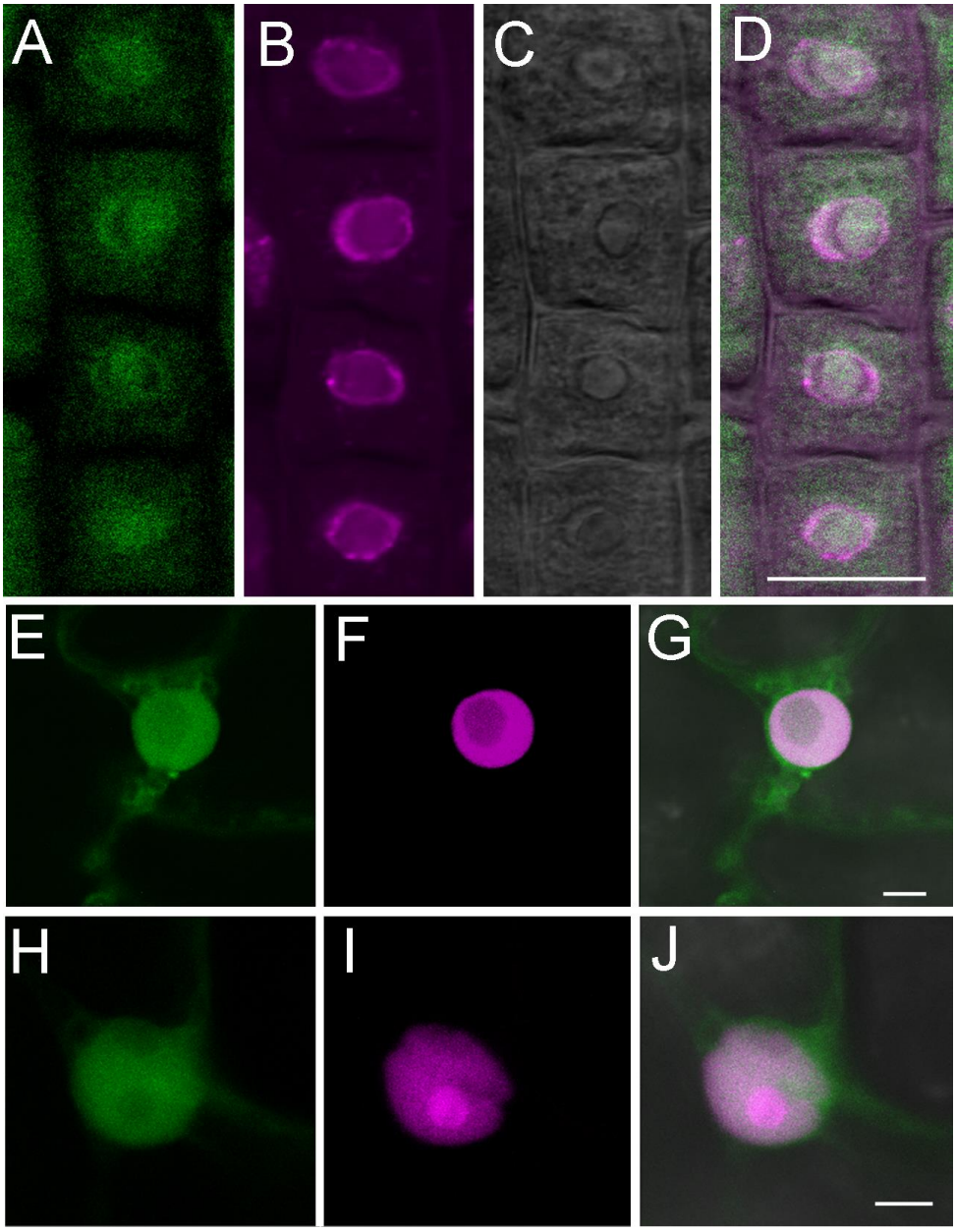
Supplemental Figure 2. Sequence alignment of CBP1 homologs from different species. Black shading with letters and gray shading with white and black letters reflect 80, 60 and 40% sequence conservation, respectively. Two conserved domains were designated as C I and C II domain (indicated by red lines) and two highly variable regions were designated as V I and V II domain (indicated by blue lines). At, *Arabidopsis thaliana*; Al, *Arabidopsis lyrata*; Bn, *Brassica napus*; Vv, *Vitis vinifera*; Gm, *Glycine max*; Nt, *Nicotiana tomentosiformis*; Mt, *Medicago truncatula*; Zm, *Zea mays*; Sb, *Sorghum bicolor*; Oj, *Oryza sativa Japonica*; Pp, *Physcomitrella patens*.

