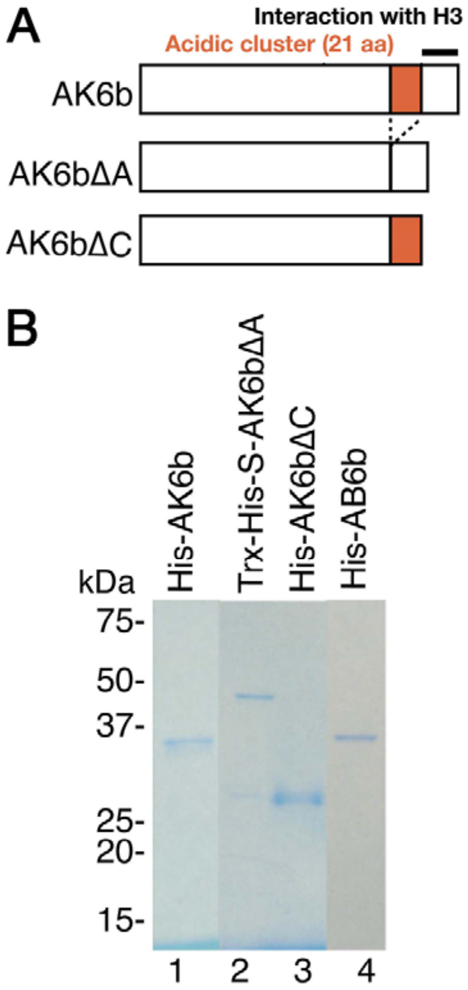


Supplemental Figure 1.
(A) Schematic representation of the structural organization of the AK6b protein [208 amino-acid (aa) residues] derived from *A. tumefaciens* AKE10 and of its mutant derivatives. The acidic region (from aa164 through 184) is shown in orange. The site of interaction with histone H3 is indicated by solid line.
(B) Characterization of proteins used in the callus-formation assay and the protein-binding assay. Recombinant proteins, as indicated, were produced in *Escherichia coli*, purified with cobalt beads, fractionated by SDS-PAGE (10.5% acrylamide), and visualized by staining with Coomassie Brilliant Blue.

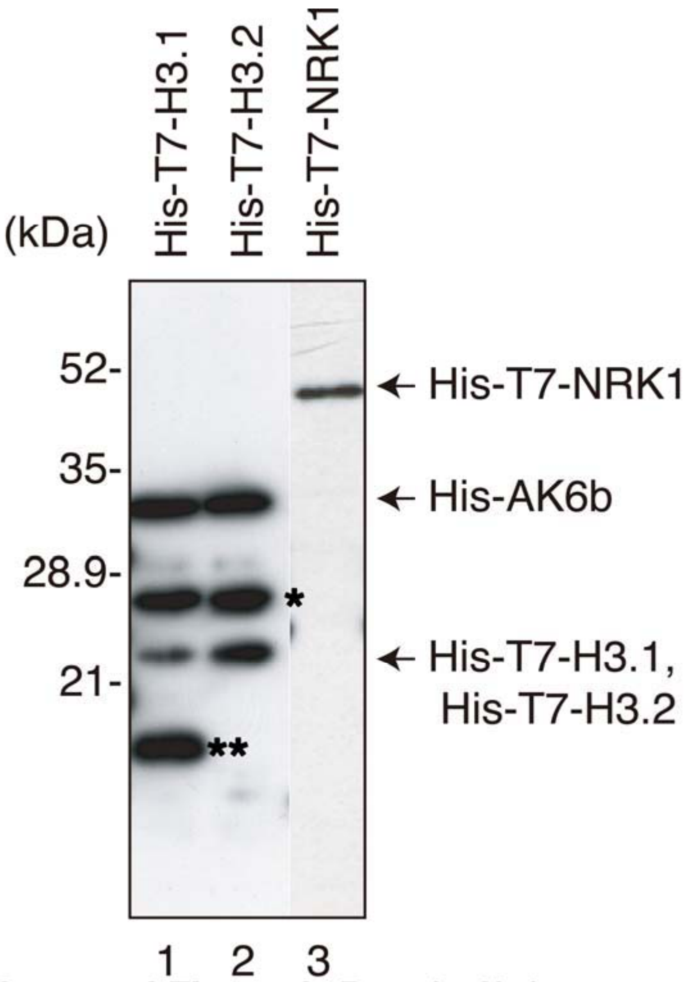
Clone 1 (H3.1)

```
                     20                  40                  60
            .         .         .         .         .         .
(M)ARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRFRPGTVALREIRKYQKSTEL
                                 -         -
                     80                  100                 120
            .         .         .         .         .         .
   LIRKLPFQRLVREIAQDFKTDLRFQSSAVAALQEAAEAYLVGLFEDTNLCAIHAKRVTIM
                             -  -

            .
   PKDIQLARRIRGERA
```

