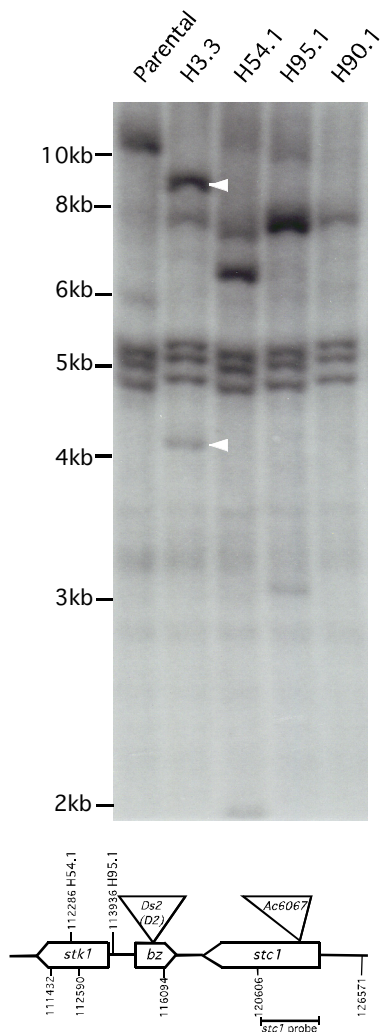


**Supplemental Figure 1.** DNA gel blot analysis of *bz-s* derivatives (PstI digest; *bz* probe).

PstI digests of genomic DNAs from *bz-m2(D2) Ac6067* and *bz-s* derivatives H1.1, H1.4, H1.5, H3.3, H54.1, H56.1, H90.1 and H95.1 were hybridized to a *bz* probe. The positions of the *bz* fragment used as probe and the location of the PstI sites in the 226-kb McC *bz* haplotype contig (GenBank AF391808) are shown below the map; the asterisks represent PstI sites known to be methylated in genomic DNA. The location of the inferred *e-f* transposition target site in each *bz-s* derivative is shown above the map.

The following bands are detected by the *bz* probe. Parental: 7.7 and 4.0 kb, *Ds* occupied and somatic xis sites respectively; H3.3, MTn transposition to unmapped 9S location: 5.6 kb, MTn xis site; H54.1, MTn transposition to *stk1* exon 3: 5.0 and 1.3 kb (not shown), transposed MTn with *Ds* (germinal) and without *Ds* (somatic xis), respectively, and 5.6 kb, MTn xis site; H95.1, MTn transposition in reverse orientation to *stk1* 5' UTR: 8.5 and 4.8 kb, transposed MTn with *Ds* (germinal) and without *Ds* (somatic xis), respectively (the MTn xis site and the transposed MTn are in the same PstI fragment); H90.1, MTn xis: 5.6 kb, MTn xis site; H1.1, 4.8-kb adjacent inversion: 9.2 and 5.5 kb, inversion with *Ds* (germinal) and without *Ds* (somatic xis), respectively; H1.4, 106-kb adjacent inversion: 7.7 and 4.0 kb, inversion with *Ds* (germinal) and without *Ds* (somatic xis), respectively; H56.2, 0.2-kb adjacent inversion on the *Ac* side: 12.7 kb, inversion with *Ac* and *Ds*; H1.5, ITS rearrangement: 9.4 kb, rearrangement with *Ds* and 3.1 kb, rearranged *stc1* fragment from the middle of ITS.



**Supplemental Figure 2.** DNA gel blot analysis of *bz-s* derivatives (*SacI* digest; *stc1* probe).

*SacI* digests of genomic DNAs from *bz-m2(D2) Ac6067* and *bz-s* derivatives H3.3, H54.1, H95.1 and H90.1, which carry transposed MTNs, were hybridized to an *stc1* probe. The position of the *stc1* fragment used as probe and the location of the *SacI* sites in the 226-kb *McC bz* haplotype contig (GenBank AF391808) are shown below the map.

The following bands are detected by the *stc1* probe. Parental: 10.5 and 6 kb, *Ac* occupied and somatic *xis* sites respectively; H3.3, MTn transposition to unmapped 9S location: 9.0 and 4.1 kb (white arrowheads), transposed MTn with *Ac* (germinal) and without *Ac* (somatic *xis*), respectively, and 7.5 kb, MTn *xis* site; H54.1, MTn transposition to *stc1* exon 3: 6.6 and 2 kb, transposed MTn with *Ac* (germinal) and without *Ac* (somatic *xis*), respectively, and 7.5 kb, MTn *xis* site; H95.1, MTn transposition in reverse orientation to *stc1* 5' UTR: 7.6 and 3 kb transposed MTn with *Ac* (germinal) and without *Ac* (somatic *xis*), respectively, and 10.1 kb, MTn *xis* site with *Ds*; H90.1 (MTn *xis*): 7.5 kb, MTn *xis* site.

