

Supporting Information

Fu et al. 10.1073/pnas.1303944110



Fig. S1. Phenotype of Duplication 3a (Dp3a) kernels. A mature kernel containing the Dp3a chromosome with the dominant alleles of *A1* and *Sh2* in a background of *anthocyaninless1 (a1)* and *shrunken2 (sh2)*, which are revealed by mosaic loss of Dp3a. The *A1* allele produces purple anthocyanin pigment in the aleurone layer, and the *Sh2* allele produces normal starch in the endosperm. When the Dp3a is lost during development of the kernel, sectors are produced that do not have normal starch production and are lacking pigment in the corresponding aleurone. These indented regions are characteristic of mutant starch production and also have no anthocyanin pigment.

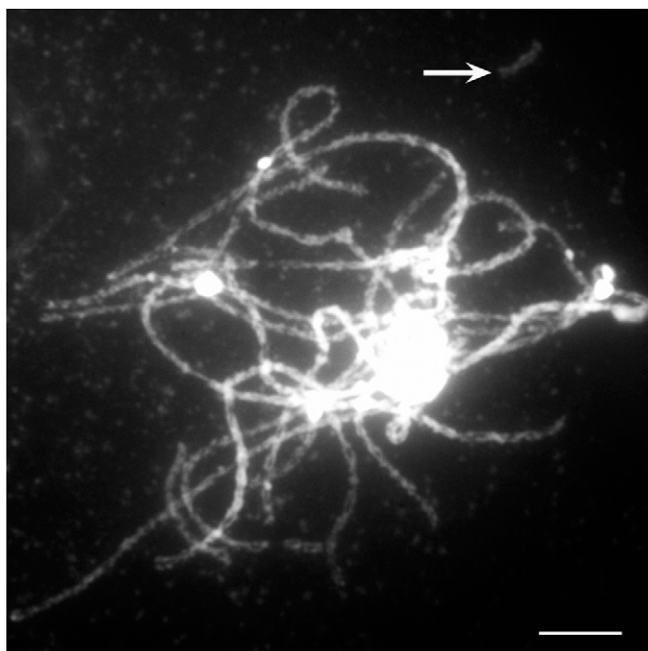


Fig. S2. Duplication 3a (Dp3a) in meiotic pachynema. The DAPI-stained pachytene chromosome image was converted to gray value. Arrow indicates that the Dp3a chromosome did not pair with chromosome 3.

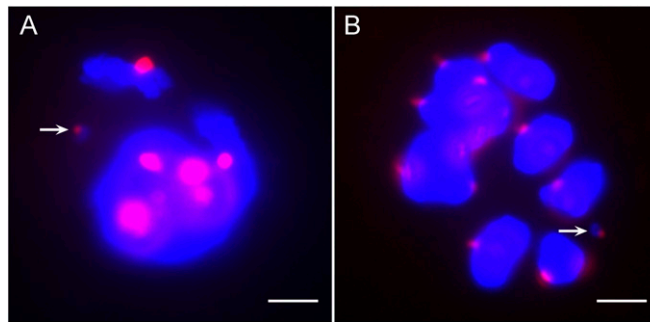


Fig. 53. Immunostaining of Dp3a for CENP-C, a foundational kinetochore protein, at different stages of meiosis. Immunolocalization analysis of CENP-C in meiosis of plants containing one Dp3a chromosome. (A) Diplotene. (B) Metaphase I. Red represents the signal of CENP-C, which is a marker for centromere activity. DAPI-stained chromosomes are blue. The arrow denotes the Dp3a chromosome with one site of CENP-C binding. (Scale bars, 10 μm .)