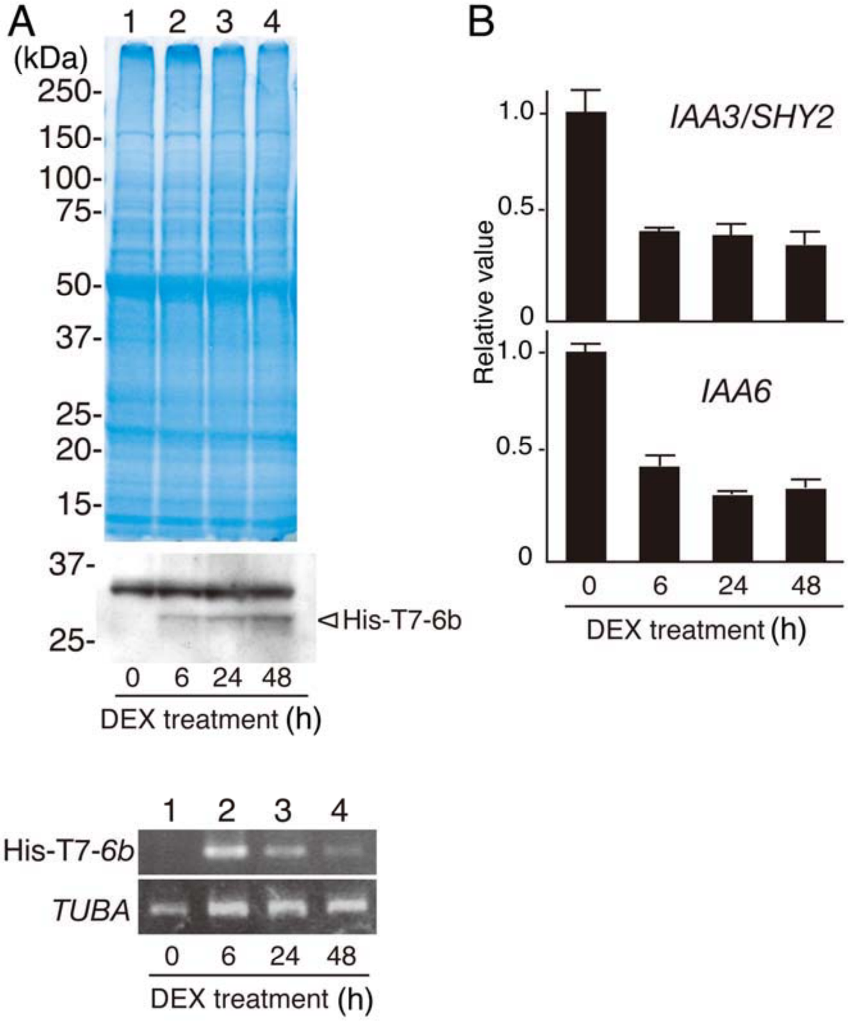
Clone 2 (H3.2)

```
                     20                  40                  60
            .         .         .         .         .         .
(M)ARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTEL
                                 -         -
                     80                  100                 120
            .         .         .         .         .         .
   LIRKLPFQRLVREIAQDFKTDLRFQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTIM
                             -  -

            .
   PKDIQLARRIRGERA
```

Supplemental Figure 2. Amino acid sequences deduced from tobacco cDNAs that were identified by the yeast two-hybrid screening. Amino acid residues that are underlined differ between the two sequences.



Supplemental Figure 3. Protein 6b interacts with histones H3.1 and H3.2 of *Arabidopsis* in vitro. His-T7-epitope tagged histone H3.1 (lane 1), histone H3.2 (lane 2) and NRK1 MAP kinase (lane 3, used as a negative control; Soyano et al., 2003) were incubated with His-epitope tagged AK6b. Complexes were immunoprecipitated with T7-specific antibodies. Proteins in recovered complexes were subjected to SDS-PAGE (10.5% acrylamide) and western blotting analysis with His-specific antibodies. Arrows indicate positions of the proteins. The proteins indicated by an asterisk and double asterisks might represent degradation products of the recombinant His-AK6b and histone proteins, respectively.



Supplemental Figure 4. Effects of the synthesis of His-T7-6b on levels of *IAA3/SHY2* and *IAA6* transcripts in *Arabidopsis* plants.

(A) DEX-inducible accumulation of His-T7-6b protein. Transgenic *Arabidopsis* plantlets (14 DAG), which carried a DEX-inducible His-T7-*6b* construct, were cultured in liquid MS medium that contained 10 μM DEX for 0, 6, 24 and 48 h with rotation at 120 r. p. m. in darkness. The plantlets were collected and total proteins and RNA were prepared. Proteins were fractioned by SDS-PAGE (10-20% acrylamide). Total proteins and His-T7-6b protein were visualized by staining with Coomassie Brilliant Blue (upper) and western blotting with T7-specific antibodies (middle), respectively. RNAs for His-T7-6b and α tubulin (*TUBA*) were analyzed by RT-PCR (bottom).

(B) Accumulation of transcripts of the *IAA3/SHY2* and *IAA6* genes after induction of the synthesis of His-T7-6b protein. Levels of transcripts of these genes were measured by real-time PCR. Each level was normalized by reference to that of the transcript of the *ACTIN2* gene. Relative values were calculated by dividing the values from plants incubated for indicated times by the values from samples analyzed at time 0.

Supplemental Table S1: Clones of tobacco cDNAs that were isolated by the yeast-two hybrid screening.

Clone	Insert size	Accession number	Annotation in database	In this study
Clone 1	467 bp	AB331236	Histone H3 (identical to the amino acid sequence of H3.1 of *Arabidopsis*: AT5G65360)	H3.1
Clone 2	570 bp	TC6946[1)]	Histone H3 (identical to the amino acid sequence of H3.2 of *Arabidopsis*: AT4G40030)	H3.2
Clone 3	686 bp	EB681212	Unknown	H2B-histone-fold-like
Clone 4	385 bp	EB680442	Unknown	Unknown

1) The accession number and annotation of TC6946 refer to a database of the Gene Index Project (http://compbio.dfci.harvard.edu/tgi/cgi-bin/tgi/gimain.pl?gudb=tobacco).