**Supplemental Table 1.** Sequence of excision footprints and new TE junctions in bz-s derivatives

Class	Category	bz-s derivative	Figure 2	<i>xis</i> footprint	New <i>Ds</i> end junction <sup>1</sup>	New <i>Ac</i> end junction <sup>2</sup>
4	<i>Ds</i> 5' adjacent deletion	H1.6	B		GCCGGGCACGGGCTC-- CAGGGATGAAAGTAG	
5	<i>Ds</i> 3' adjacent del + <i>Ac</i>	H3.7	C		TTCATCCCTA-- CGCGTGTCTTGGTTAC	
		H3.8			TTCATCCCTA-- CCCTTGTTGCGGCCAT	
		H3.10			TTCATCCCTA-- GTATTAACAACATATGC	
6	<i>Ds</i> 3' adjacent del - <i>Ac</i>	H68.2			TTTTTCATCCCTA-- CTACTAGCGGGGCGGC	
		H98.1			TTTTTCATCCCTA-- GGCGGCCCTGCTGGTG	
7	<i>Ac</i> 5' adjacent deletion	H62.1	D			GGAACCTGCGCTTCGT-- CAGGGATGAAAGT
8	Inversion, ITS deletion	H1.1	E		AAACTCATGCTAGAAAC-- TAGGGATGAAAA	GGTGTTGTTTCTAG-- CAGGGATGAAAGT
		H1.4	F		GTGGTGCTGGCGAT-- TAGGGATGAAAA	CATGCCAATCGCCAG-- CAGGGATGAAAGT
		H56.1	G		TTTTTCATCCCTA-- AGCACGGTCCAGCGG	TACTTTCATCCCTG-- ACCGTGCTGCTAGC
		H56.2			TTTTTCATCCCTA-- AGCACGGTCCAGCGG	TACTTTCATCCCTG-- ACCGTGCTGCTAGC
9	MTn transposition	H3.3		CACCGCATGGGGCAG-- TCTTTCGCCTGCC	GGATGGGTATCATGAGTC-- CAGGGATGAAAG	
		H54.1	H	CACCGCATGGGGCAG-- TCTTTCGCCTGCC	ACCGGGCCTCGTGGG-- CAGGGATGAAAGTAG	CCGTTTTTCATCCCTA-- CTCGTGGGACATGCCG
		H95.1			CACCGCATGGGGCAG-- TCTTTCGCCTGCC	CTACTTTCATCCCTG-- GGCACGCCGGGAGGG
10	MTn excision	H34.1		CACCGCATGGGGCA-- CTCTTTCGCCTGCC		
		H40.1		CACCGCATGGGGCA-- CTCTTTCGCCTGCC		
		H70.1		CACCGCATGGGGCAC-- CTTTCGCCTGCC		
		H77.3		CACCGCATGGGCAG-- TCTTTCGCCTGCC		
		H85.1		CACCGCATGGGGCACT-- TCTTTCGCCTGCC		
		H90.1	I	CACCGCATGGGGCA-- AGTCTTTCGCCTGCC		
		H90.2			CACCGCATGGGGCA-- AGTCTTTCGCCTGCC	
11	ITS rearrangement	H57.3		CGTCCTTTTC-- GGGGCAGTGCCTC	GACCGTTTTTCATCCCTA-- ACCGACGCCACCCGGC	CCTCCAGCACCGACGC-- CAGGGATGAAAGT
		H72.3		CGTCCTTTTC-- AGGGCAGTGCCTC	GACCGTTTTTCATCCCTA-- TGCGCCGGACGGAGG	GGGCGCACGTGCGCCGG-- CAGGGATGAAAGT
		H75.1		CGTCCTTTTC-- GGGGCAGTGCCTC	GACCGTTTTTCATCCCTA-- ATGGATGGTACATCGAG	CTCGACAGGCATGGATGG-- CAGGGATGAAAGT
		H87.1		CGTCCTTTTC-- GGGGCAGTGCCTC	GACCGTTTTTCATCCCTA-- GCAAGGGCCAAGGAGC	CGGATGAGGGCAAGGGC-- CAGGGATGAAAGT
		H1.5	J	GGAGGCACTGCC-- CGAAAGAGGACGATG	TTTTTCATCCCTA-- CTTGTCACCTCTTGT	TGGCCTTGTCACCT-- CAGGGATGAAAGT
14	3-ended <i>Ds</i> (two 3' ends)	H81.1			GTTTTTCATCCCTA-- GTAGCAAGTGGCTCCTCT	
					<sup>1</sup> <i>Ds</i> 5' end sequence in red; 3' end in blue	<sup>2</sup> <i>Ac</i> 5' end sequence in red; 3' end in blue
					<b>TSD</b> in bold	<b>TSD</b> in bold