Supplemental Figure 3



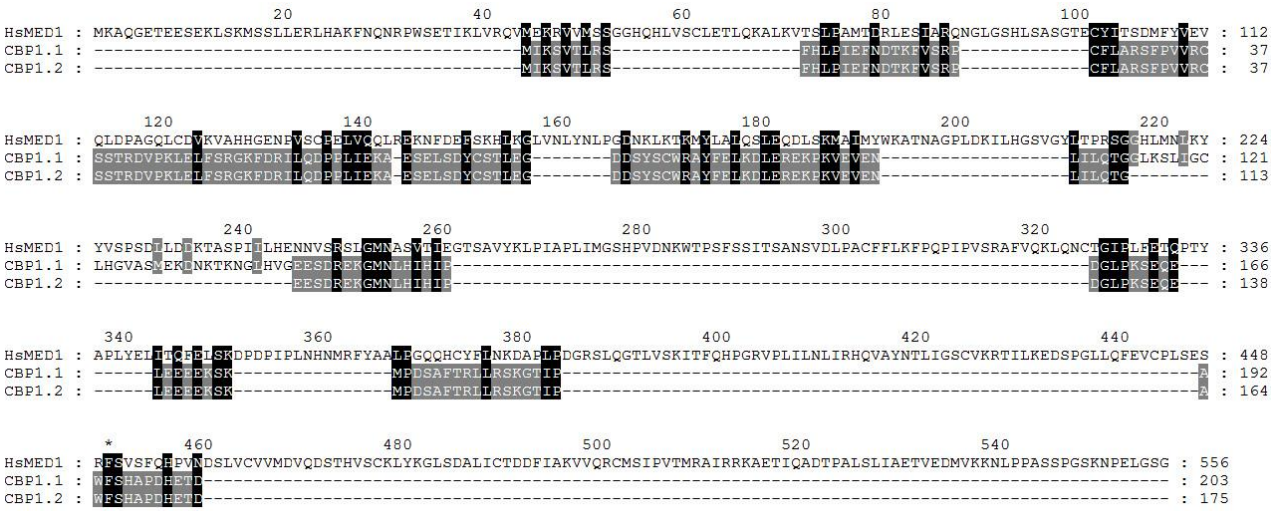
Supplemental Figure 3. CBP1-3×GFP fluorescence is predominantly localized in the central cell. (A-C). The same CLSM image of an ovule showing the fluorescence of CBP1-3×GFP under the native promoter. D. Ovules of the *amiRCBP1* knock-down plants in the background of *pCBP1:CBP1-3×GFP* exhibit no GFP signal. The fluorescence intensity was measured by Zeiss LSM image browser profiling tool (Version 4.2). The y-axes of the green lines are the relative pixel intensity of the GFP signal. The x-axes are the distance from the start point of the measurement in 2D dimension. cc, central cell; s, synergids; i, integument. Bar: 20 μm.