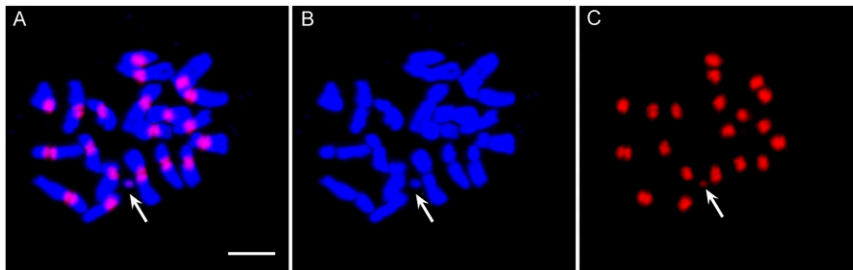


Fig. 54. Phosphorylation of H3-ser-10 on the Dp3a somatic chromosome. Immunofluorescence assay using anti-H3S10ph (red) antibody on mitotic metaphase chromosomes. (A) Merged images. (B) DAPI channel. (C) The red channel is the H3S10 antibody. Arrows indicate the Dp3a chromosome. (Scale bar, 10 μm .)

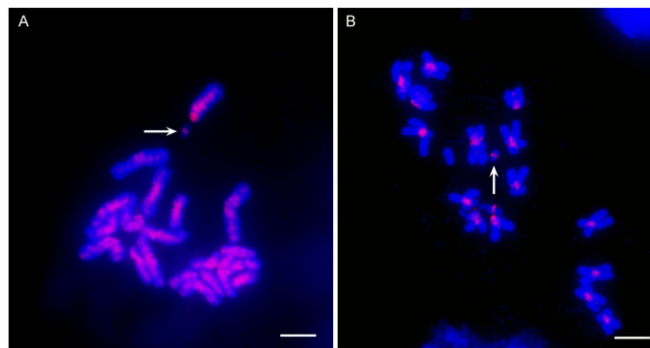


Fig. 55. Sites of H3T3 phosphorylation on the Dp3a somatic chromosome. H3T3 phosphorylation antibody localizes in the inner centromeric region during metaphase. (A) Early metaphase. (B) Metaphase. Arrows indicate the Dp3a chromosome. The red channel is H3T3ph antibody; DAPI-stained chromosomes are blue. (Scale bars, 10 μm .)

