Supporting Information

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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.

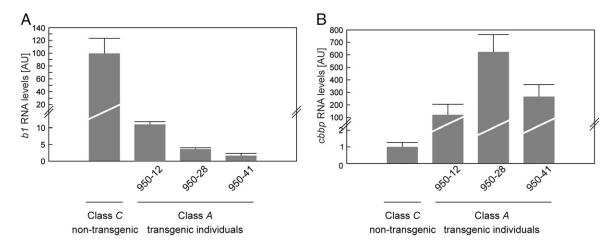


Fig. S2. (A) Expression of b1 in transgenic FLAG-cbbp plants. b1 transcript levels in three class A individuals and a nontransgenic class C sibling were analyzed by quantitative RT-PCR. Results were normalized to actin, and transcript levels are shown in arbitrary units (AU). Mean values from three technical 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.

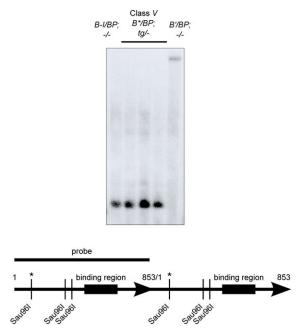


Fig. S3. DNA methylation analysis on Sau96-I site in b1 repeats. DNA samples extracted from B-I/B-Peru, B'/B-Peru and three class V (B*/B-P; tg/-, see Fig. 4) plants that showed silencing were digested with Sau96-I DNA methylation sensitive enzyme. Digested DNA was analyzed by Southern blot with the 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.

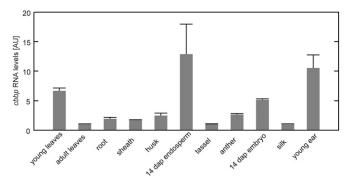


Fig. S4. RNA levels of *cbbp* in different tissues. Total RNA samples extracted from different tissues of the B73 genotype were analyzed by quantitative RT-PCR with primers specific to *cbbp*. Results were normalized to *actin*. RNA levels shown in arbitrary units (AU). Mean values from three technical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

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

		ss A nic plants	Class C nontransgenic plants		
Family	<i>B-I</i> phenotype	B* and B' 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	

Table S2. Heritability and paramutagenicity of B^* epiallele

Parent	Cla	ss I		Class II	Clas	s IV	Class	s VIII
Phenotype	B-I	В*	B-I	B* and B'	B-I	В′	B-I	В*
950–28	1	0	7	0	1	0	0	5
950-54	10	2	9	8	3	0	0	14
952–27	5	3	5	2	8	0	0	8

Table S3. Sequences of the PCR primers

Primer	Sequence		
P1	CCATGGGTTTGCTGCATCCTTGAC		
P2	ACCCTATCCACTGAAGGTAGTC		
P3	AGACTACCTTCAGTGGATAGGG		
P4	GTTGTGTACTGCAGTGTTAGGTAG		
P5	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGCTGAAGTTGGTCC		
P6	GGGGACCCATTTGTACAAGAAAGCTGGGTCCTATTCAGCTTTACGACGACGTT		
P7	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGATGGTGATGGCTGCAAAAC		
P8	GGGGACCCATTTGTACAAGAAAGCTGGGTCCTATTTACGGCCGAACGGGTTAC		
P9	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGTTGGCGTGATTCTGGACGG		
P10	GGGGACCCATTTGTACAAGAAAGCTGGGTCCTAAACCAGGGATTTCATTTTGC		
P11	TTACTGTGTGCTTTGCTT		
P12	AGCCTGACTTCTTGCATGTG		
P13	TTCACCGGAGGTTTAATTTGAAAGG		
P14	ATCTGCCTGAAGAATAACCAACAGT		
P15	CAATAGGCACCCTCCACTTCGTGTC		
P16	GATCGACGGTATGGGCCAGGGGAG		
P17	TCCGACAGGAAGAGGAGGA		
P18	CCAGAAGCAAAGCACACAGT		
P19	GATGATGCGCCAAGAGCTG		
P20	GCCTCATCACCTACGTAGGCAT		
P21	ATGGCGCTCTCAGCTTGCCC		
P22	GGACCAGAAGAGGGAATAGC		
P23	TGAGATTTGAAATGATGACT		
P24	GAGATGCAACAATATCCATT		