

Supporting Information

Brzeska et al. 10.1073/pnas.1001576107

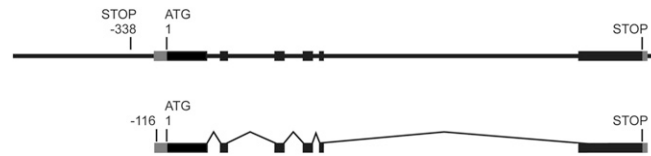


Fig. S1. A schematic representation of the longest *cbbp* cDNA recovered in the yeast one-hybrid screening (*Lower*) with corresponding genomic DNA (*Upper*). Exons are indicated as thick boxes. First ATG codon and nearest upstream STOP codon in the genomic DNA are indicated. There is no in-frame ATG codon in between. STOP codon present in the CBBP cDNA is also indicated. Putative 5' UTR and 3' UTR are indicated in gray.

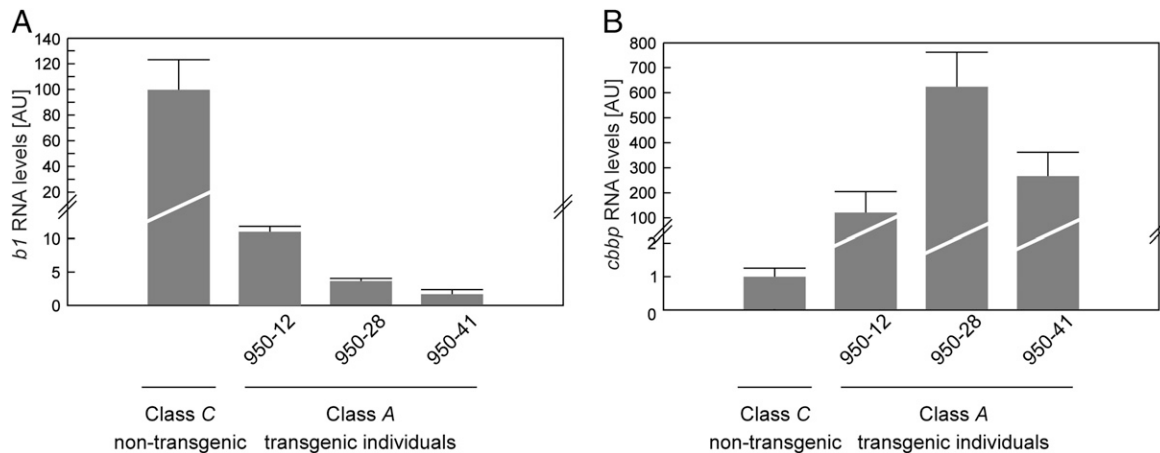


Fig. S2. (A) Expression of *b1* in transgenic *FLAG-cbbp* plants. *b1* transcript levels in three class A individuals and a nontransgenic class C sibling were analyzed by quantitative RT-PCR. Results were normalized to *actin*, and transcript levels are shown in arbitrary units (AU). Mean values from three technical replicates are shown with error bars indicating SD. (B) Total *cbbp* RNA levels in the same class A and class C nontransgenic plants as shown in A. Results were normalized to *actin*, and transcript levels are shown in AU. Mean values from three technical replicates are shown with error bars indicating SD.

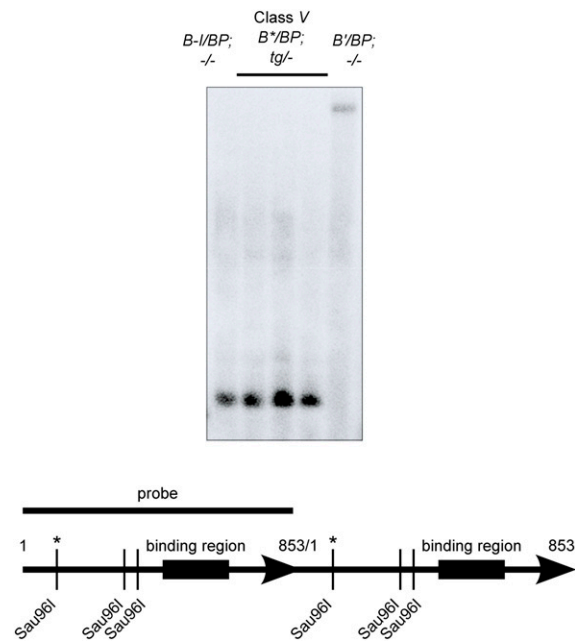


Fig. S3. DNA methylation analysis on Sau96-I site in *b1* repeats. DNA samples extracted from *B-I/B-Peru*, *B'/B-Peru* and three class *V* (*B*/B-P*; *tg*^{-/-}, see Fig. 4) plants that showed silencing were digested with Sau96-I DNA methylation sensitive enzyme. Digested DNA was analyzed by Southern blot with the probe corresponding to the full-length repeat unit. The probe position and Sau96-I sites relative to the repeats are diagramed below the blot. The Sau96-I sites that are differentially methylated in *B-I* and *B'* are indicated by asterisks. The two other Sau96-I sites are usually methylated in both epialleles. Only two repeat units are shown.

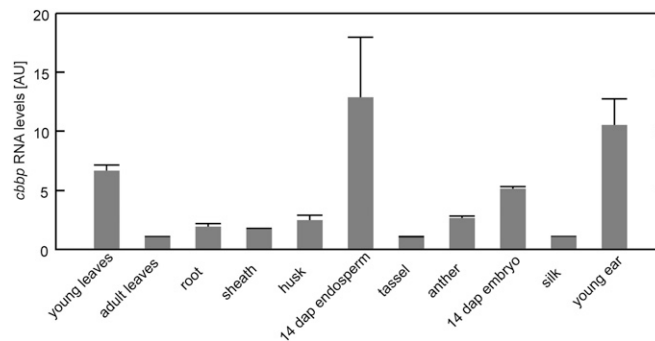


Fig. S4. RNA levels of *cbbp* in different tissues. Total RNA samples extracted from different tissues of the B73 genotype were analyzed by quantitative RT-PCR with primers specific to *cbbp*. Results were normalized to *actin*. RNA levels shown in arbitrary units (AU). Mean values from three technical replicates are shown with error bars indicating SD.

Table S1. FLAG-*cbbp* transgene correlates with *B-I* silencing

Family	Class A transgenic plants		Class C nontransgenic plants	
	<i>B-I</i> phenotype	<i>B*</i> and <i>B'</i> phenotype	<i>B-I</i> phenotype	<i>B'</i> phenotype
V950	0	22	26	0
V952	4	10	19	1
V954	0	3	3	0
V956	4	3	3	0
V1351	0	3	5	0
V1353	0	5	2	0
V1355	0	4	6	0
V1357	1	4	4	0
V1361	0	1	3	0