Supplemental Figure 4



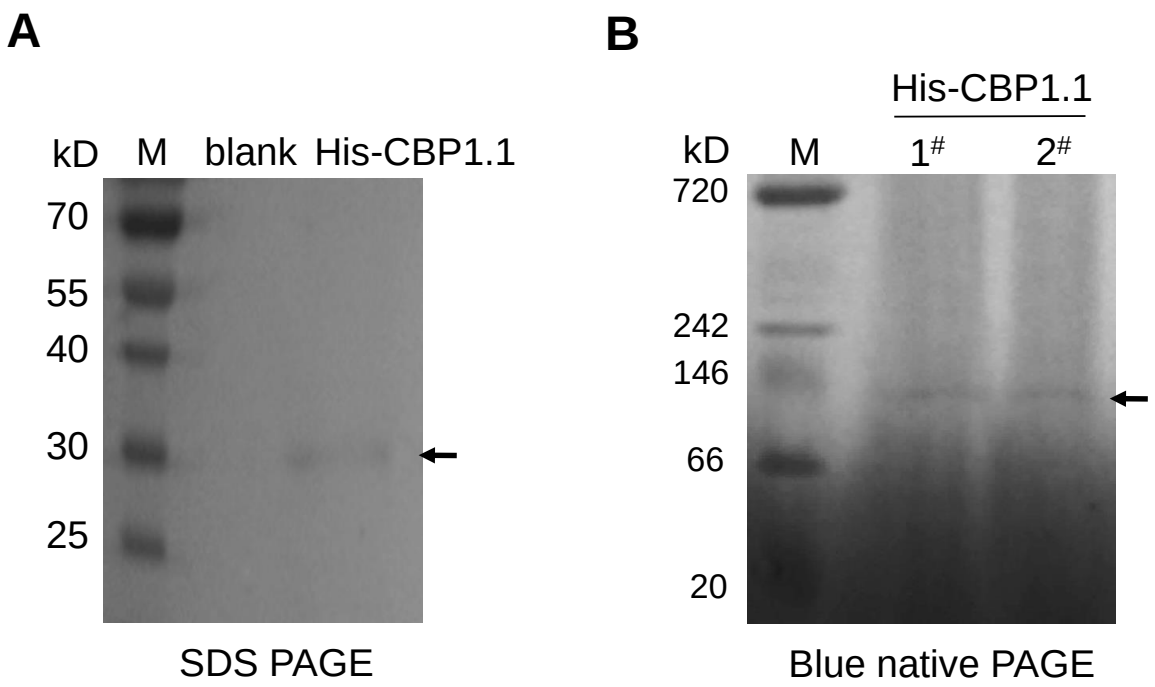
Supplemental Figure 4. CBP1 localization in the nucleus and cytoplasm. Subcellular localization analysis in *Arabidopsis* roots transformed with *pCBP1:CBP1-3×GFP* (A-D) and tobacco leaf epidermal cells transiently transformed with CBP1-GFP and the nucleus fluorescent marker H_2B-mCherry (E-J). (A) Fluorescence of CBP1-3×GFP; (B) Fluorescence of DNA 49, 6-diamidino-2-phenylindole (DAPI) staining of the nucleus; (C) Image of bright field. (D) Merged images. (E) CBP1.1-GFP; (F, I) H_2B-mCherry; (H) CBP1.2-GFP; (G, J) merged images of two channels. Bar: 5 μm.

Supplemental Figure 5



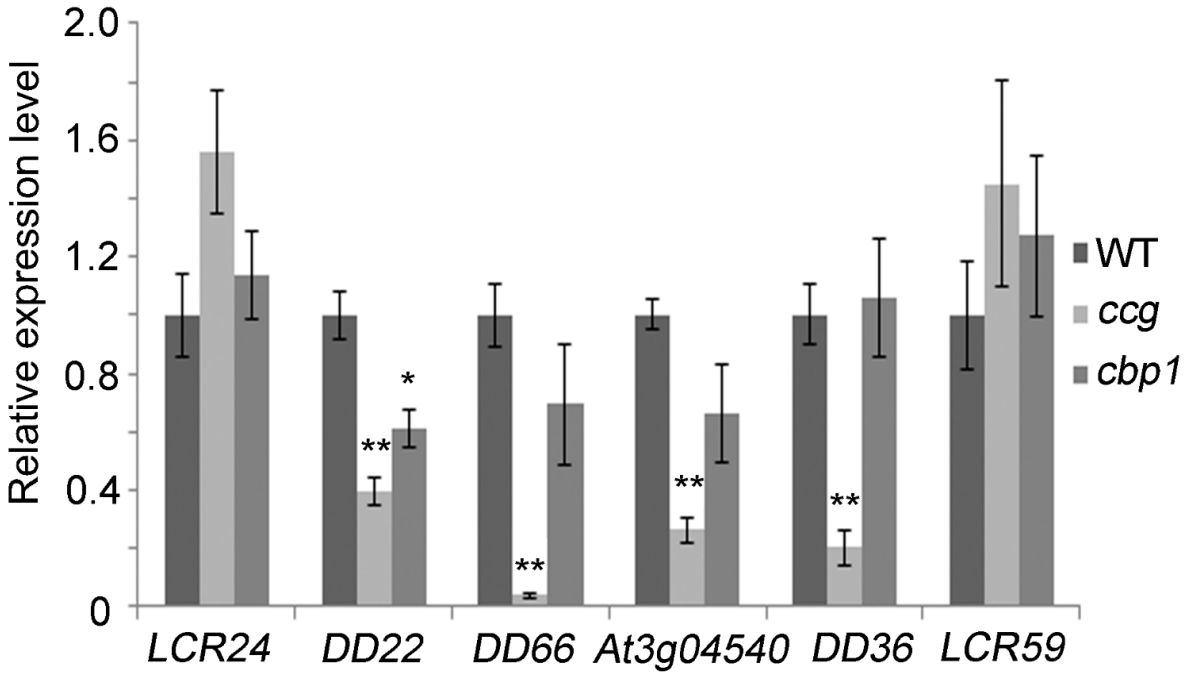
Supplemental Figure 5. Protein alignment between MED1 from *Homo sapiens* and CBP1. Black shading with letters and gray shading with white and black letters reflect 80, 60 and 40% sequence conservation, respectively.