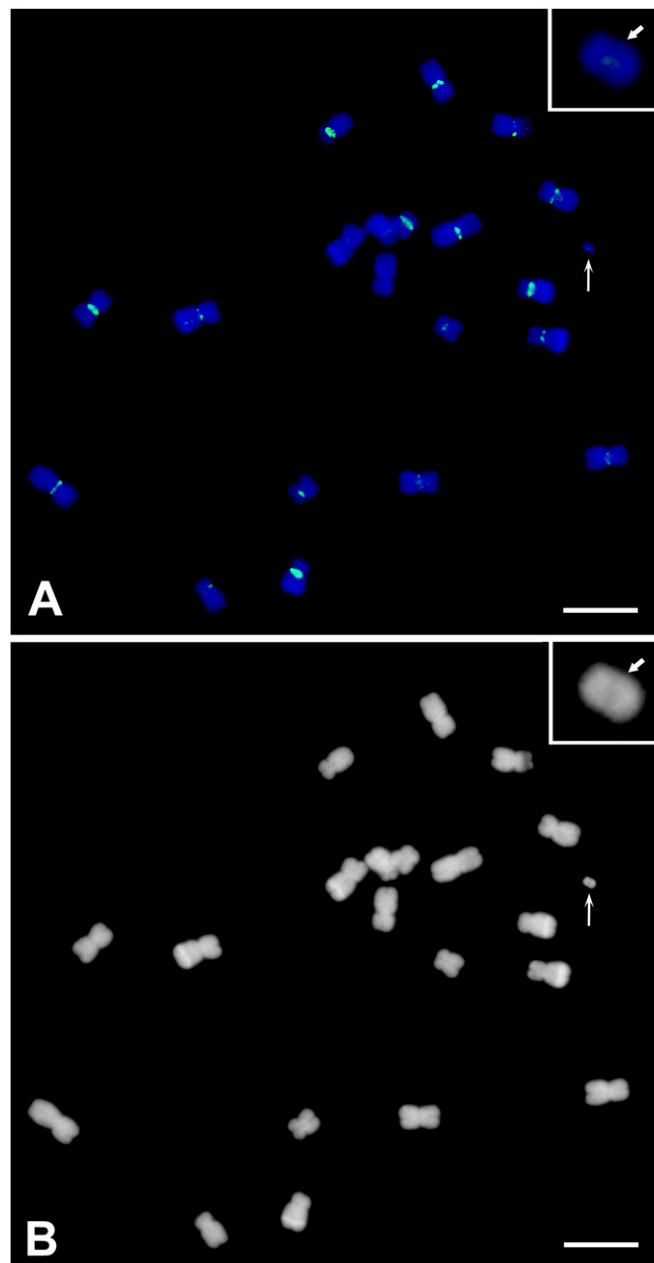


Fig. S6. Confirmation of ChIP-DNA location to centromeric regions. (A) FISH analysis using DNA from ChIP as a probe to detect the location of the ChIP-DNA sequences. The green signals indicate that the ChIP-DNA sequences are located in centromere regions. DAPI-stained chromosomes are blue. Arrow designates Dp3a. *Inset* shows an enlarged image of Dp3a. (B) Gray-value image of A. (Scale bar, 10 μm .)

Table S1. Mapping results from ChIP-Seq

Sequence Reads	Control, pair-end 100 nt		Dp3a, pair-end 100 nt	
	Reads	Percentage	Reads	Percentage
Total reads	51,453,782	100	30,902,058	100
Total mapped	39,326,480	76.43	23,364,933	75.61
Uniquely and nonredundantly mapped	33,992,185	66.06	19,700,469	63.75

Table S2. Genes located in the 350-kb region of Dp3a

Fig. 4B

Gene Number designation	Name	Protein	Nucleotide position	CENH3 above control
1	GRMZM2G045565	Protein of unknown function DUF538 family protein	218,891,348–218,892,450	–
2	GRMZM2G045318	Hypothetical protein	218,893,373–218,896,627	–
3	GRMZM5G815568	Hypothetical protein	218,893,525–218,896,628	–
4	GRMZM2G045275	Putative early flowering 3-like	218,897,671–218,903,527	–
5	GRMZM2G045268	Like ubiquinol-cytochrome c reductase complex	218,910,518–218,916,860	–
6	AC207396.3_FG004	Hypothetical protein	218,923,790–218,924,035	+
7	AC207396.3_FG003	Hypothetical protein	218,926,785–218,927,030	+
8	AC207396.3_FG002	Hypothetical protein	218,927,716–218,928,003	+
9	AC207396.3_FG001	Hypothetical protein	218,928,547–218,928,792	–
10	GRMZM2G125571	Uncharacterized protein LOC100501661 precursor	219,063,340–219,064,565	+
11	GRMZM2G342653	Uncharacterized protein LOC100272281	219,075,234–219,076,412	+
12	AC209738.3_FG002	Uncharacterized protein LOC100272281	219,075,562–219,076,050	+
13	AC209738.3_FG003	Tetratricopeptide repeat domain 4	219,097,302–219,099,416	+
14	GRMZM2G342693	Hypothetical protein	219,099,193–219,101,141	+
15	GRMZM5G882921	Hypothetical protein	219,099,460–219,099,789	+
16	AC209738.3_FG005	<i>Zea mays</i> RNA-binding protein (LOC100285689)	219,104,042–219,104,893	–
17	GRMZM2G342711	RNA-binding protein	219,104,793–219,106,389	–
18	GRMZM2G342719	Cell division protein ftsZ	219,107,045–219,108,925	–
19	GRMZM2G508066	Hypothetical protein	219,111,436–219,111,834	–
20	GRMZM2G040905	Uncharacterized protein LOC100277351	219,117,645–219,126,756	+
21	GRMZM2G702260	<i>Zea mays</i> B73 monoterpene synthase (tps26) gene	219,164,362–219,164,942	+
22	GRMZM2G081816	bHLH transcription-like	219,181,998–219,184,295	–

+, binding with CENH3; –, no binding with CENH3.