**Supplemental Table 2.** BFB activity of *bz-s* derivatives from *bz-m2(D2) Ac6067*

<b>Class</b>	<b>Category</b>	<b>bz-s derivative</b>	<b># BFB kernels</b>	<b>Adjusted Total kernels<sup>1</sup></b>	<b>BFB Fraction</b>
4	<i>Ds</i> 5' adjacent deletion	H3.17			NT
		H95.2	47	197	0.238
		H110.1			NT
5	<i>Ds</i> 3' adjacent del. + <i>Ac</i>	H3.7	355	414	0.857
		H3.8	373	420	0.888
		H3.10	150	197	0.760
		H95.3	135	194	0.695
		H45.1			NT
		H69.1	150	158	0.947
		H73.1	123	135	0.910
6	<i>Ds</i> 3' adjacent del. - <i>Ac</i>	H57.2	0	190	0.000
		H59.1	0	164	0.000
		H74.3	0	180	0.000
		H64.1	1	201	0.005
		H64.3	0	169	0.000
		H66.1	0	106	0.000
		H68.2			NT
		H77.6	2	148	0.014
		H85.3	1	148	0.007
		H98.1	0	158	0.000
7	<i>Ac</i> 5' adjacent deletion	H3.1			NT
		H3.11			NT
		H34.2			NT
		H34.3	0	180	0.000
		H34.4	2	158	0.013
		H39.1	0	4	0.000
		H43.1	3	201	0.015
		H49.3	4	190	0.021
		H57.4			NT
		H58.1			NT
		H98.2	0	127	0.000
		H81.2			NT
		H86.1	0	158	0.000
		H60.1	0	169	0.000
		H60.2	2	137	0.015
		H61.2	9	116	0.077
		H62.1	10	185	0.054
H64.2	1	127	0.008		
H83.1	2	137	0.015		
H93.1			NT		
H96.1	3	201	0.015		
H99.1	1	275	0.004		
H105.1	0	53	0.000		
H112.1	3	127	0.024		
H114.1	2	153	0.013		
H85.2	1	169	0.006		
8	Inversion, ITS deletion	H3.2	0	330	0.000
		H3.4	0	300	0.000
		H3.5	376	400	0.940
		H3.6	120	206	0.583

1 Adjusted for reduced transmission of *sh-bz-X2* homolog

**Supplemental Table 2.** BFB activity of *bz-s* derivatives from *bz-m2(D2) Ac6067*

<b>Class</b>	<b>Category</b>	<b>bz-s derivative</b>	<b># BFB kernels</b>	<b>Adjusted Total kernels<sup>1</sup></b>	<b>BFB Fraction</b>
		H3.9	0	360	0.000
		H3.12	90	340	0.265
		H3.13	26	280	0.093
		H40.2	0	116	0.000
		H42.1	0	106	0.000
		H43.2	0	106	0.000
		H45.2	1	121	0.008
		H48.1	0	232	0.000
		H48.2	0	158	0.000
		H48.3			NT
		H49.1			NT
		H49.2	171	197	0.866
		H56.1	194	200	0.972
		H56.2	134	143	0.940
		H56.3			NT
		H58.2			NT
		H61.1	11	169	0.065
		H61.3	1	158	0.006
		H63.1	42	127	0.331
		H63.2			NT
		H68.1	0	53	0.000
		H69.2	64	102	0.625
		H72.1			NT
		H72.2	0	180	0.000
		H74.1	130	148	0.879
		H74.2	147	154	0.953
		H77.1	0	127	0.000
		H77.5	2	253	0.008
		H84.1	198	211	0.938
		H92.1	173	199	0.871
		H101.1	82	87	0.947
		H102.1	174	184	0.947
		H104.1	4	70	0.057
		H107.1	138	162	0.854
		H107.2	0	8	0.000
		H107.3	117	148	0.791
		H110.2	4	232	0.017
		H112.2	111	133	0.834
		H114.2	2	148	0.014
9	MTn transposition	H3.3	387	432	0.896
		H54.1	87	111	0.785
		H95.1	134	163	0.824
10	MTn excision	H34.1	0	222	0.000
		H40.1	0	127	0.000
		H70.1			NT
		H77.3	3	201	0.015
		H85.1	0	158	0.000
		H90.1	0	137	0.000
		H90.2	0	106	0.000