Supplemental Figure 6



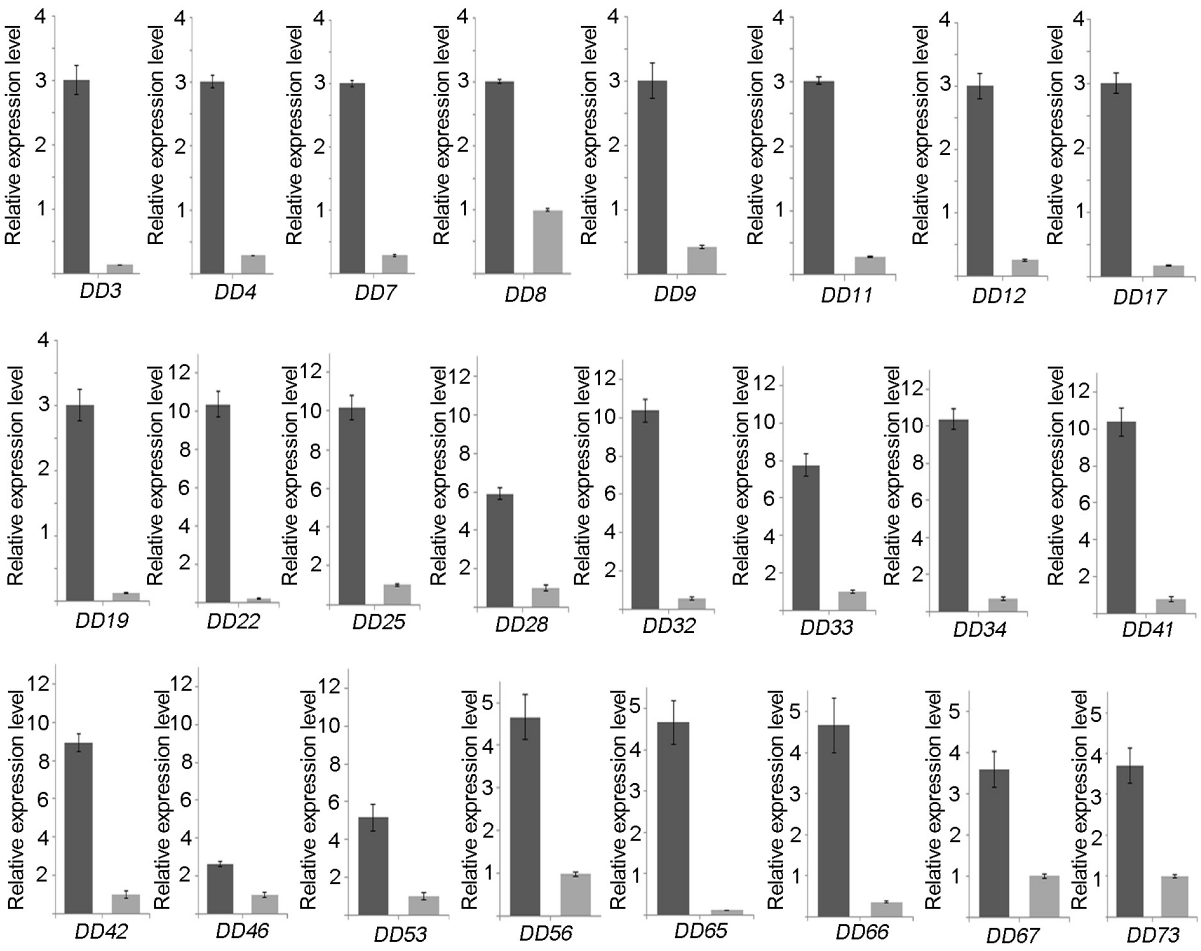
Supplemental Figure 6. CBP1 forms a tetramer *in vitro*. (A) SDS-PAGE separation of purified His-CBP1 with a predicted molecular weight of 29 kD. (B) Separation of purified His-CBP1 on the blue native gel showing a molecular weight of a tetramer. The loading amount in $2^{\#}$ is 1.5 fold of that in $1^{\#}$. (A-B) Coomassie blue staining. Arrows indicate the target fusion proteins.

Supplemental Figure 7



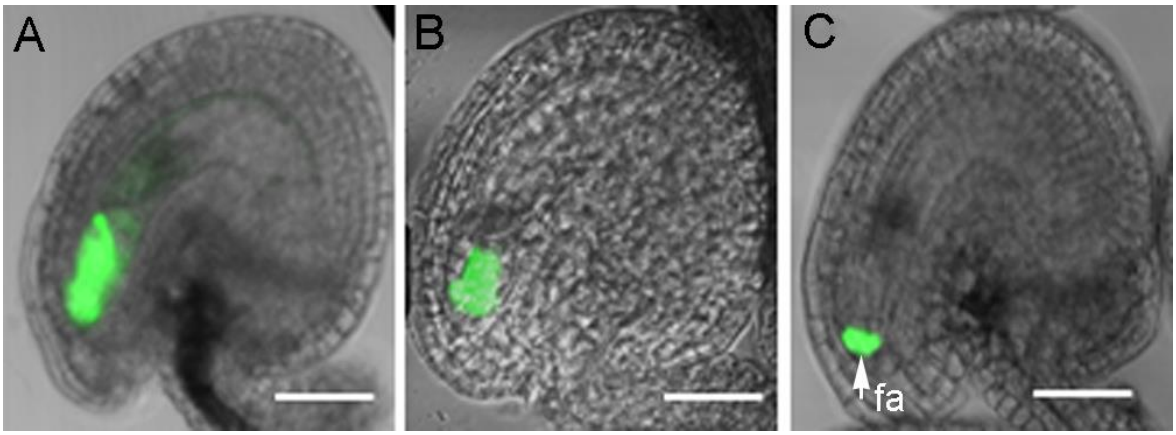
Supplemental Figure 7. Central cell-expressed *CRPs* are down-regulated in *ccg* and *cbp1* ovules. Relative expression level of *CRP* genes in *ccg* and *cbp1* ovules. Data are normalized to ***eIF1α***. (n=3, mean ± SD). Student's *t*-test, **p<0.01, *p<0.05.

Supplemental Figure 8



Supplemental Figure 8. *MYB98* and the DD-type genes downstream of *MYB98* are down-regulated in *ccg* ovules. Relative expression level (y-axis) of DD-type genes in *ccg* and wild-type ovules. Total RNA was isolated from mature ovules. Data were normalized to *eIF1α*. (n=3, means ± SD).

Supplemental Figure 9



Supplemental Figure 9. *CRP810.2* genes are expressed in the synergid cells. (A) *ProCRP810.2.1:GFP*; (B) *ProCRP810.2.2:GFP*; (C) *ProCRP810.2.3:CRP810.2.3-GFP*. fa: filiform apparatus. Scale bar: 20 μm.

Table S1. Genetic complementation data of *ccg* by expression of *CCG* under the *CBP1* promoter

Transgenic plants	The ovule abortion ratio of transgenic plants	Kan ^{R}/Kan ^{S} (T2)
1	13.4% (n= 216)	1.97 (n=214)
2	17% (n= 314)	2.37 (n=662)
3	15.8% (n=203)	1.68 (n=451)

For all the above scores, Students *t*-test, $p<0.01$.