1 Adjusted for reduced transmission of *sh-bz-X2* homolog

**Supplemental Table 2.** BFB activity of *bz-s* derivatives from *bz-m2(D2) Ac6067*

<b>Class</b>	<b>Category</b>	<b>bz-s derivative</b>	<b># BFB kernels</b>	<b>Adjusted Total kernels<sup>1</sup></b>	<b>BFB Fraction</b>
11	ITS rearrangement	H57.3	106	145	0.733
		H72.3	85	106	0.805
		H75.1	64	206	0.311
		H87.1	215	238	0.905
12	Tn recombination to <i>Ac</i>	H54.2	10	211	0.047
		H77.2			NT
		H77.4	0	48	0.000
		H81.3	10	162	0.062
		H82.1	4	148	0.027
13	Tn recombination to <i>Ds</i>	H57.1	0	158	0.000
		H80.1	0	169	0.000
		H77.7			NT
		H112.3	1	264	0.004
		H112.4	0	211	0.000
14	3-ended <i>Ds</i> (two 3' ends)	H81.1	0	148	0.000

<sup>1</sup> Adjusted for reduced transmission of *sh-bz-X2* homolog

**Supplemental Table 3.** Primers for dicentric bridge PCR amplification

	Nested PCR primers		1st round PCR primers	
Fixed	bz-a	ATTGCGCGCGGGTTTGATGA	bz-y3	GCGACCAGGGTGCGTTGGATT
	Ac-3	GTGTGCTCCAGATTTATATGGA		
Variable	mkk-C	AGCGAATCTGGAATGCGAATGGA	mkk-A	AGCGGCAGTGGGGAGGAGAAGAAT
	mkk-D	AATCCGACCTGCCTTTCTTA	mkk-C	AGCGAATCTGGAATGCGAATGGA
	stk-P	AAGAGGGGATGGCTGAAGGATGAT	stk-O	TTGGCTGCGGGGACACATTCTCGT
	stk-Q	CTTCATGTCCACACCGCCGTC AAC	stk-P	AAGAGGGGATGGCTGAAGGATGAT
	stk-4	AACAGGTACACGGCAATGGCAGAG	Del-7	ACCCGATGGAGGAGATTTGATTAG
	stk-C	ACTCCGGGTCGATGTAGCAGA	Ins1	CGGGCACGGCCGGGTCCAG
	stk-H	CGTCGGGCCGGAGCACCTTGAT	stk-G	GCAGCTCAGCACCTCCACCTC
	stkF1	GGCGGCCGGTGCTGCTGACAAA	stkF-2	GCCGAGGGAGCAGAAGGAAGAGC
	stkP-1	GCGGCGTACGTGATTGCTCCTCCTA	Del-1	TGCGGGTCCGTCCGGCTGCTTGAA
	bz-N	CACGCTCTCGTTCCTCTCCA	bz-y5	GGGTGTGTCCAGAATGTACCTA
	bz-y3	GCGACCAGGGTGCGTTGGATT	bz-N	CACGCTCTCGTTCCTCTCCA
	bz-a	ATTGCGCGCGGGTTTGATGA	bz-y3	GCGACCAGGGTGCGTTGGATT
	bz-y10	TGCAGGAAGAACTTCGACA	by-y15	GCGAGGACTCGTGGCCGCA
	bz-y14	GCAATTTGTGTACGCGTCA	stc-R1	CACAACCATGCATGGGGCATCACAAAC
	stc1-proR2	CCTTCTGAAGGGACGACGTGG	stc1-a	AGCGCAAGATTAACGAGTCCAGA
	LhAcF1	CCTGCTGGTGCAACCAAT	LHAcF2	ACGGTGGCACTAGCAGAGA